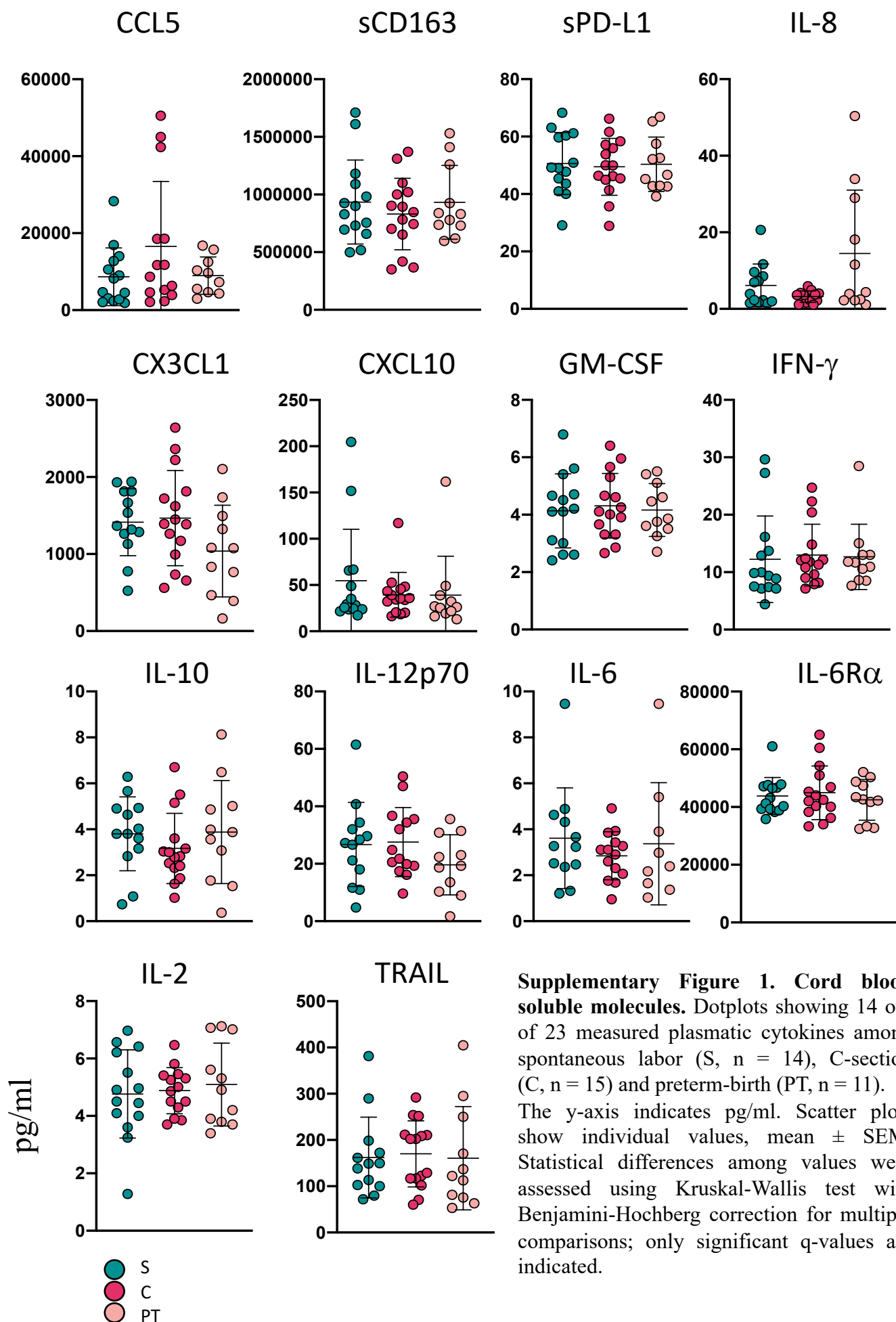


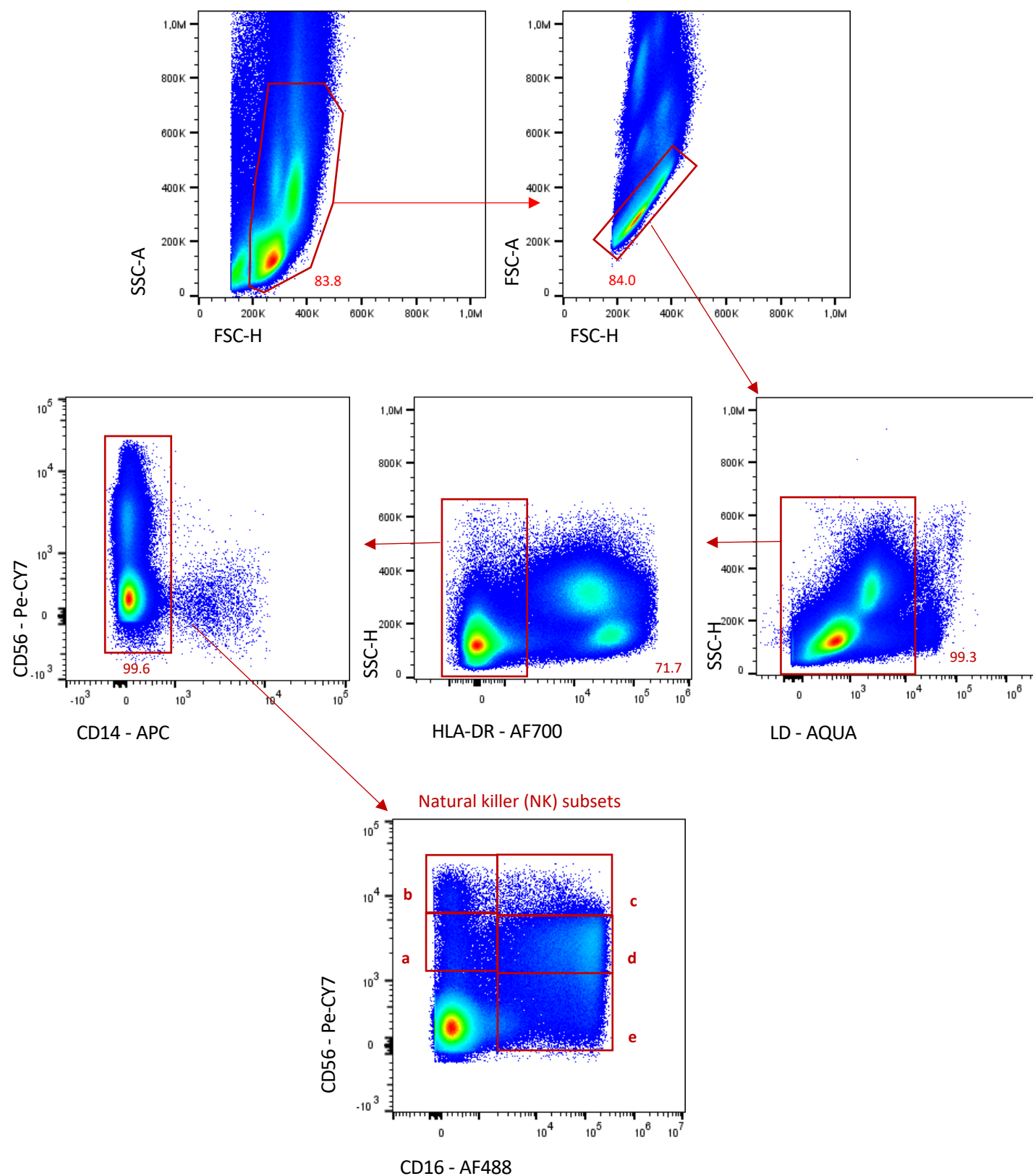
Specificity	Dye	Clone	Manufacturer	Cat.	Lot	Dil. (μ l)
CD14	APC	63D3	BioLegend	367118	B275678	0.3
CD16	AF488	3G8	BioLegend	302019	B216866	0.3
HLA-DR	AF700	LN3	BioLegend	327014	B275239	0.3
PD-L1	PE	MIH1	Thermo Fisher	12-5983-41	2017815	5.0
CCR2	BV605	K036C2	BioLegend	357214	B253733	0.3
CCR5	BV421	J418F1	BioLegend	359118	B249331	0.3
CD56	PE-CY7	MEM-188	BioLegend	304628	B283573	1.25
CX3CR1	APC-CY7	2A9-1	BioLegend	341616	B334395	1.25
CD13	PerCP/Cyanine5.5	WM15	BioLegend	301714	B313626	2.50
LIVE/DEAD	AQUA		Thermo Fisher	L34957A	2268305	1.25
True-Stain Monocyte Blocker			BioLegend	426102	B343281	5.0

Cat, category number; Dil, dilution; Lot, lot number.

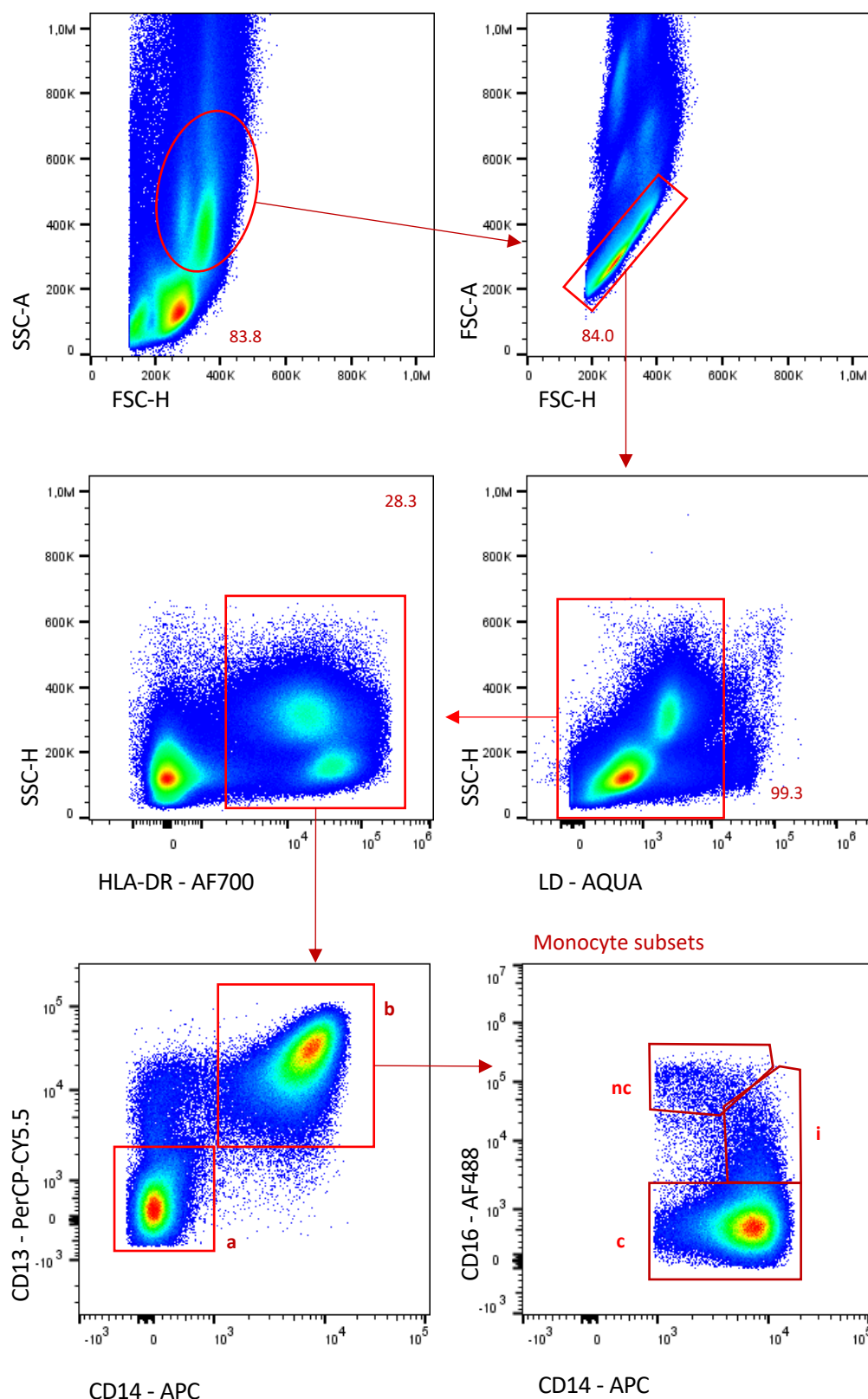
Supplementary table 1. List of monoclonal antibodies used in the monocyte flow cytometry panel.



Supplementary Figure 1. Cord blood soluble molecules. Dotplots showing 14 out of 23 measured plasmatic cytokines among spontaneous labor (S, n = 14), C-section (C, n = 15) and preterm-birth (PT, n = 11). The y-axis indicates pg/ml. Scatter plots show individual values, mean $\pm$ SEM. Statistical differences among values were assessed using Kruskal-Wallis test with Benjamini-Hochberg correction for multiple comparisons; only significant q-values are indicated.

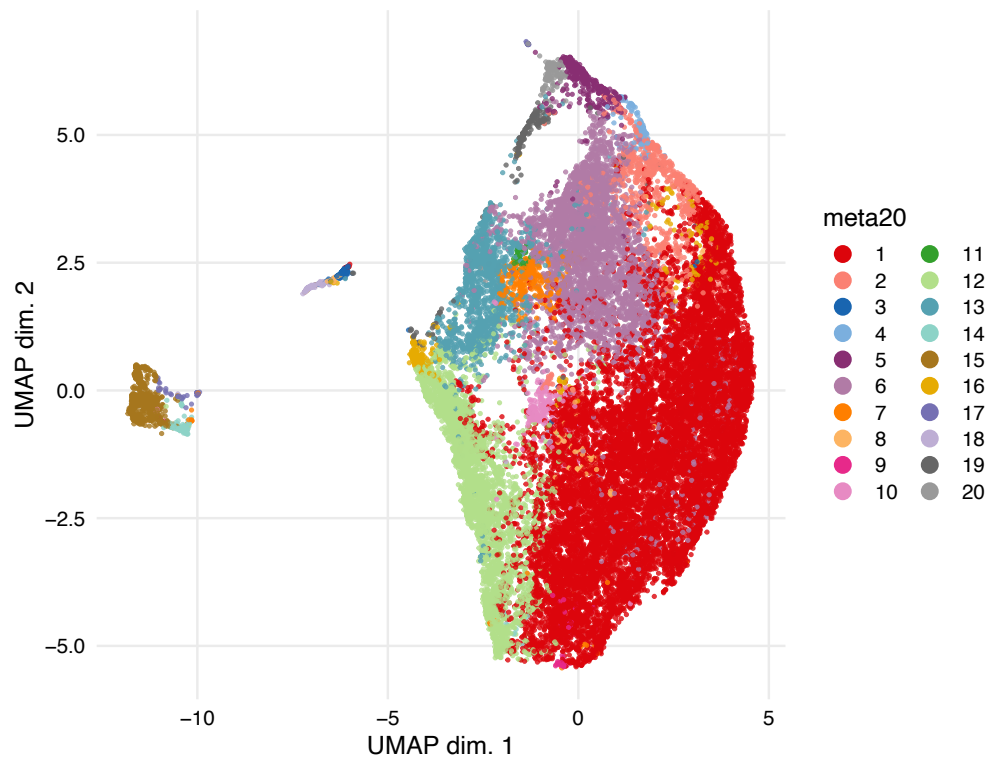


Supplementary Figure 2. Natural killer (NK) subsets in cord blood. Gating strategy used to identify NK subsets based on the expression of CD16 and CD56. PBMCs were gated according to physical parameters and aggregates were removed from the analysis by using FSC-A vs FSC-H gate. Living (Live/Dead, LD⁻) cells and HLA-DR⁻ cells were identified. Then, a gate was set on CD14⁻CD56⁺ cells and CD16 expression versus CD56 expression is shown. From left to right is possible to identify five different NK subsets: (a) CD56⁺CD16⁻, (b) CD56⁺⁺CD16⁻, (c) CD56⁺⁺CD16^{+/-}, (d) CD56^{+/+}CD16⁺, (e) CD56⁻CD16⁺.

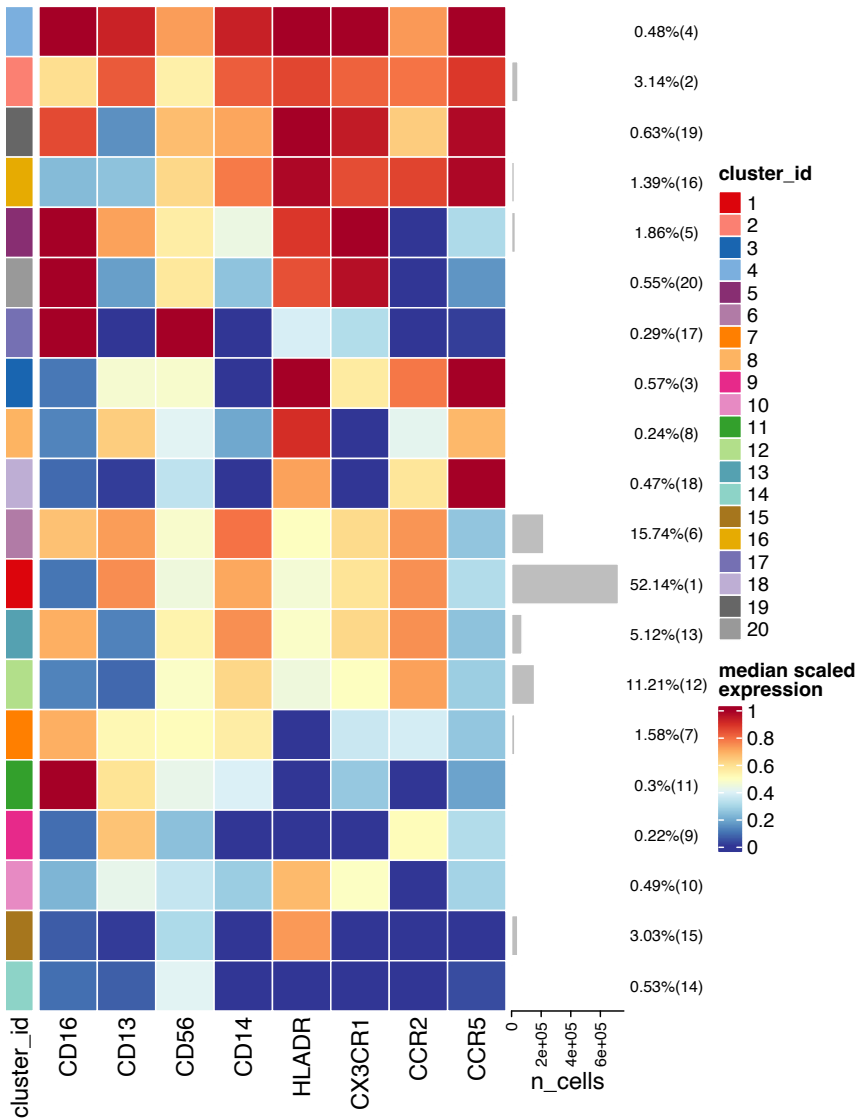


Supplementary Figure 3. Monocyte subsets in cord blood. Gating strategy used to analyse markers related to different stage of maturation and differentiation of monocytes. PBMCs were gated according to physical parameters and aggregates were removed from the analysis. Living (Live/Dead, LD⁻) cells and HLA-DR⁺ cells were identified. Immature monocytes are identified as CD13⁻CD14⁻ (**a**), mature monocytes are CD13⁺CD14⁺ (**b**). Within the mature monocyte, it is possible identify three monocyte subsets based on CD14 and CD16 expression: classical monocytes are defined as CD14⁺CD16⁻ (**c**), intermediate monocytes are CD14⁺CD16⁺ (**i**) and nonclassical monocytes are CD14^{+/−}CD16⁺ (**nc**).

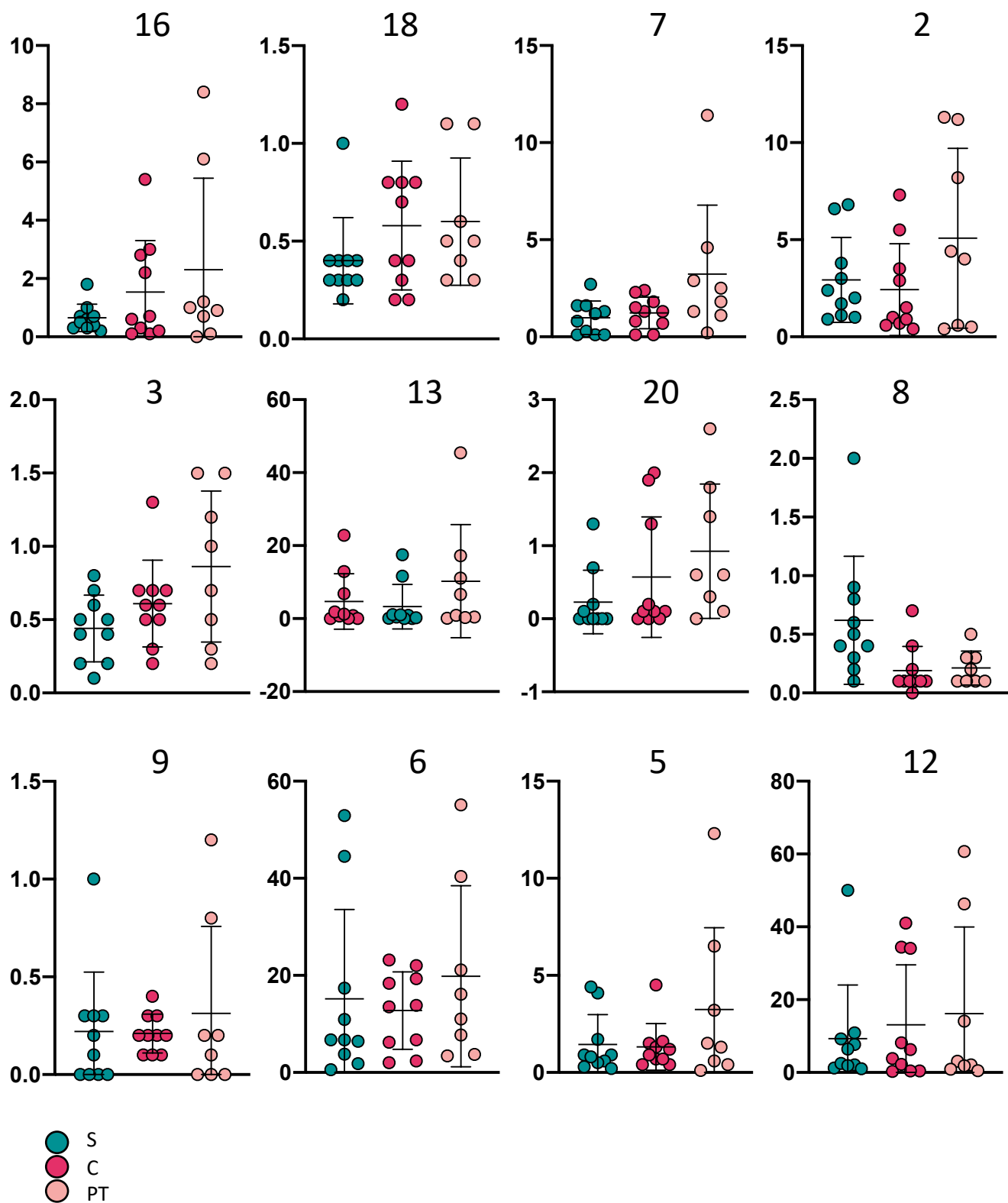
A



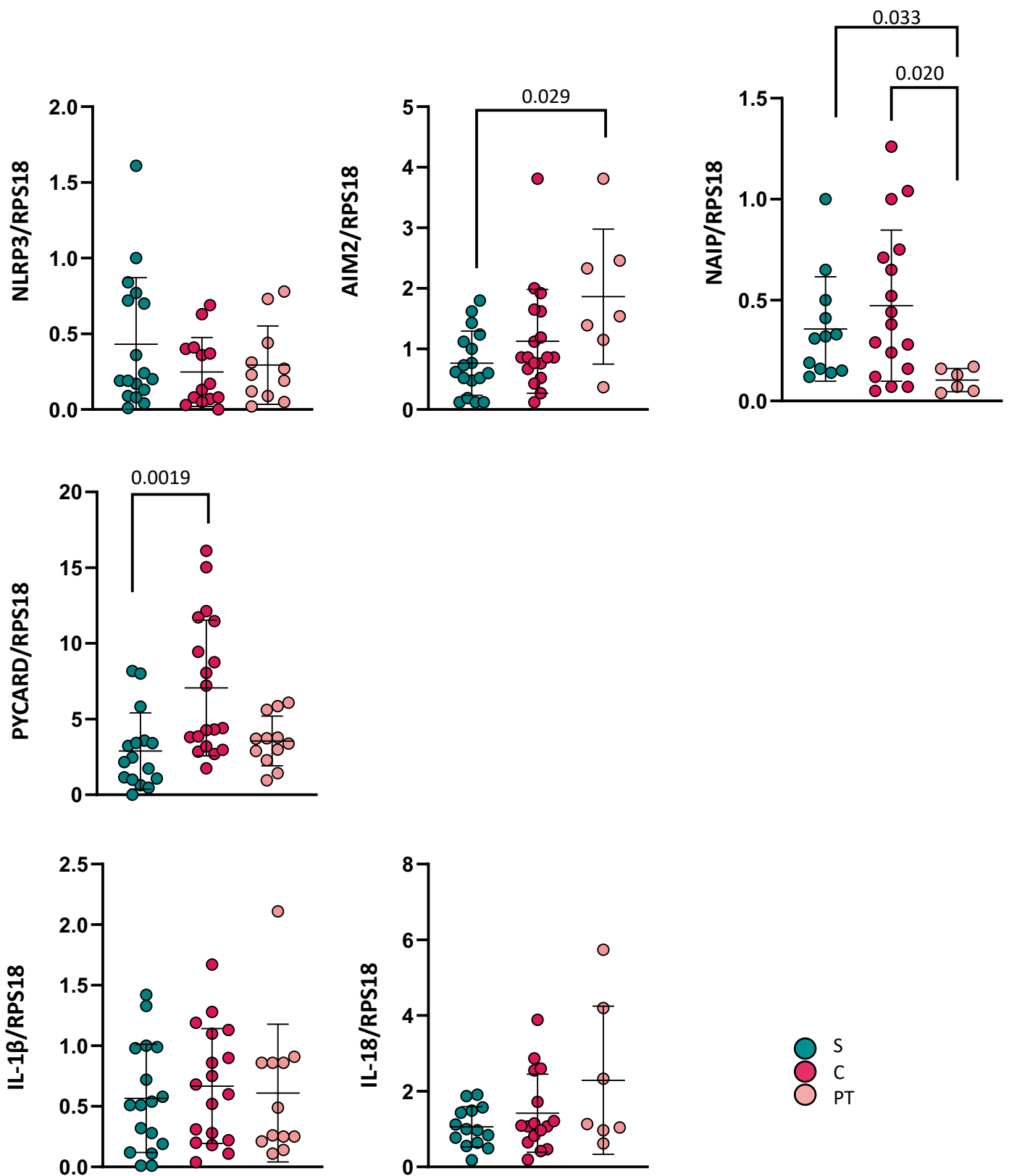
B



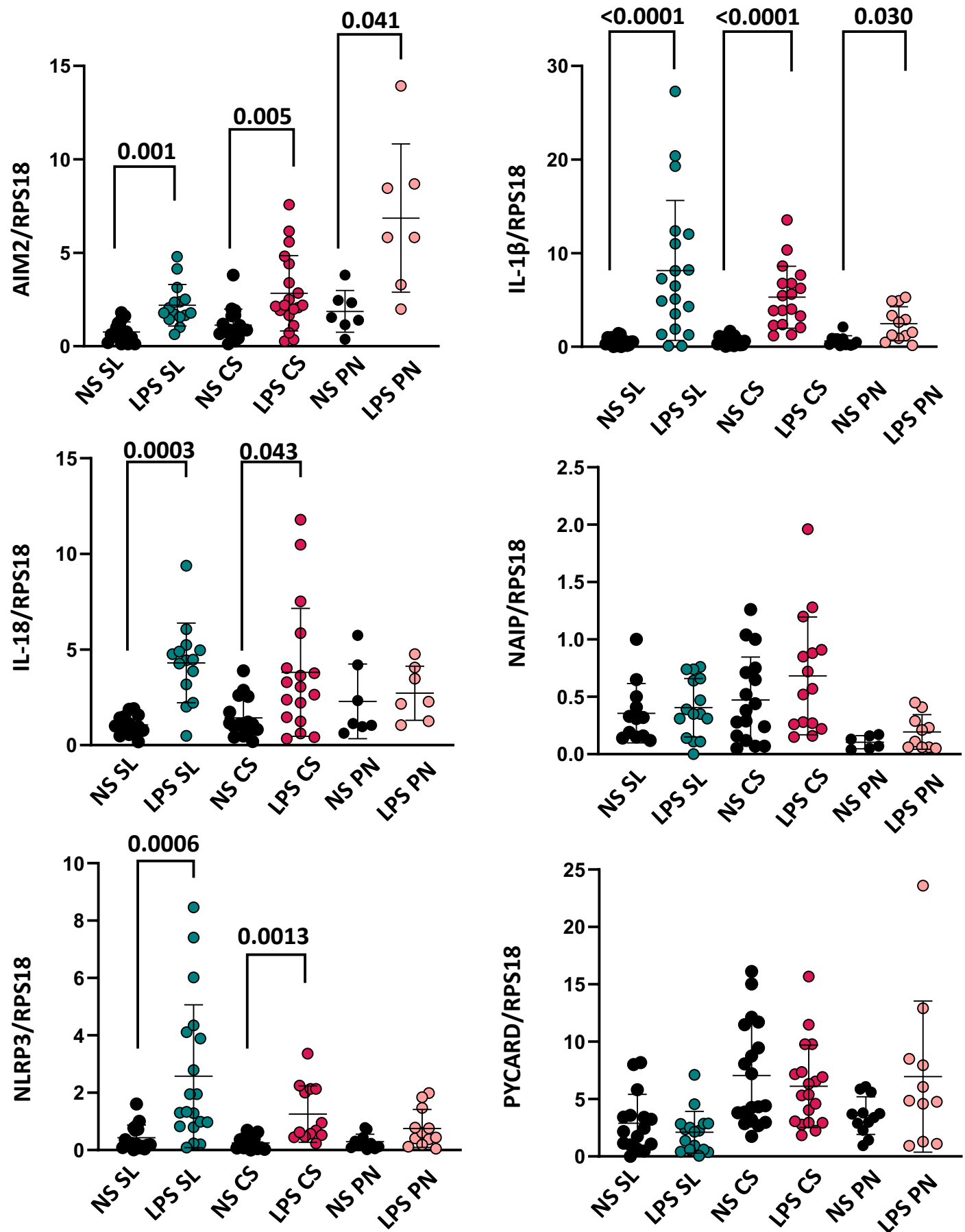
Supplementary Figure 4.
A) UMAP plot showing the 2D spatial distribution monocytes among S (n = 10), C (n = 10), and PT (n = 8) embedded with FlowSOM clusters; **B)** Monocytes heatmap showing the median marker intensities of the 8 lineage markers across the 20 cell populations obtained with FlowSOM after the manual metaclusters merging.



Supplementary Figure 5. Monocyte subsets in cord blood. Dotplots show the relative cells percentage of the 12 clusters among S (n = 10), C (n = 10) and PT (n = 8) newborns. The central bar represents the mean $\pm$ SEM. GLMM test was used for the statistical analysis. Exact p-values are reported in the figure, if significant.

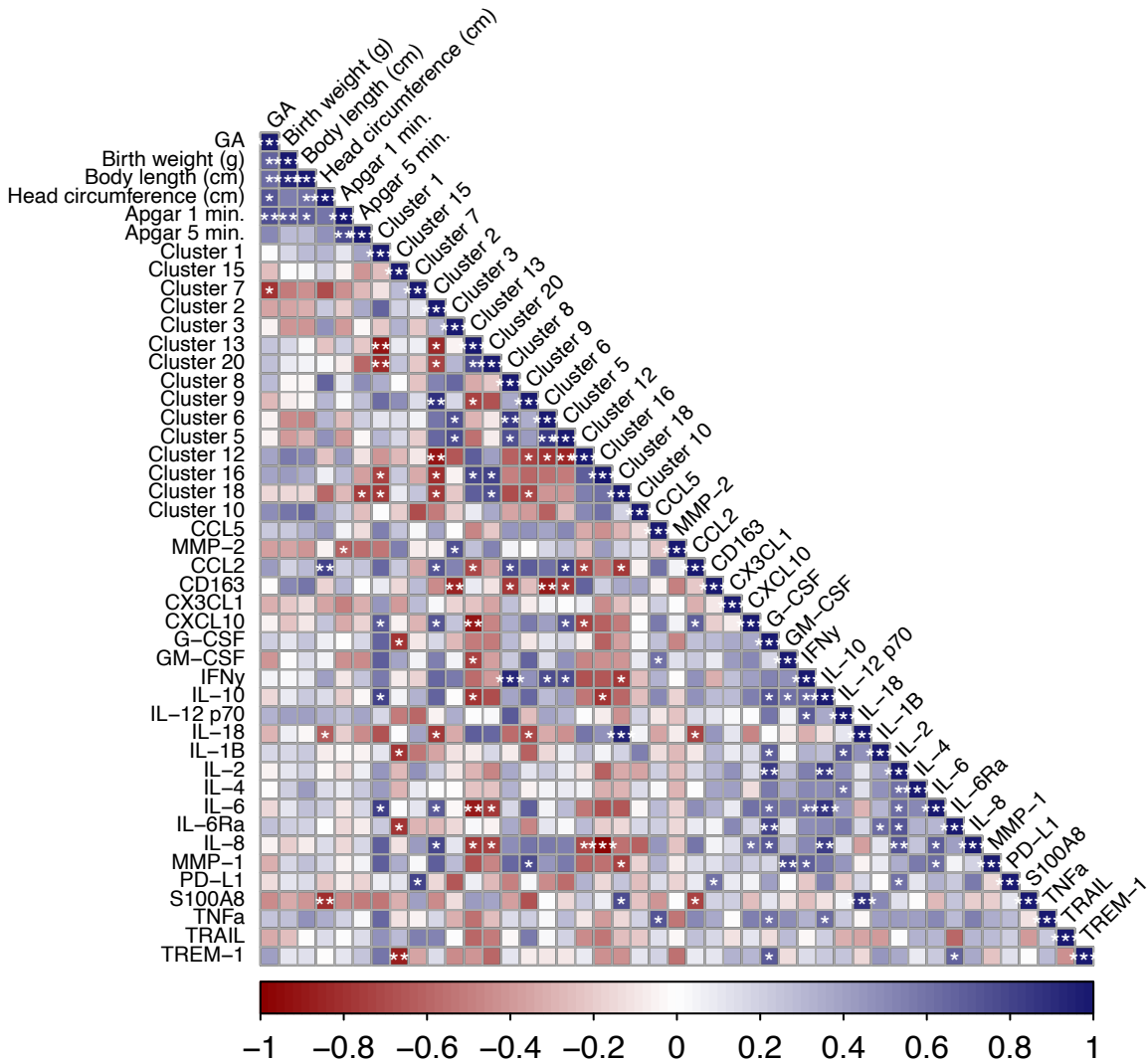


Supplementary Figure 6. Inflammasome genes relative expression in NS condition. Changes in gene expression were evaluated in non-stimulated monocytes among S (n = 19), C (n = 19) and PT (n = 12) newborns. Kruskal Wallis Test with original FDR method of Benjamini and Hochberg correction was used to test differences among groups and adjusted q-value is shown. Each dot represented one sample as mean value of two replicates and the central bar correspond to mean $\pm$ standard deviation (SD). Results were normalized to *RPS18* (Ribosomal Protein S18) expression for each sample.



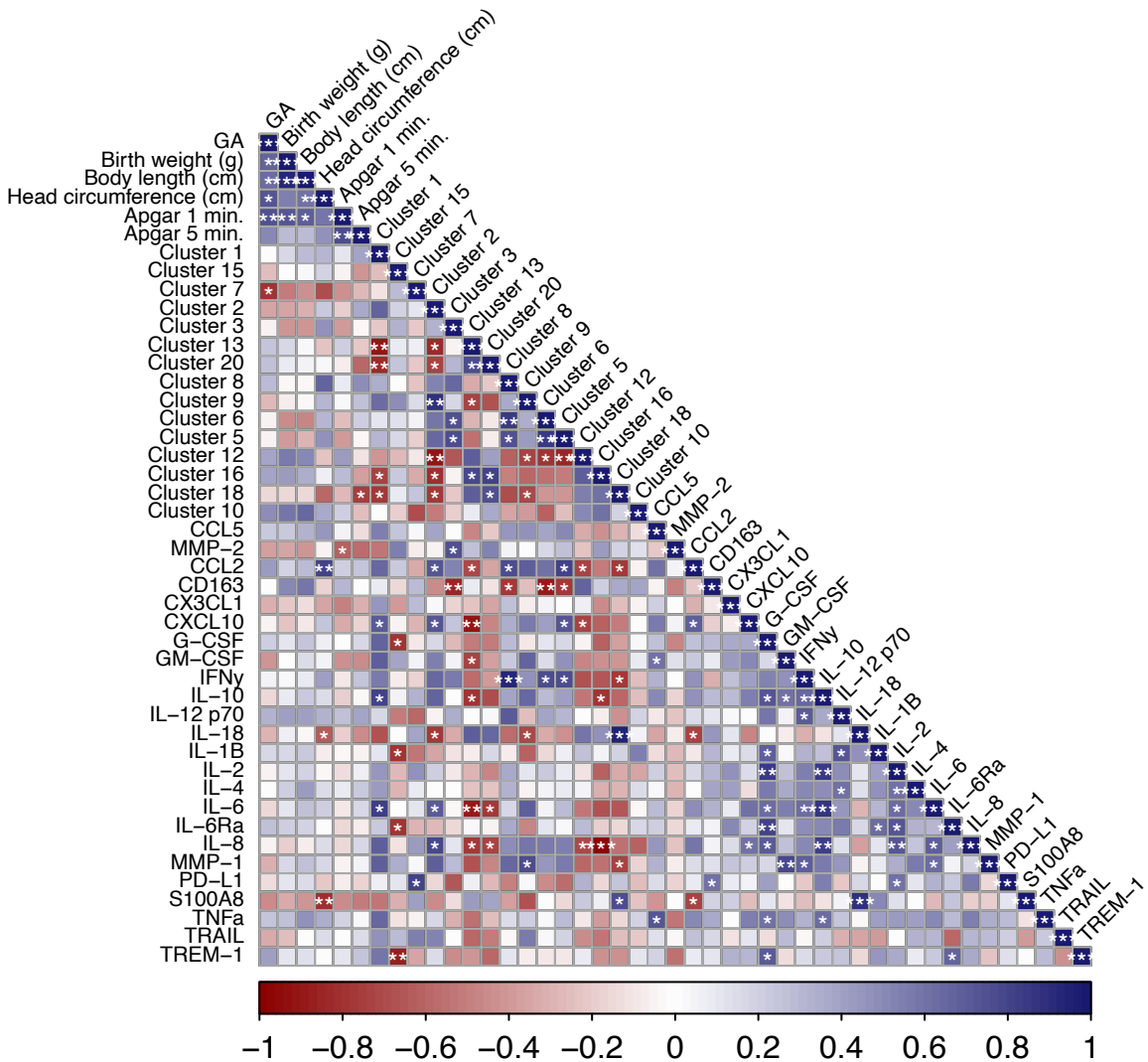
Supplementary Figure 7. Inflammasome genes relative expression. Relative mRNA expression for target genes relative to inflammasomes. Not stimulated (NS) and stimulated (LPS) conditions are shown for each group. Scatter plots show individual values, mean $\pm$ SEM. Kruskal-Wallis test with Benjamini-Hochberg correction for multiple comparisons was used to test the differences among the three groups: S (n = 19), C (n = 19) and PT (n = 12) .

S

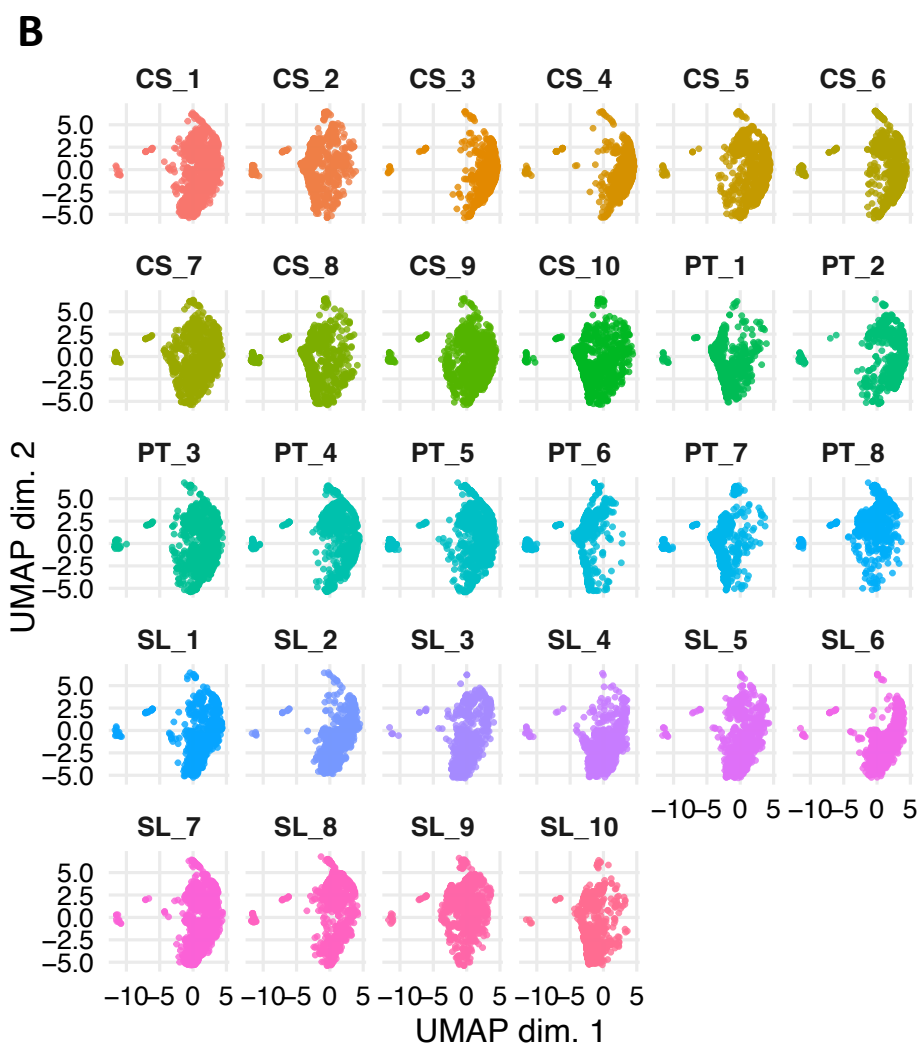
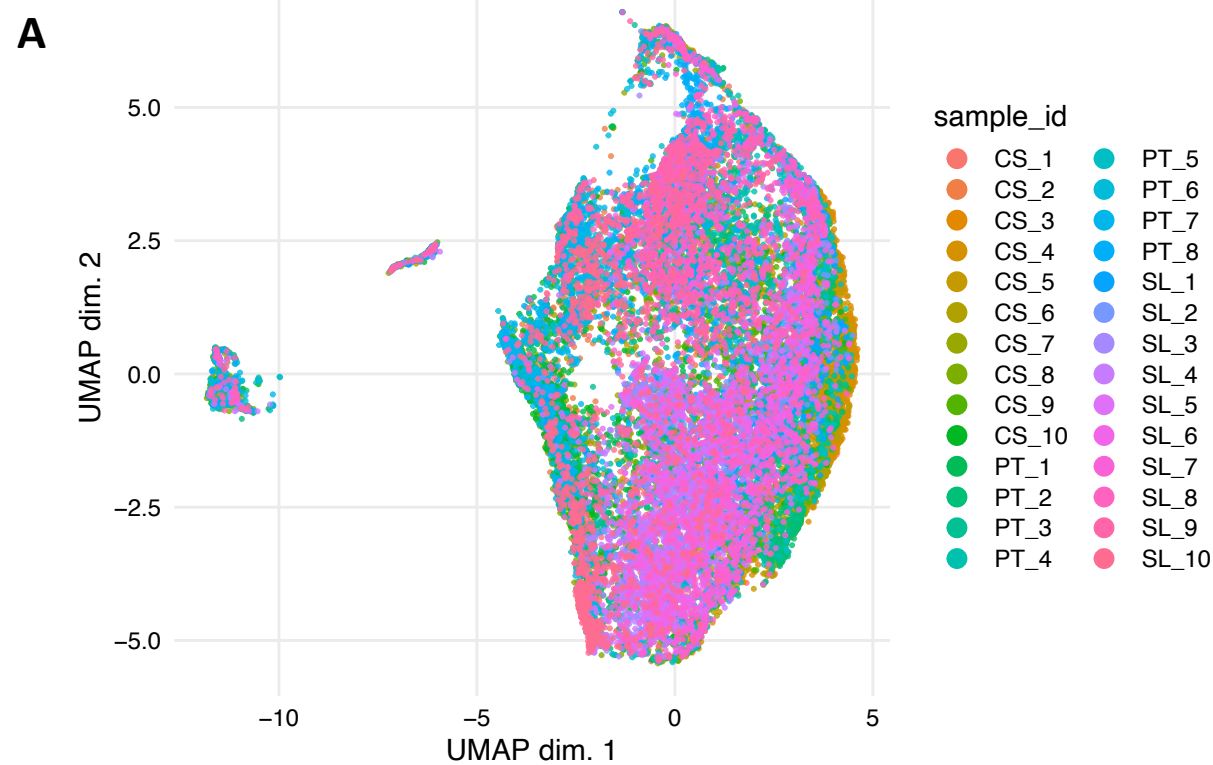


Supplementary Figure 8. Correlogram showing immunological-clinical correlations in S donors. Correlogram of S. Spearman R (ρ) values are shown from red (-1.0) to blue (1.0); specific R values are indicated by the square color. Blank fields with dots indicate lack of signal. Spearman rank two-tailed p-value was indicated by *P < 0.05, **P < 0.01, and ***P < 0.001.

C

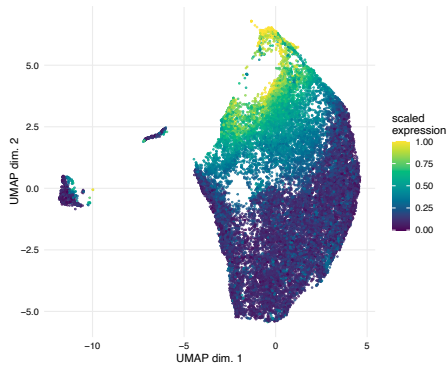


Supplementary Figure 9. Correlogram showing immunological-clinical correlations in C donors. Correlogram of C Spearman R (ρ) values are shown from red (-1.0) to blue (1.0); specific R values are indicated by the square color. Blank fields with dots indicate lack of signal. Spearman rank two-tailed p-value was indicated by *P < 0.05, **P < 0.01, and ***P < 0.001.

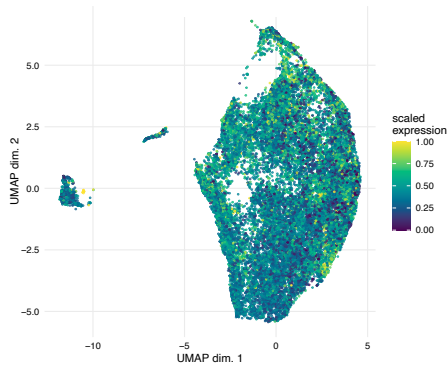


Supplementary Figure 10. A) UMAP graph monocytes overlaid by patients; B) Projection of UMAP graph stratified by sample.

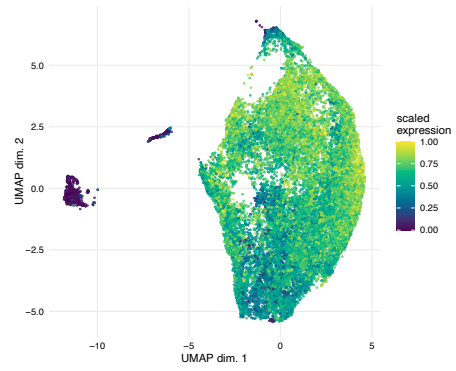
CD16



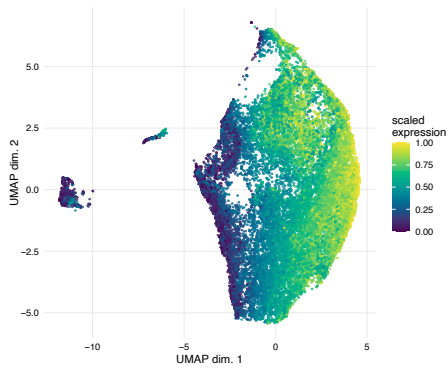
CD56



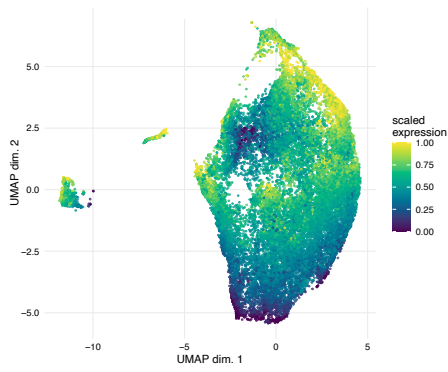
CD14



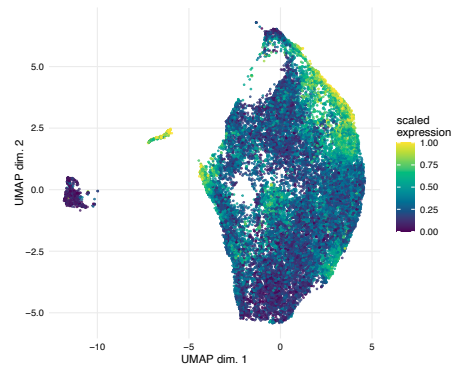
CD13



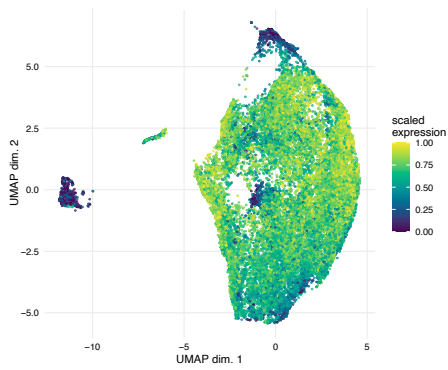
HLA-DR



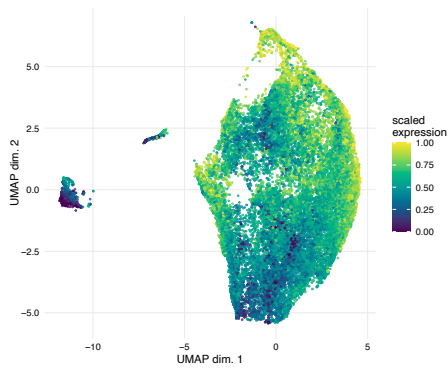
CCR5



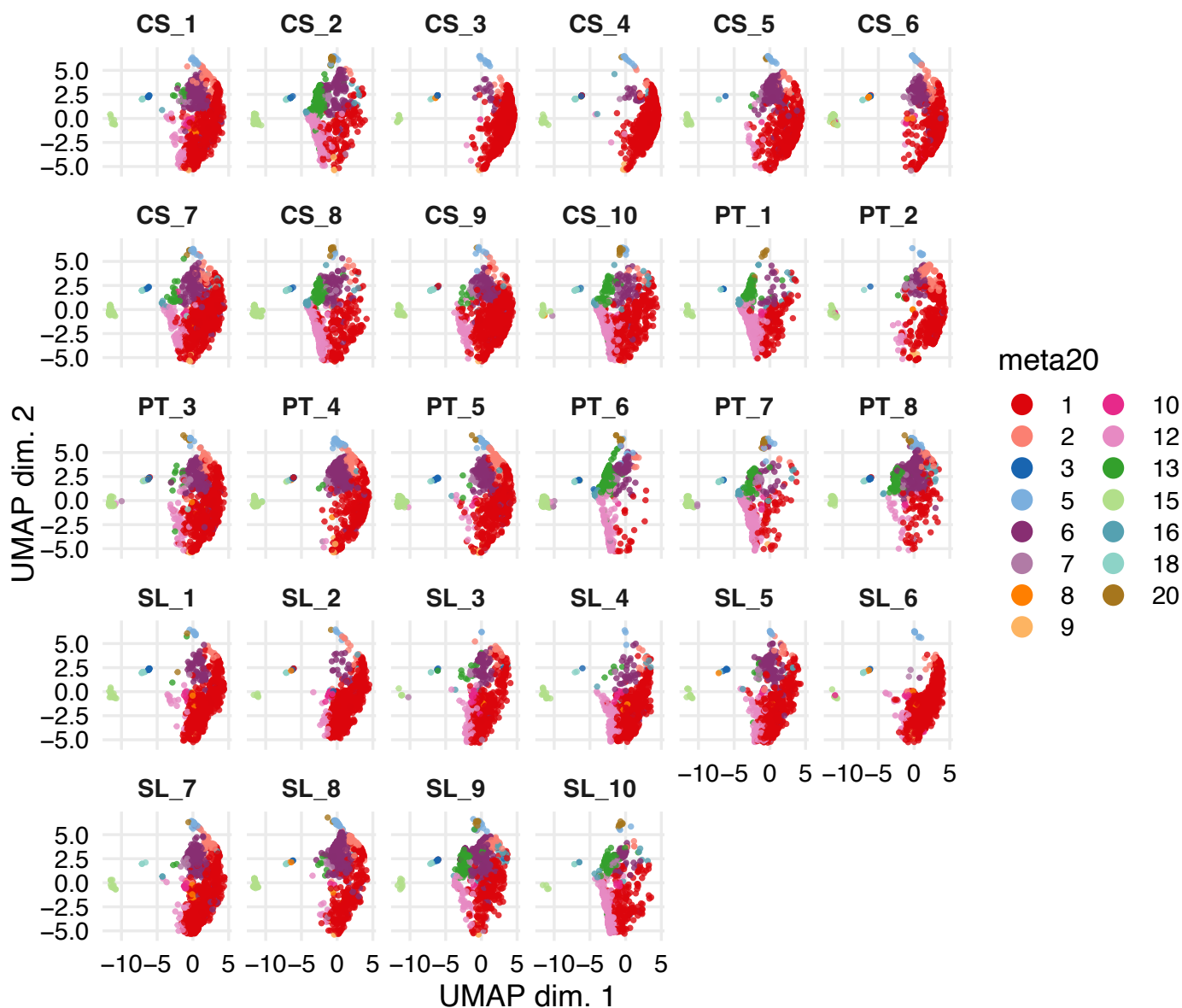
CCR2



CX3CR1



Supplementary Figure 11. UMAP graphs colored by the expression of 8 markers used for monocytes phenotyping.



Supplementary Figure 12. Projection of UMAP graphs stratified by patients showing the FlowSOM clusters.