

Figure S1. Gating strategy of flow cytometry. Sequential gating strategy for the identification of lymphocytes subpopulations:  $CD45^+$  cell identification (A), setting a logical limitation for area A based on Forward Scatter and Side Scatter (B), CD3 receptor expression histogram on white blood cells (C), identification of  $CD45^+CD3^+CD19^-$  corresponding to T-cells and  $CD45^+CD3^-CD19^+$  corresponding to B-cells phenotypes (D), identification of  $CD45^+CD3^-CD56^+$  phenotypes corresponding to NK-cells;  $CD45^+CD3^+CD56^-$  corresponding to NKT-cells (E), identification of  $CD45^+CD3^+CD4^+$  phenotypes corresponding to T-helper cells;  $CD45^+CD3^+CD8^+$  corresponding to T-cytotoxic lymphocytes;  $CD45^+CD3^+CD4^+CD8^+$  corresponding to a heterogeneous population of double positive T-cells (F-H).

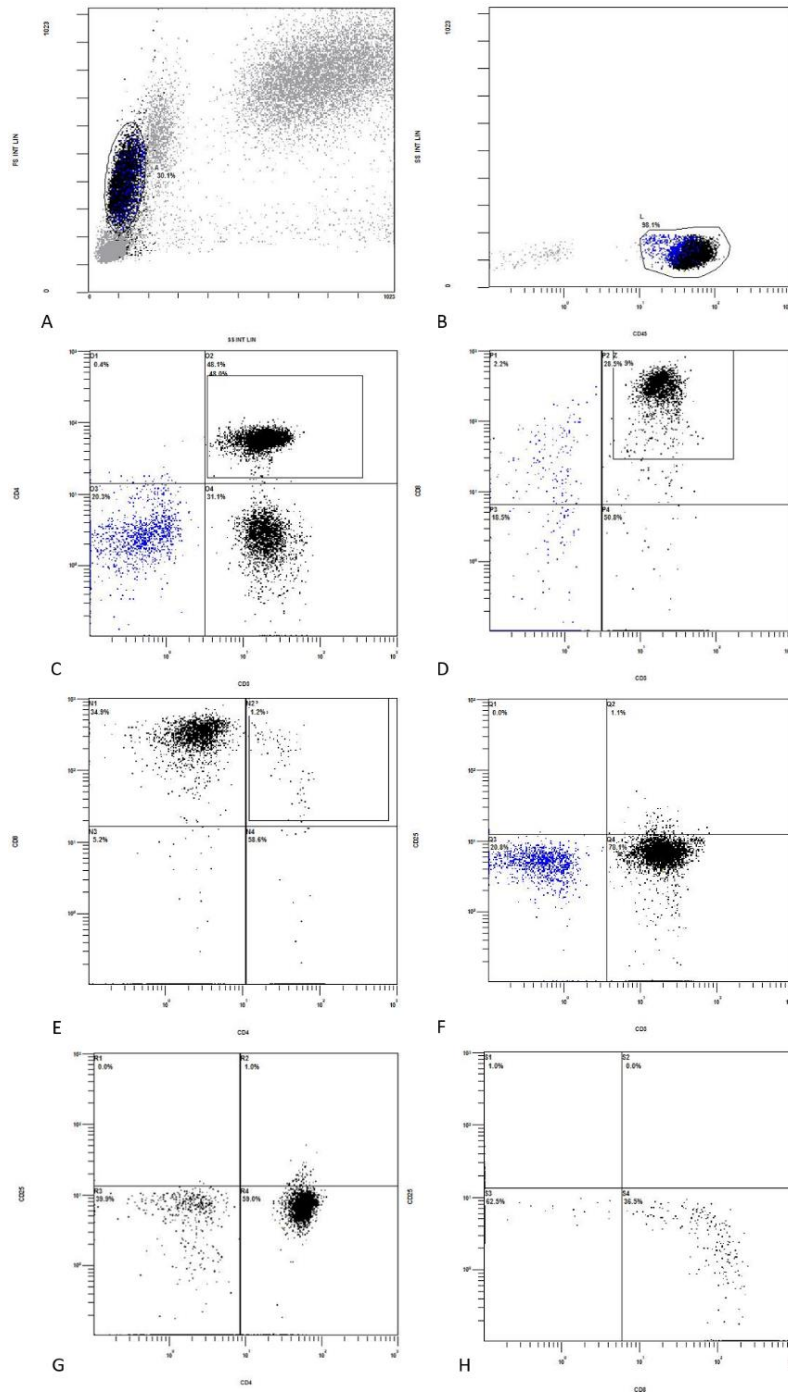


Figure S2. Gating strategy of flow cytometry. Sequential gating strategy for the identification of  $CD25^+$  T cells subpopulations: setting a logical limitation for area A based on Forward Scatter and Side Scatter with lymphocyte population isolation (A), setting a logical limitation for area A with identification of  $CD45^+$  cells (B), identification of  $CD45^+CD3^+CD4^+$  phenotypes corresponding to T-helper cells;  $CD45^+CD3^+CD8^+$  corresponding to T-cytotoxic lymphocytes;  $CD45^+CD3^+CD4^+CD8^+$  corresponding to a heterogeneous population of double positive T-cells (C-E), identification of CD25-expressing T-cell phenotypes (including T-helper and T-cytotoxic lymphocytes) based on CD3, CD4, CD8 and CD25 expression (F-H).

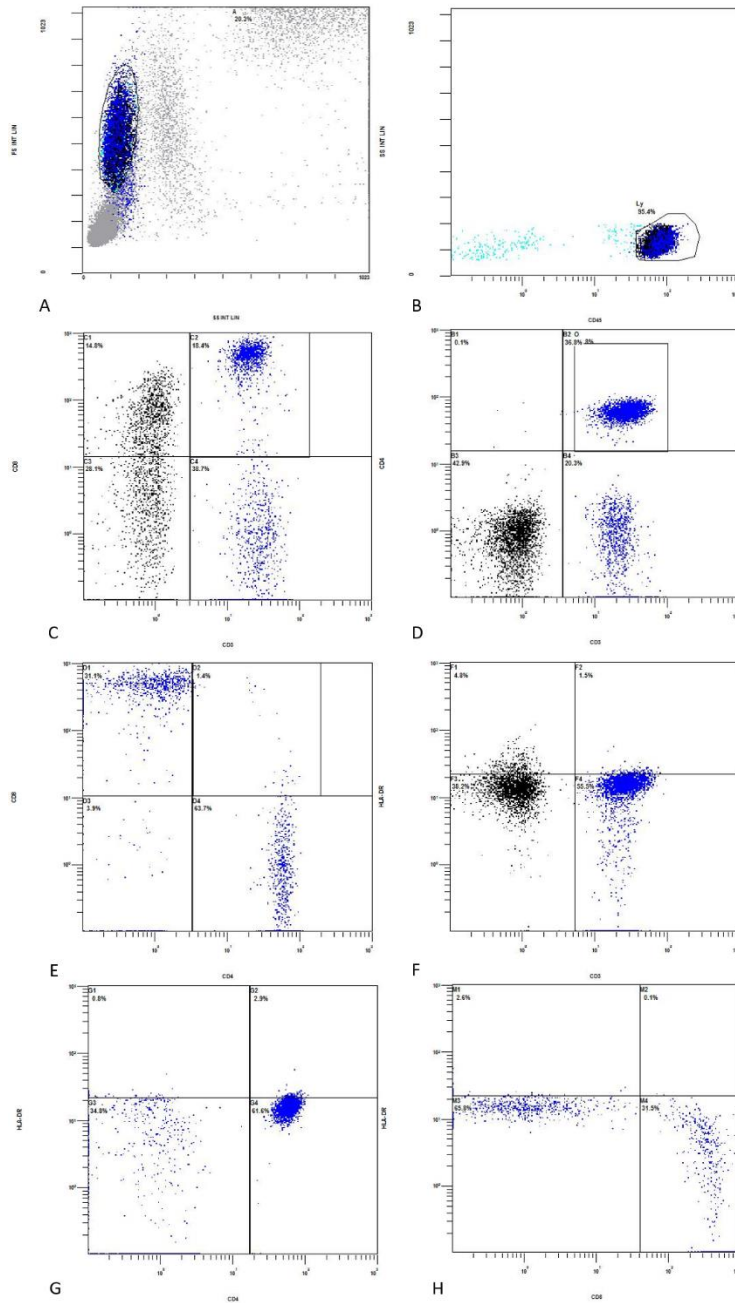


Figure S3. Gating strategy of flow cytometry. Sequential gating strategy for the identification of HLA-DR<sup>+</sup> T cells subpopulations: setting a logical limitation for area A based on Forward Scatter and Side Scatter with lymphocyte population isolation (A), setting a logical limitation for area A with identification of CD45<sup>+</sup> cells (B), identification of CD45<sup>+</sup>CD3<sup>+</sup>CD4<sup>+</sup> phenotypes corresponding to T-helper cells; CD45<sup>+</sup>CD3<sup>+</sup>CD8<sup>+</sup> corresponding to T-cytotoxic lymphocytes; CD45<sup>+</sup>CD3<sup>+</sup>CD4<sup>+</sup>CD8<sup>+</sup> corresponding to a heterogeneous population of double positive T-cells (C-E), identification of HLA-DR-expressing T-cell phenotypes (including T-helper and T-cytotoxic lymphocytes) based on CD3, CD4, CD8 and HLA-DR expression (F-H).

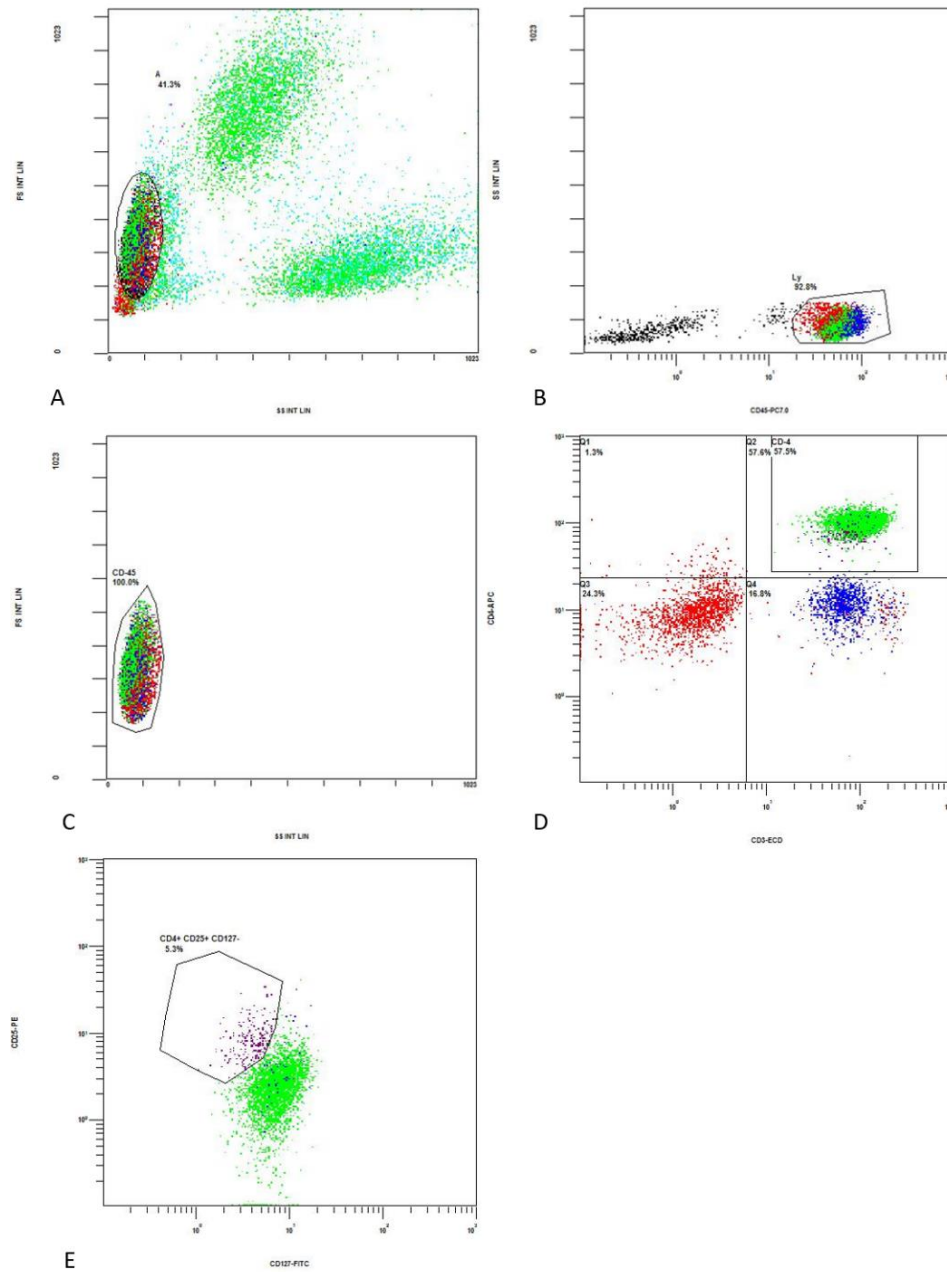


Figure S4. Gating strategy of flow cytometry. Sequential gating strategy for the identification of T-regulatory lymphocytes subpopulations: setting a logical limitation for area A based on Forward Scatter and Side Scatter with lymphocyte population isolation (A), setting a logical limitation for area A with identification of CD45<sup>+</sup> cells (B), setting a second logical limitation for the lymphocytic region based on Forward Scatter and Side Scatter (C), identification of CD45<sup>+</sup>CD3<sup>+</sup>CD4<sup>+</sup> phenotypes corresponding to T-helper cells (D), identification of CD45<sup>+</sup>CD3<sup>+</sup>CD4<sup>+</sup>CD25<sup>+</sup>CD127<sup>-</sup> phenotypes corresponding to T-regulatory cells (E).

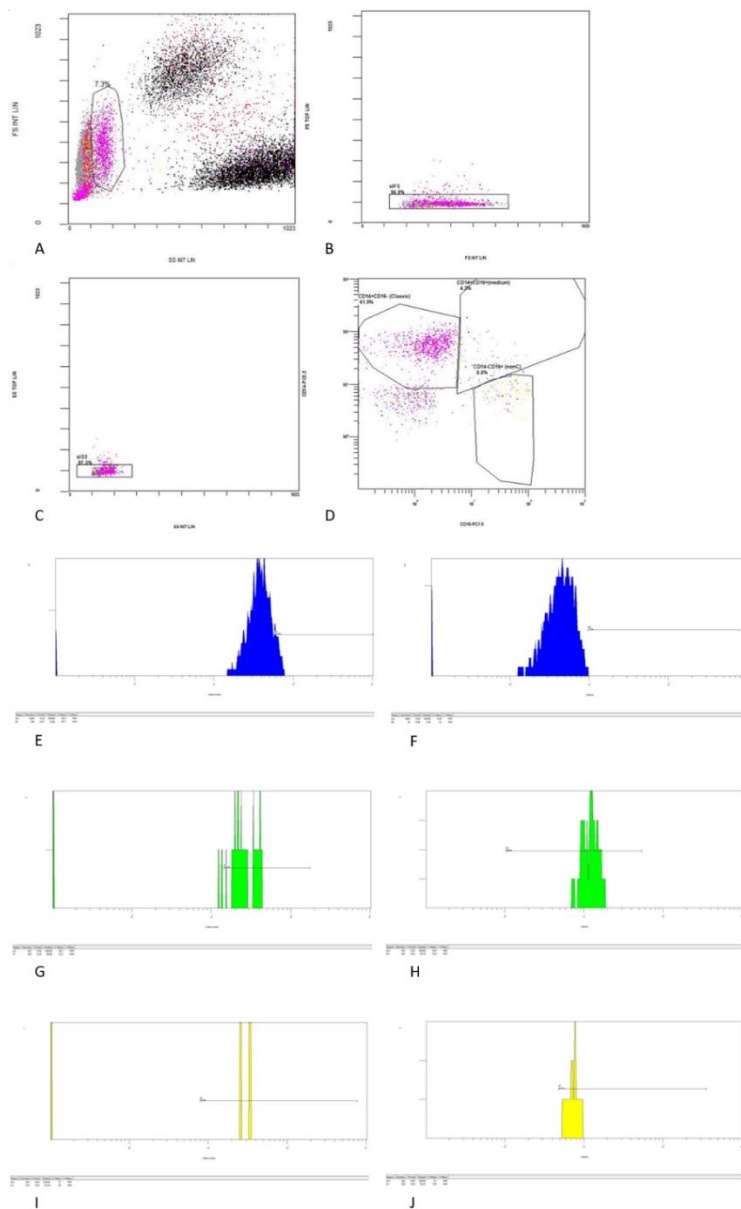


Figure S5. Gating strategy of flow cytometry. Sequential gating strategy for the identification of monocytes subpopulations: setting a logical limitation for area A based on Forward Scatter and Side Scatter with monocyte population isolation (A), gating for single cells in a FS TOF vs FS INT plot (B), gating for single cells in a SS TOF vs SS INT plot (C), identification of CD14<sup>+</sup>CD16<sup>-</sup> phenotypes corresponding to classical monocytes, CD14<sup>+</sup>CD16<sup>+</sup> phenotypes corresponding to intermediate monocytes, CD14<sup>-</sup>CD16<sup>+</sup> phenotypes corresponding to non-classical monocytes (D), identification of TLR2 and TLR4 expression levels on classical monocytes, as well as the number of TLR2- and TLR4-positive classical monocytes (E-F), identification of TLR2 and TLR4 expression levels on intermediate monocytes, as well as the number of TLR2- and TLR4-positive intermediate monocytes (G-H), identification of TLR2 and TLR4 expression levels on non-classical monocytes, as well as the number of TLR2- and TLR4-positive non-classical monocytes (I-J).