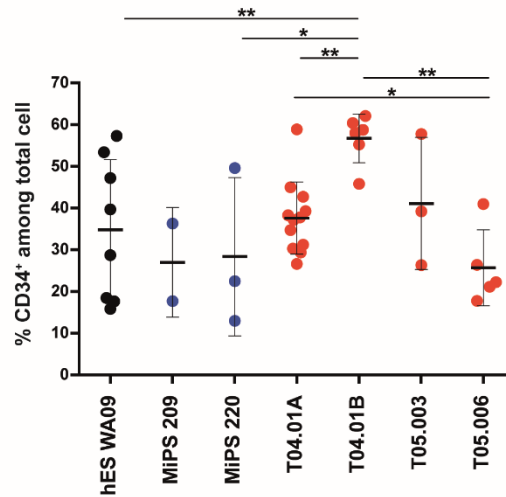
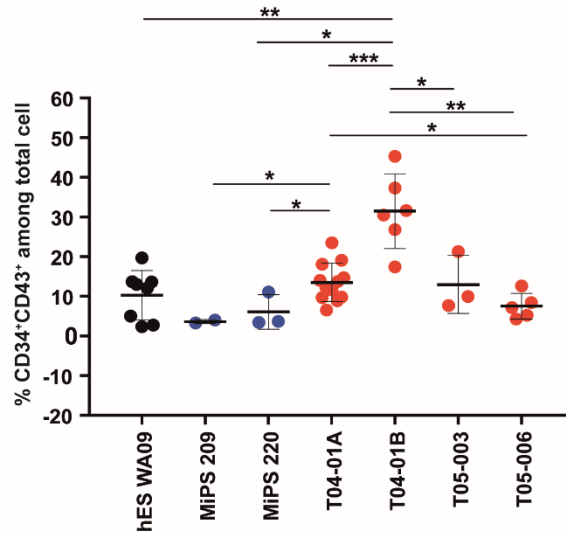


A



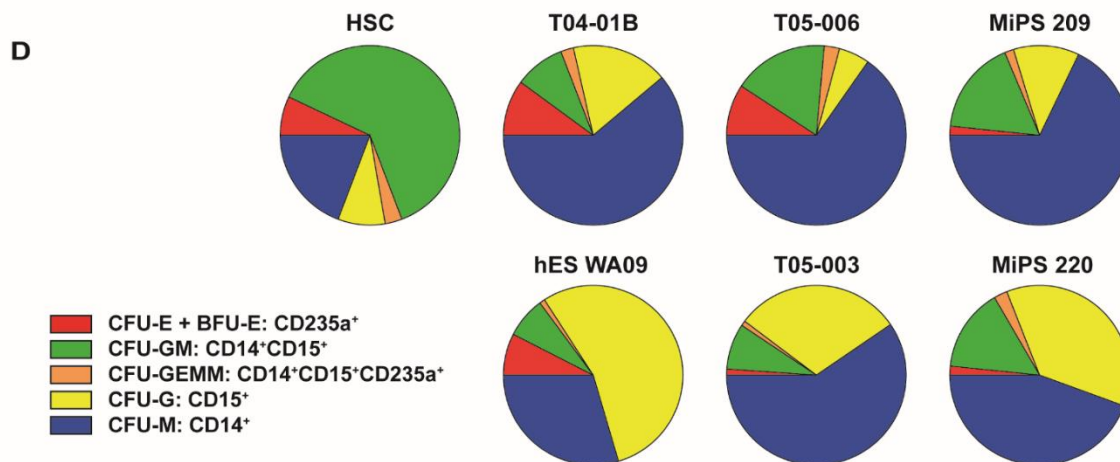
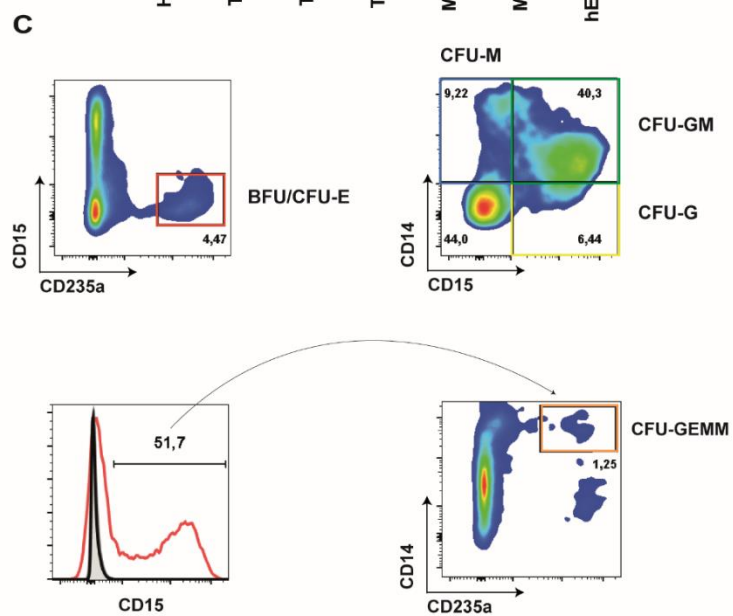
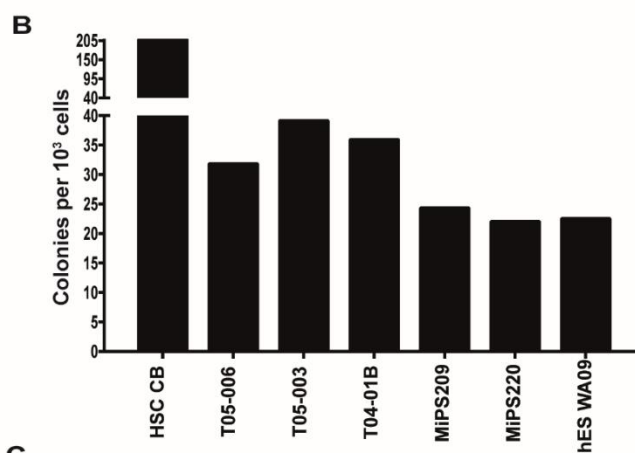
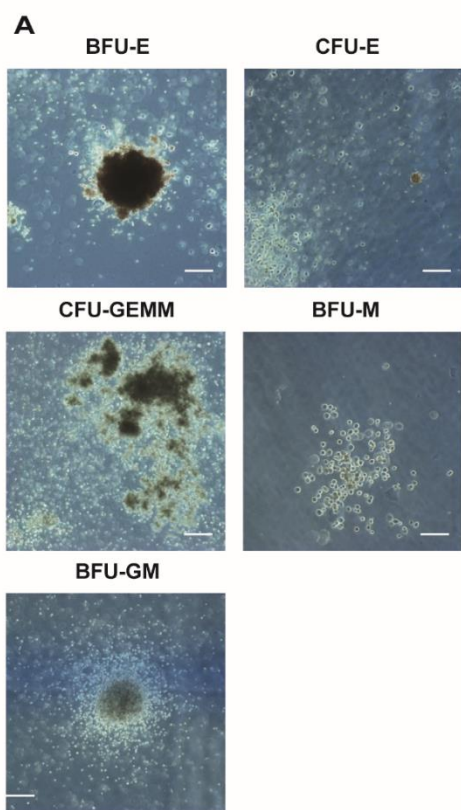
B



Supplementary Figure S1: Expression of CD34 and CD43 in HPSCs differentiated from several hiPSCs sources

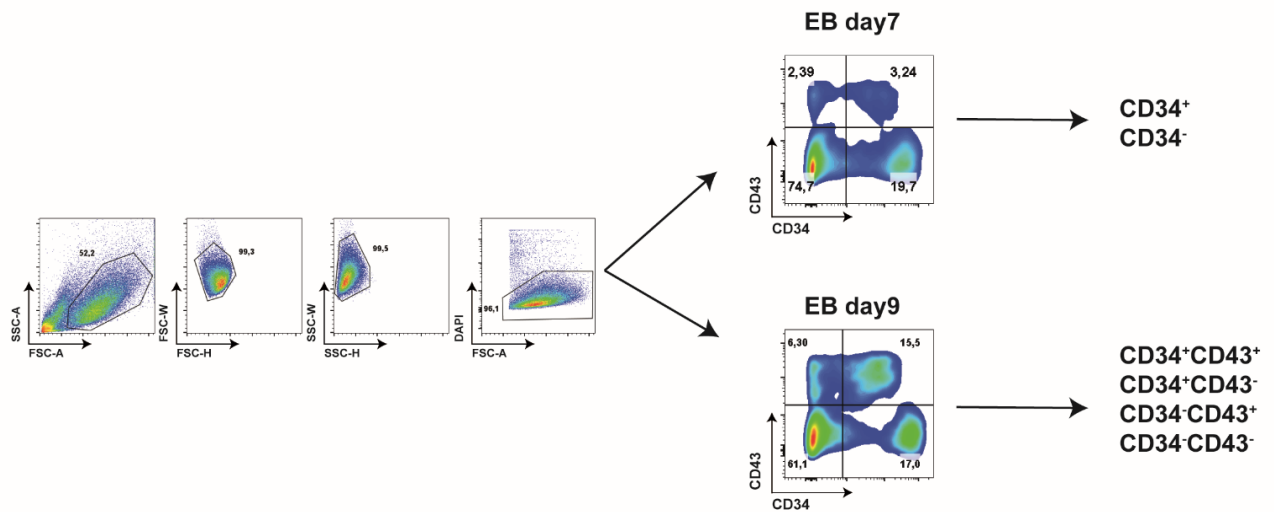
A, Percent of total cells from day 9 EBs expressing CD34, mean +/- SEM are represented. Mann Whitney test, * $p < 0,05$, ** $p < 0,001$, *** $p < 0,0001$. **B**, Percent of total cells from day 9 EBs

expressing CD34 and CD43, mean \pm SEM are represented. Mann Whitney test, * $p < 0,05$, ** $p < 0,001$, *** $p < 0,0001$.



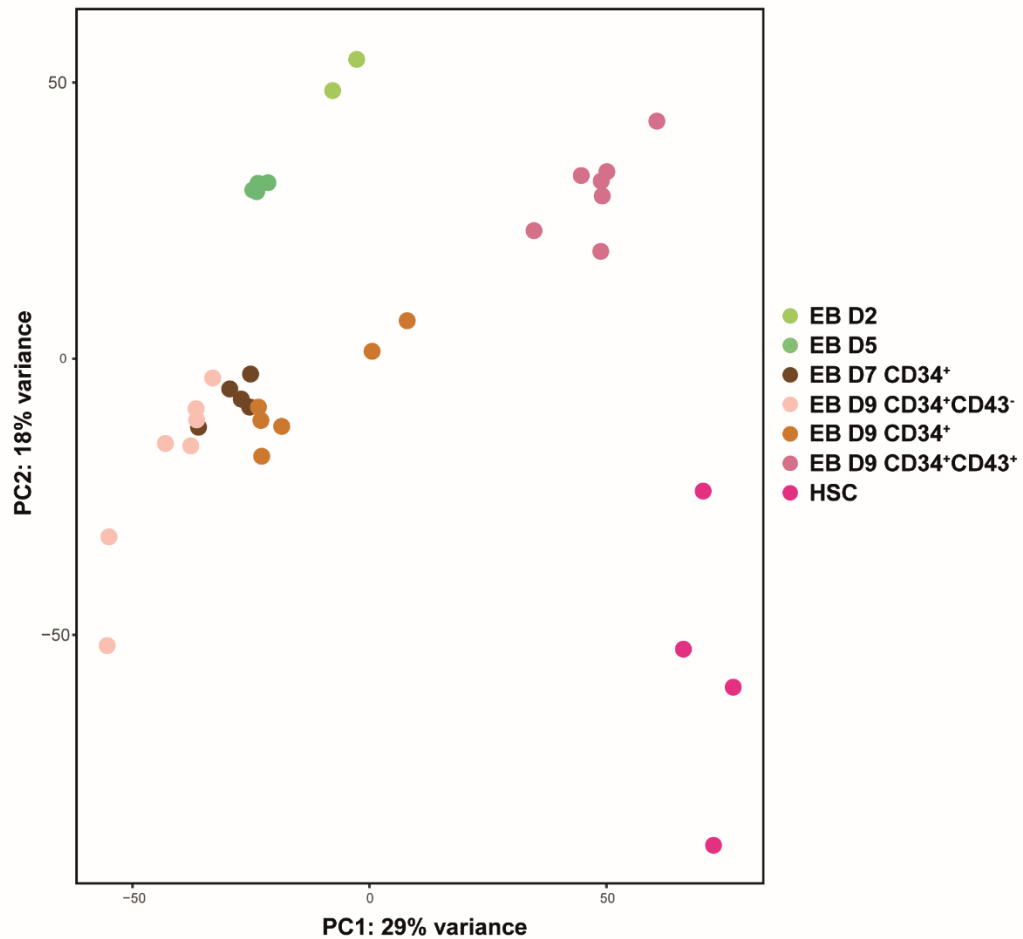
Supplementary Figure S2: Multipotent HPSCs derived from hPSCs

A, Representative photos of blood colonies BFU-E, CFU-E, CFU-GEMM, CFU-M and CFU- GM from hPSCs. **B**, Total colonies number per 1000 CD34+ cells seeded cells in methyl-cellulose in indicated cell lines. **C**, After 14 days in methyl-cellulose, the cells are analyzed by flow-cytometry for the expression of CD14, CD15 and CD235a markers and according to the following gating strategy. The combination of these markers allows to determine the different blood colonies. **D**, Summary of flow-cytometry analysis of CFU assay blood colonies for the indicated cell lines.



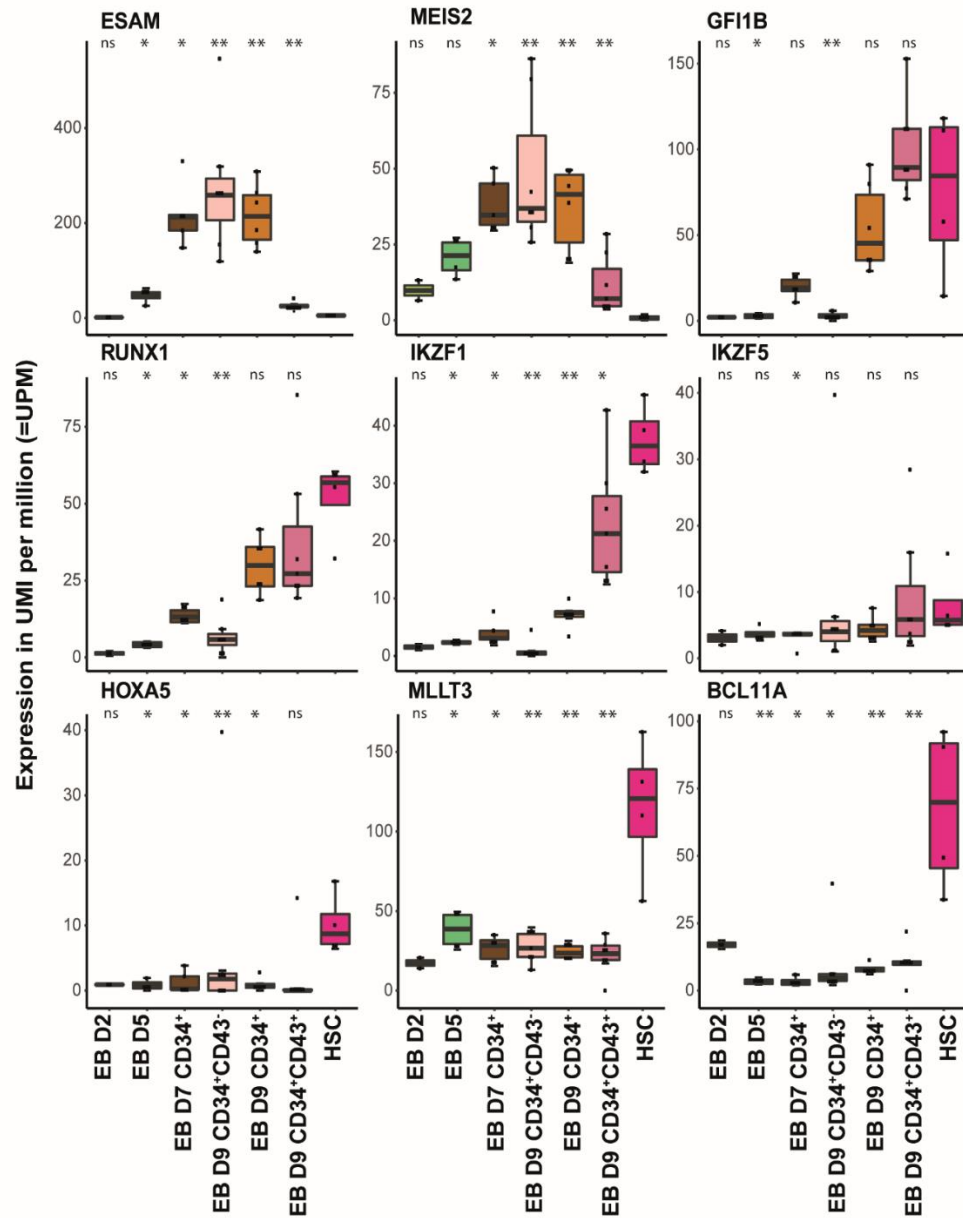
Supplementary Figure S3: Gating strategy of multipotent HPSCs derived from hPSCs sorting

Gating strategy for cell sorting by FACS Aria. Cells were selected on morphology, exclusion of doublets and dead cells (DAPI), and expression of CD34 et CD43.



Supplementary Figure S4: Principal component analysis during HPSCs differentiation

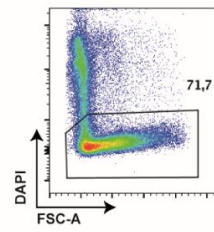
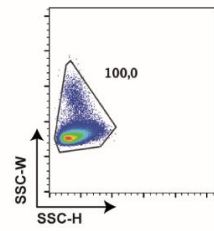
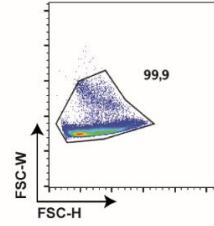
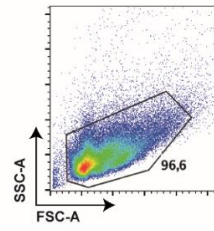
PCA analysis of EB D2 (n=2), EB D5 (n=4), EB D7 CD34⁺ (n=5), EB D9 CD34⁺CD43⁻ (n=7), EB D9 CD34⁺ (n=6), EB D9 CD34⁺CD43⁺ (n=7) and HSC (n=4) during differentiation. PC1 and PC2 are displayed for differentiated cells. PC1 accounted for 29% of the variance and explained the stages of differentiation. PC2 accounted for 18% variance and segregated the primary cells from the differentiated cells.



Supplementary Figure S5: Molecular characterization of HSPCs derived from hPSCs

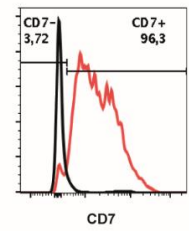
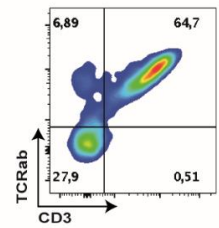
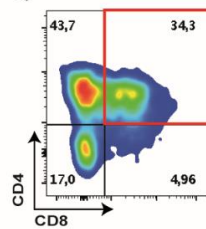
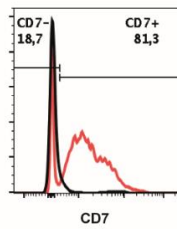
Gene expression levels of indicated lineage markers are shown for EB D2 (n=2), EB D5 (n=4), EB D7 CD34+ (n=5), EB D9 CD34+CD43- (n=7), EB D9 CD34+ (n=6) and EB D9 CD34+CD43+ (n=7) samples and HSC (n=4) are included as control. Expression levels are given as number of

transcripts per million of mRNA molecules. In each boxplot, the top and bottom of the box represent the third and first quartile, respectively; the band represents the median; and error bars show the interquartile range. A Wilcoxon-Mann-Whitney statistical test was performed for each sample, with HSC taken as the reference group. Asterisks indicate statistical significance of the difference: *p value < 0.05, **p value < 0.01, ***p value < 0.001.



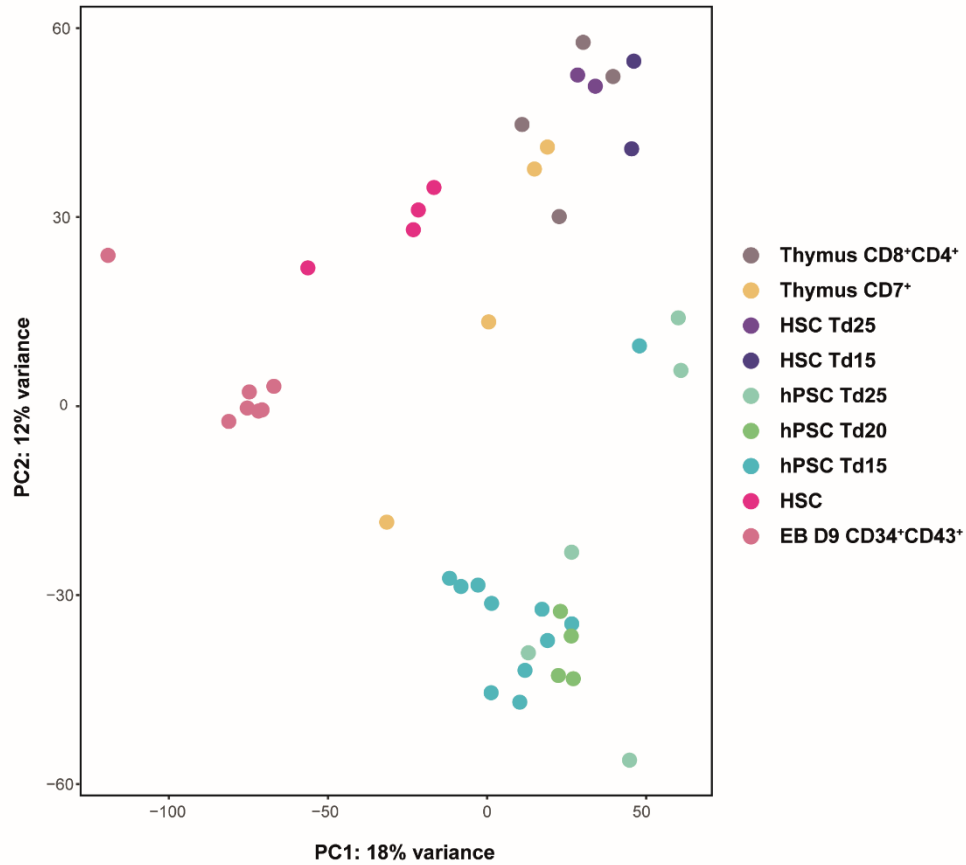
CD7⁺ and CD7⁻
SORT

CD8⁺CD4⁻
SORT



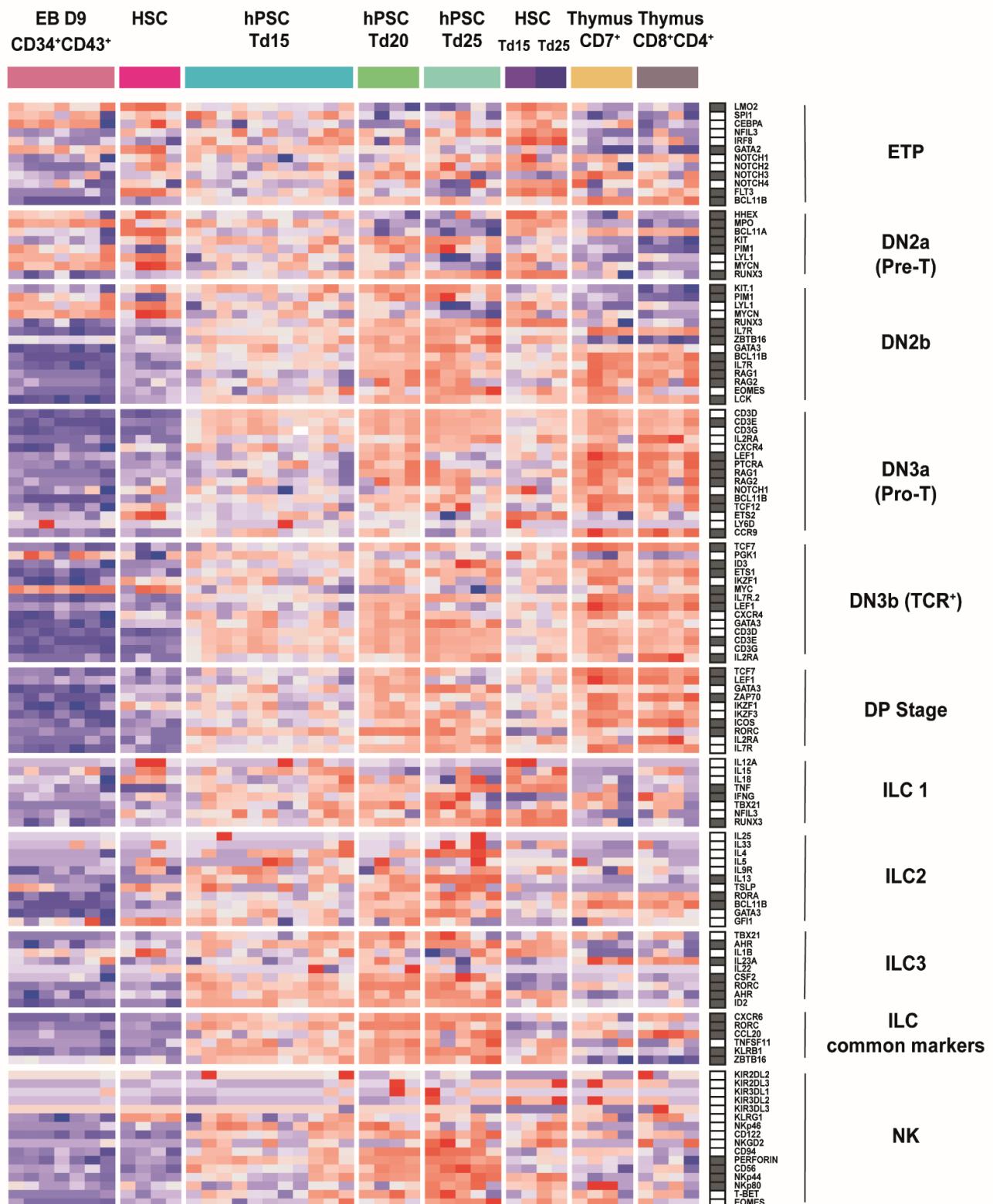
Supplementary Figure S6: Gating strategy of thymocytes sorting

Gating strategy for cell sorting by FACS Aria. Cells were selected on morphology, exclusion of doublets and dead cells (DAPI), and expression of CD7 or CD8 et CD4. 96,3% of CD8⁺CD4⁺ expressed CD7 and 64,7% CD3 and TCRαβ.



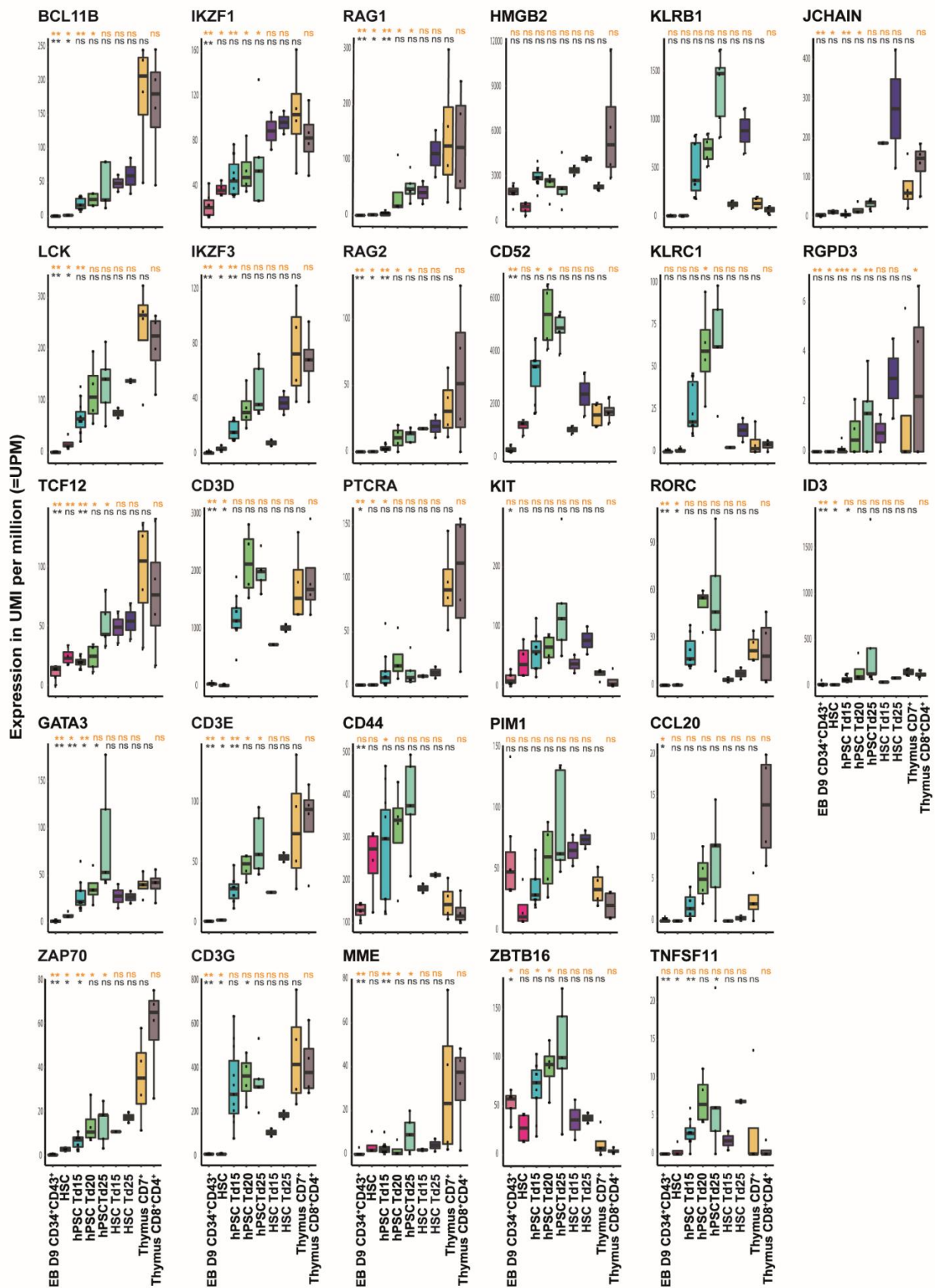
Supplementary Figure S7: Principal component analysis during T cells differentiation

PCA analysis of EB D9 CD34+CD43+ (n=7), HSC n=4, hPSC Td15 (n=11), hPSC Td20 (n=4), hPSC Td25 (n=5), HSC Td15 (n=2), HSC Td25 (n=2), thymocytes CD7+ (n=4) and thymocytes CD8+CD4+ (n=4) during differentiation. PC1 and PC2 are displayed for differentiated cells. PC1 accounted for 18% of the variance and explained the stages of differentiation. PC2 accounted for 12% variance and segregated the primary cells from the differentiated cells.



Supplementary Figure S8: T-cell progenitor derived from hPSC are stuck at the DN3a thymocyte stage

Gene expression heatmaps of selected markers associated in T-cells, Innate cells like (ILCs) and Natural Killer cells (NKs) development and function are shown defined by DGE-seq.



Supplementary Figure S9: Molecular characterization of T-cell progenitors derived from hPSCs

Gene expression levels of indicated lineage markers are shown for EB D9 CD34+CD43+ (n=7), HSC n=4, hPSC Td15 (n=11), hPSC Td20 (n=4), hPSC Td25 (n=5), HSC Td15 (n=2), HSC Td25 (n=2) and thymocytes CD7+ (n=4) and CD8+CD4+ (n=4) are included as control. Expression levels are given as number of transcripts per million of mRNA molecules. In each boxplot, the top and bottom of the box represent the third and first quartile, respectively; the band represents the median; and error bars show the interquartile range. A Wilcoxon-Mann-Whitney statistical test was performed for each sample, with thymocytes CD7+ (orange) and CD8+CD4+ (grey) taken as the reference group. Asterisks indicate statistical significance of the difference: *p value < 0.05, **p value < 0.01, ***p value < 0.001.

Supplementary Figure S10 (related to supplementary figure 9): Summary of Statistical Significance of Difference for each sample in T-cell differentiation

Gene expression levels of indicated lineage markers are shown for EB D9 CD34+CD43+ (n=7), HSC n=4, hPSC Td15 (n=11), hPSC Td20 (n=4), hPSC Td25 (n=5), HSC Td15 (n=2), HSC Td25 (n=2) and thymocytes CD7+ (n=4) and CD8+CD4+ (n=4) are included as control. A WilcoxonMann-Whitney statistical test was performed for each sample. Asterisks indicate statistical significance of the difference: *p value < 0.05, **p value < 0.01, ***p value < 0.001, ****p value <0.0001.