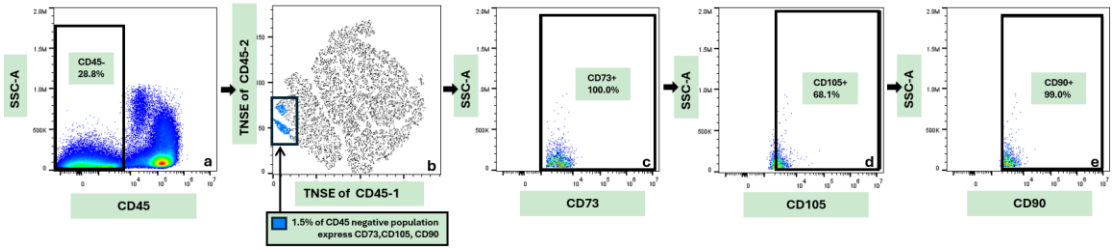
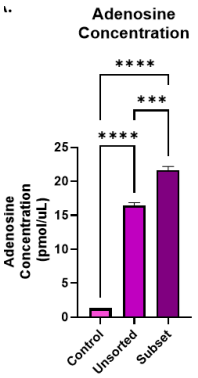
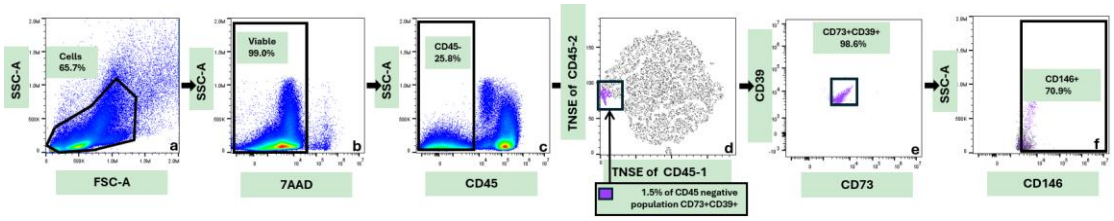


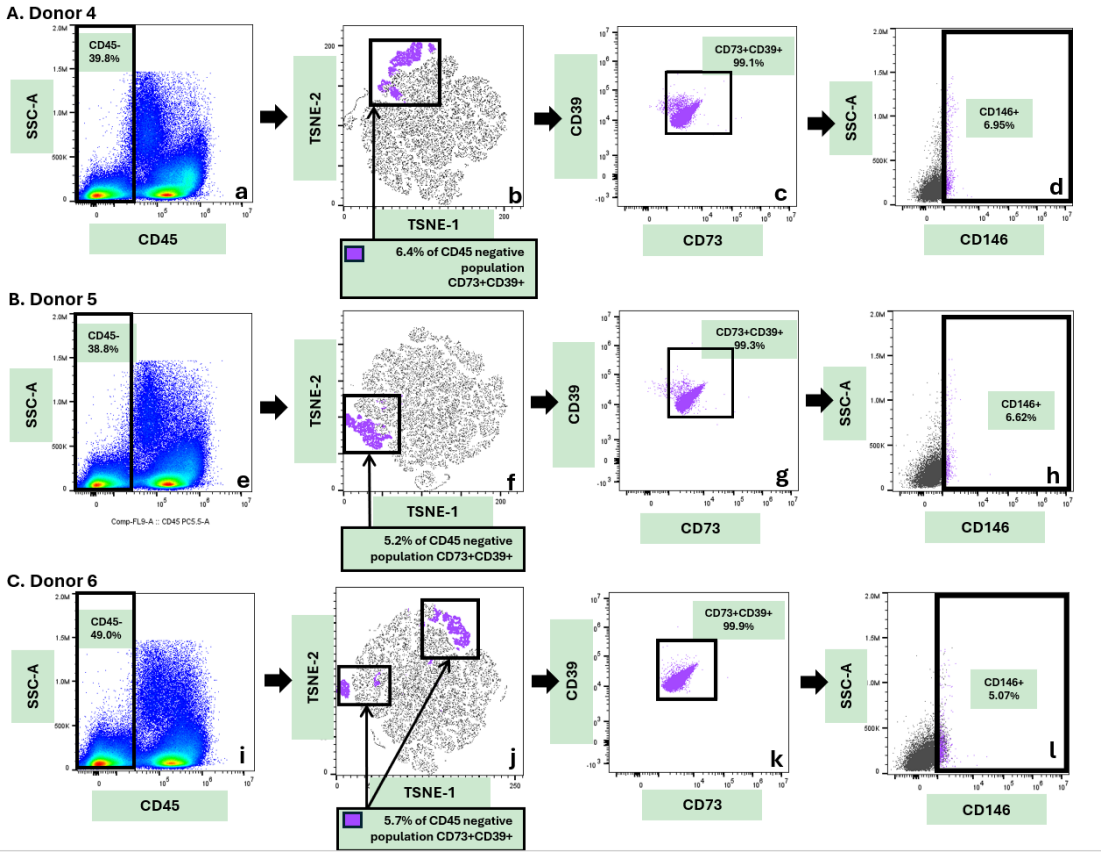
Supplementary Figure 1 Representative flow cytometry analysis for peripheral blood stem cells. The whole cell population was defined on a basis of forward scatter area (FSC-A) and side scatter area (SSC-A) and dead cells were ruled out by live-dead gating. Only the viable CD45 negative population was selected for tSNE cluster analysis (a). t-Distribution Stochastic Neighbor Embedding (tSNE) plot in combination with flowSOM and cluster explorer was used. 1.5% of the CD45- fraction express CD73, CD105, and CD90 (b). Cells which expressed CD73, CD105, CD90, and did not express CD45 were characterized as MSCs (c-e).



Supplementary Figure 2 Fluorometric adenosine assay in unsorted bone marrow-derived mesenchymal stem cells and target subset. Unsorted bone marrow-derived Mesenchymal Stem Cells (MSCs) exhibited a concentration of 16.4 pmol/uL, while the targeted subset showed a concentration of 21.6 pmol/uL (***P<0.0001). Bar graph is a result of mean ± SD (n = 3). The background sample that did not include adenosine deaminase represented the control group. The fluorescent product was detected by measuring fluorescence in a plate reader at 535/587 nm, with intensity proportional to the quantity of adenosine (Fluorometric Adenosine Assay Kit, Abcam ab211094).



Supplementary Figure 3 Representative flow cytometry analysis gating strategy for mesenchymal stem cell subset in non-mobilized mononuclear cells, single-mobilized, and dual-mobilized peripheral blood stem cells. The whole cell population was defined on a basis of forward scatter area (FSC-A) and side scatter area (SSC-A) (a). Dead cells were ruled out by 7AAD live-dead gating (b). Only the viable CD45 negative population was selected for tSNE cluster analysis (c-d). t-Distribution Stochastic Neighbor Embedding (tSNE) plot in combination with flowSOM and cluster explorer was used. 1.5% of CD45 negative cells expressed CD73 and CD39 (d). Only cells from cluster of CD45 negative fraction presented by TSNE plot were gated on and showed to co-express CD73 and CD39 at 96.8% (e). From CD45-CD73+CD39+ cells, approximately 70% are positive for CD146+ (f).



Supplementary Figure 4 Expression of the CD45-CD73+CD39+CD146+ subset in single mobilized samples from three additional donors (Donor 4, 5, and 6). A: Flow cytometry analysis showing target subset in Donor 4. Total CD45 negative fraction was gated (a). t-Distribution Stochastic Neighbor Embedding (tSNE) plot in combination with flowSOM and cluster explorer was used. 6.4% of CD45- cells expressed CD73 and CD39 (b). Cells from the CD45- fraction shown in the t-SNE plot were gated, indicating co-expression of CD73 and CD39 at 99.1% (c). From the CD45-CD73+CD39+ fraction, 6.95% of the cells co-expressed CD146+ (d). (B) Flow cytometry analysis showing the target subset in Donor 5. The total CD45 negative fraction was gated (B.e). tSNE plot in combination with flowSOM and cluster explorer was used. 5.2% of CD45- cells expressed CD73 and CD39 (f). Cells from the CD45- fraction shown in the t-SNE plot were gated, showing co-expression of CD73 and CD39 at 99.3%(g). 6.62% of the CD45-CD73+CD39+ fraction co-expressed CD146+(h). (C) Flow cytometry analysis with target subset in Donor 5. The total CD45- fraction was identified and gated (i). tSNE plot in conjunction with with flowSOM and

cluster explorer was utilized for the analysis. 5.7% of CD45- cells expressed CD73 and CD39 (j). Cells from the CD45- fraction presented in the t-SNE plot were gated, showing co-expression of CD73 and CD39 at 99.9% (k). From the CD45-CD73+CD39+ fraction, 5.07% of the cells was CD146+ (l).