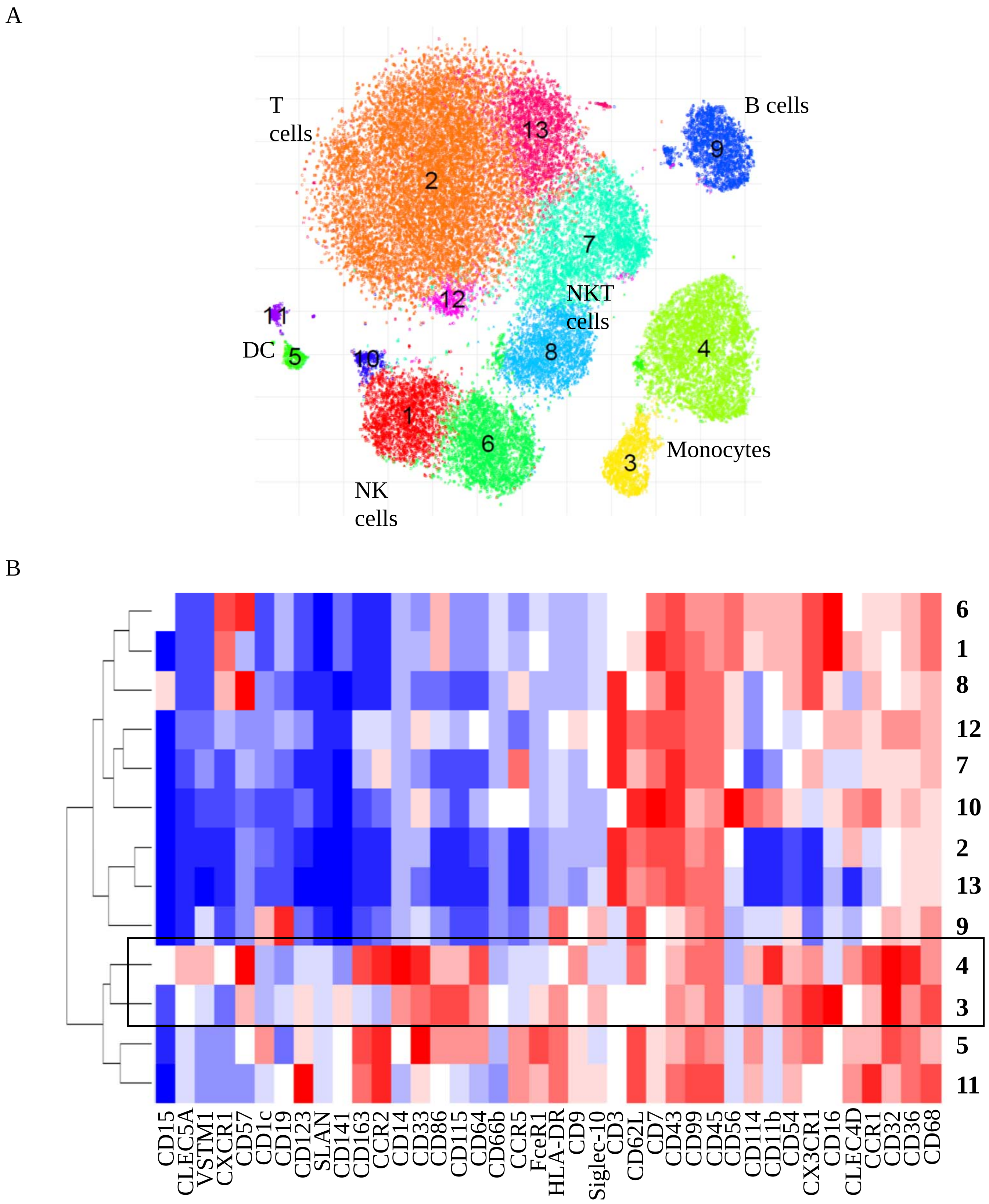
Supplementary Figure S1



Supp Figure S1. Visualization of the expression of forty markers on PBMCs. (A) *t*-SNE clustering of PBMCs based on the expression of the forty markers. **(B)** Expression level of the forty markers on each cluster in (A).

Supplementary Figure S2

CD14 CD16 CD32 CD64

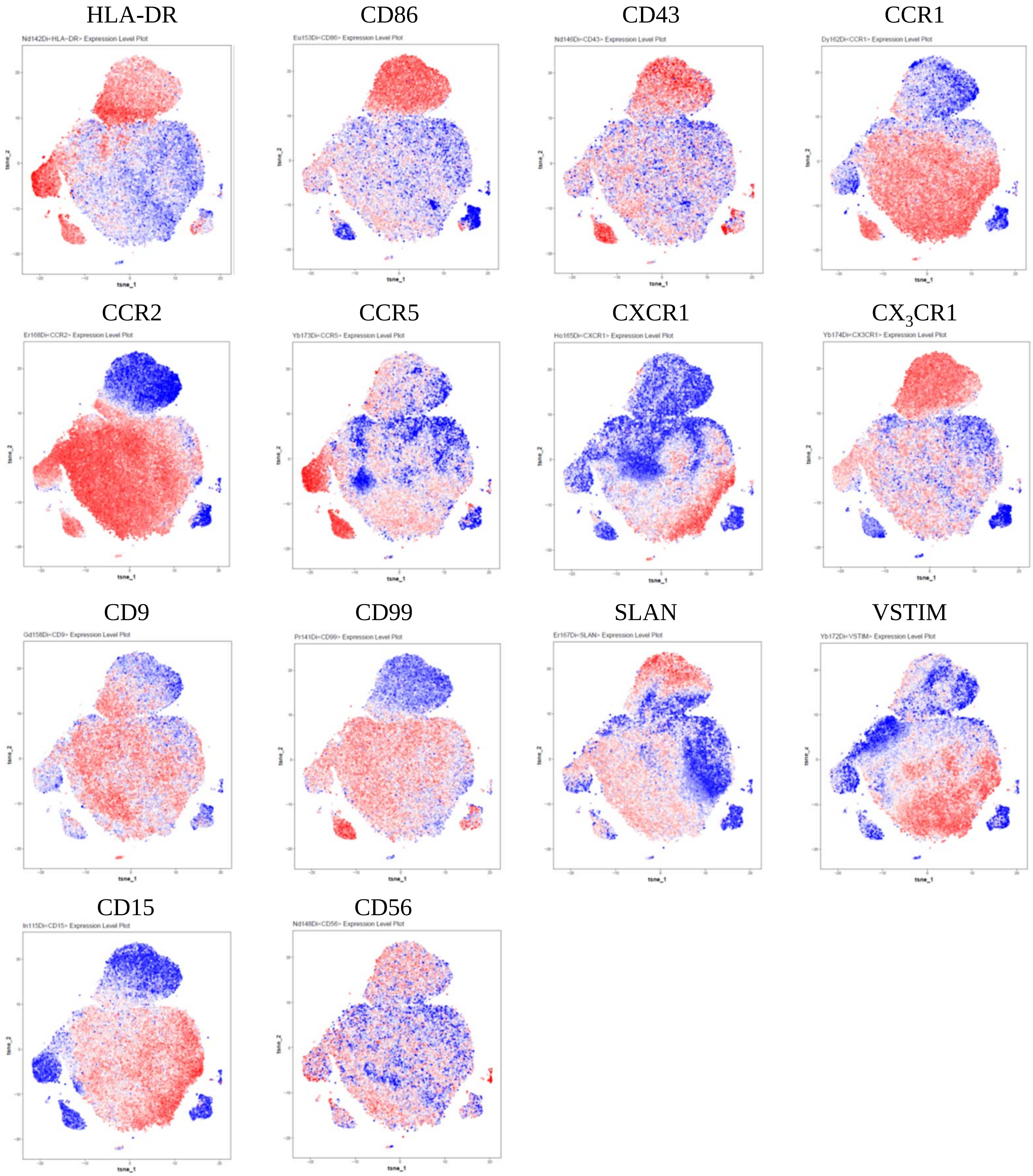
FcεR1a CD123 CD1c CD141

CD33 CD68 CD114 CD115

CD36 CD163 CLEC4D CLEC5A

CD11b CD54 CD62L Siglec-10

Supplementary Figure S2 (continued)



HLA-DR

CD86

CD43

CCR1

CCR2

CCR5

CXCR1

CX_3CR1

CD9

CD99

SLAN

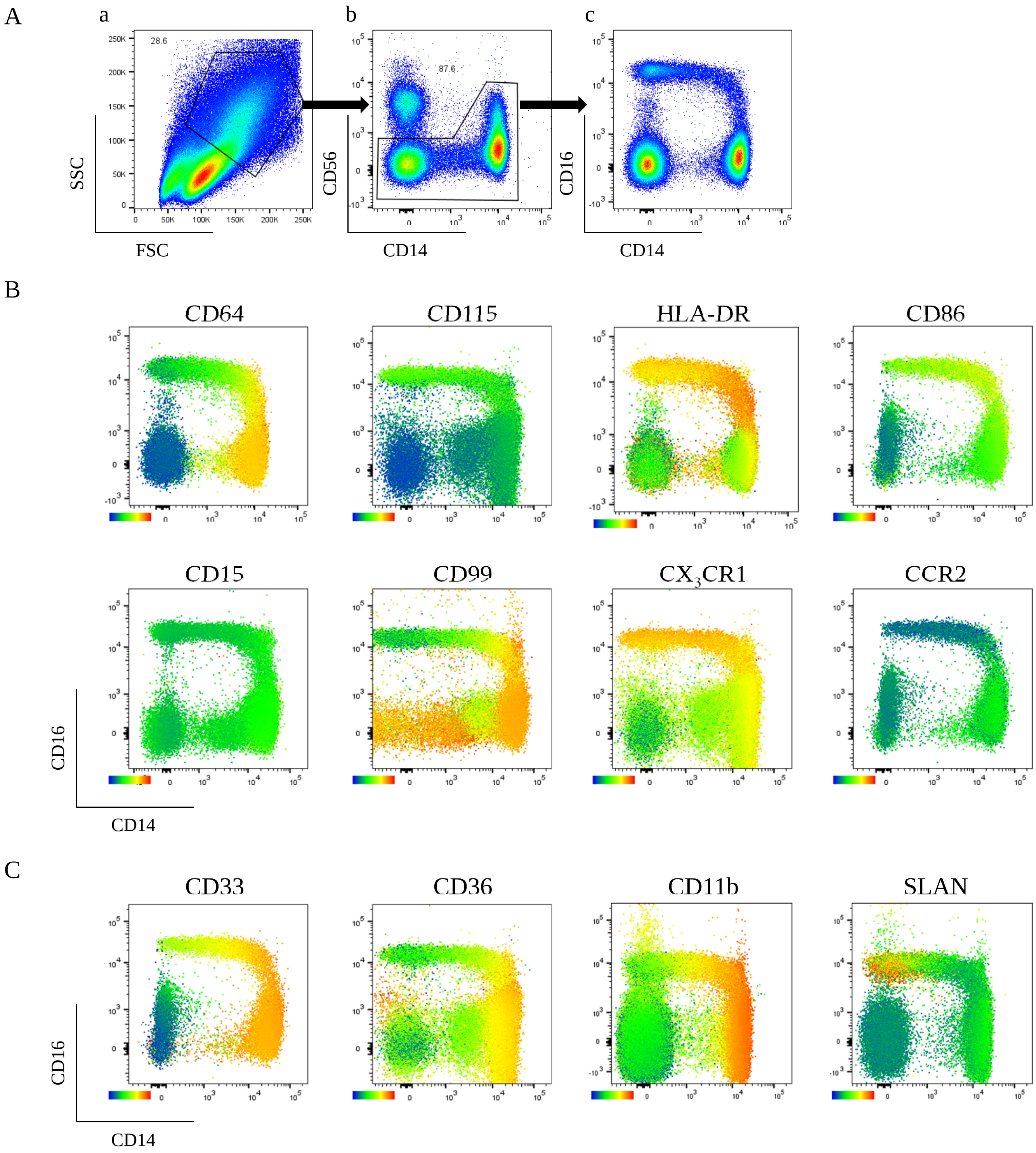
VSTIM

CD15

CD56

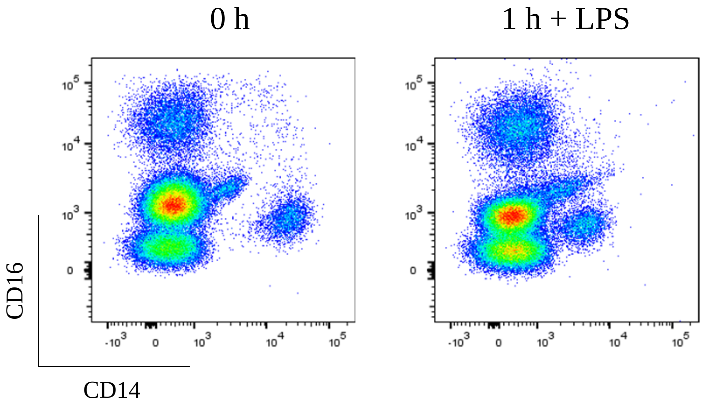
Supp Figure S2. Expression level of each of the thirty-four markers on monocytes visualized on *t*-SNE plots.

Supplementary Figure S3



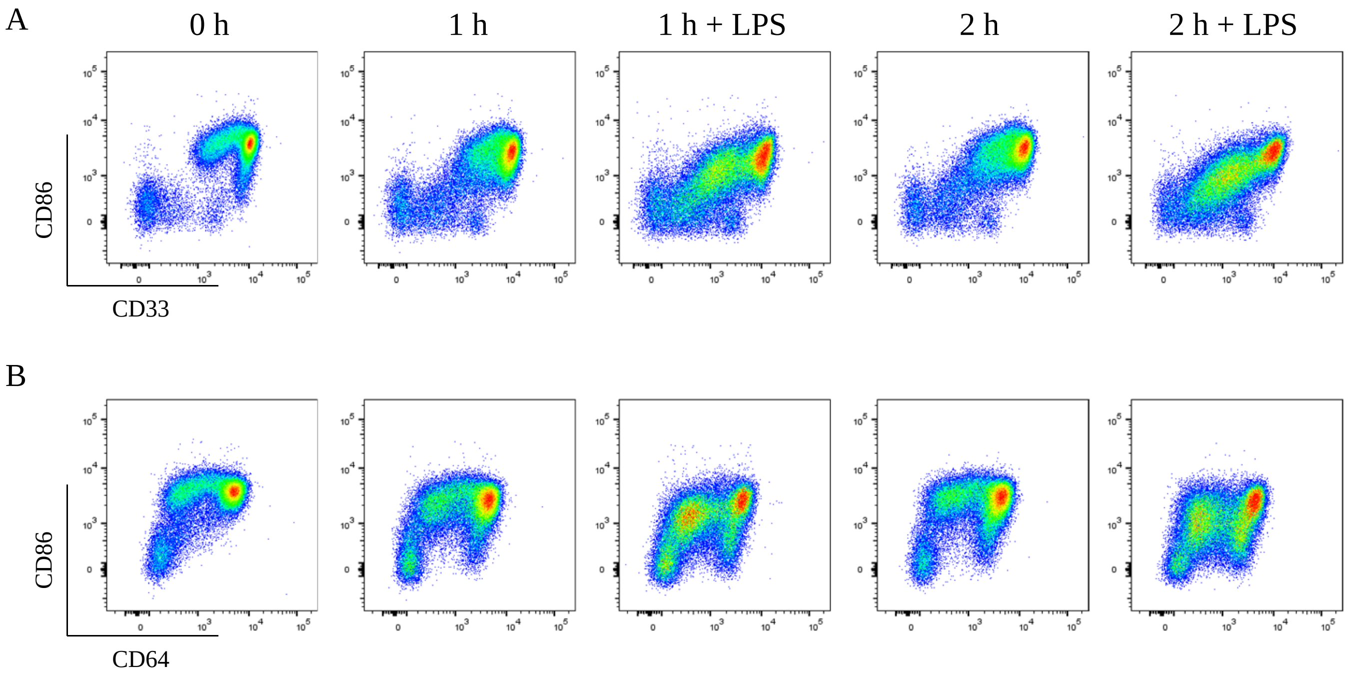
Supp Figure S3. Markers shortlisted from CyTOF data were assessed with flow cytometry on a conventional CD16-CD14 plot. (A) Enriched monocytes were gated from PBMCs for (B) and (C). Heatmap expression of markers shortlisted to separate CD16$^+$ and CD16$^-$ monocytes **(B)** and NC and ITM subsets **(C)**.

Supplementary Figure S4



Supp Figure S4. Down-regulation of CD14 and CD16 on monocytes in whole blood after 1 h of stimulation with LPS.

Supplementary Figure S5



Supp Figure S5. Expression of CD33 on monocytes **(A)** is more modulated than that of CD64 **(B)** *in vitro*.