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Supplemental Information

In Vivo Tracking of Human Hematopoiesis Reveals Patterns of Clonal Dynamics during Early and Steady-State Reconstitution Phases

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Figure S1

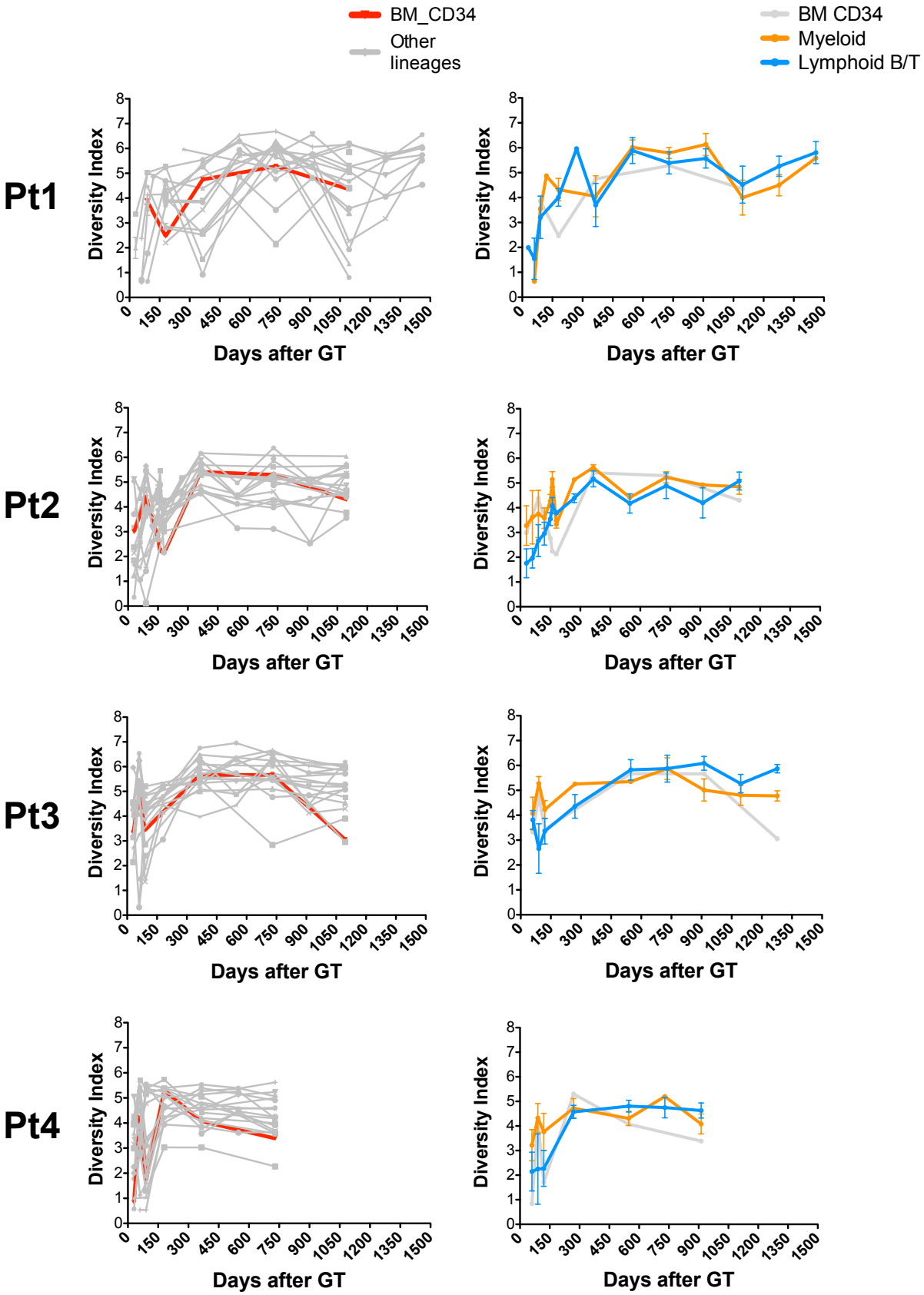

BM_CD34
Other lineages
BM CD34
Myeloid
Lymphoid B/T
Pt1
Pt2
Pt3
Pt4
Diversity Index
Days after GT
0
150
300
450
600
750
900
1050
1200
1350
1500
1
2
3
4
5
6
7
8

Figure S2

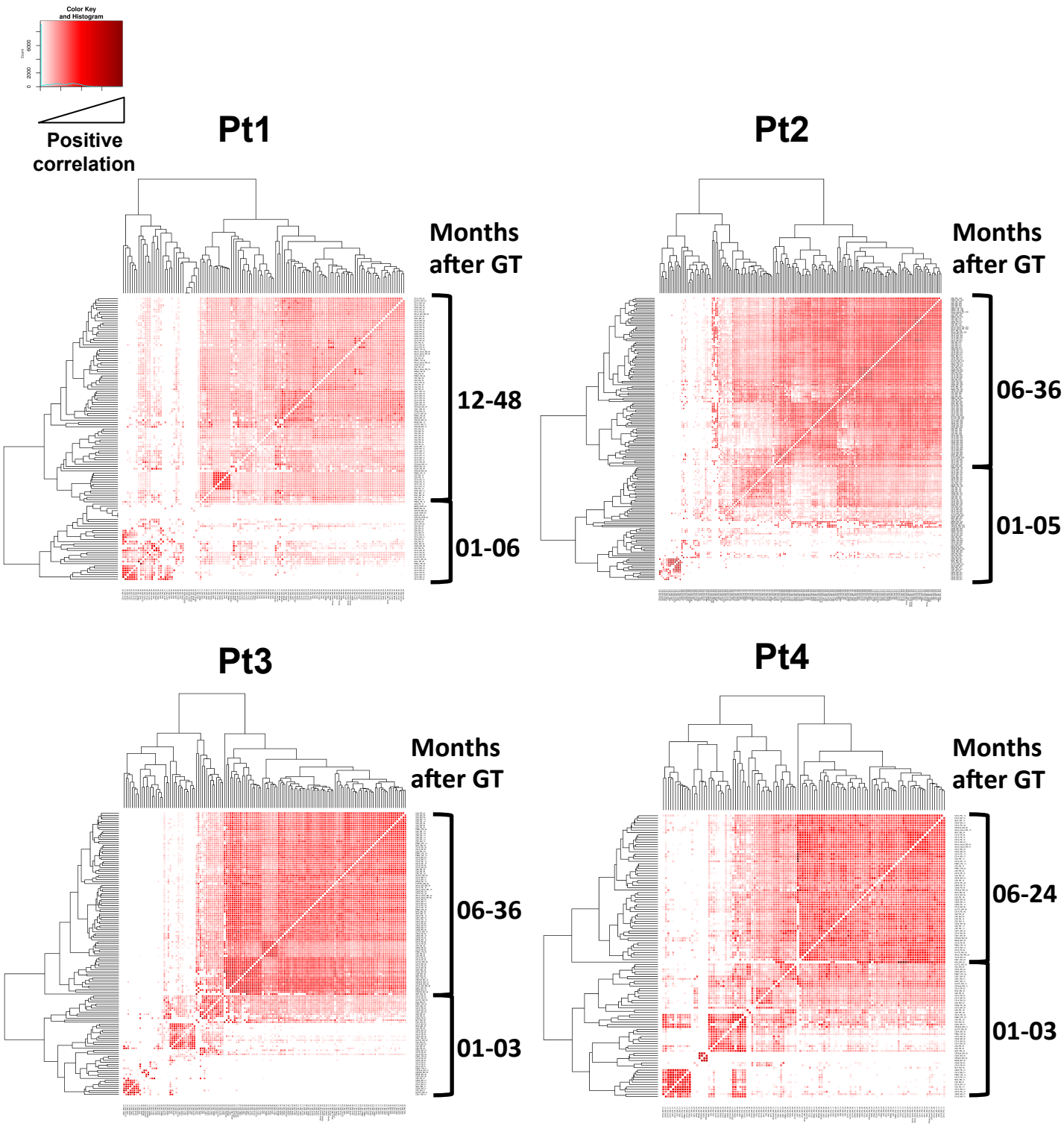

Color Key and Histogram
Positive correlation
Pt1
Months after GT
12-48
01-06
Pt2
Months after GT
06-36
01-05
Pt3
Months after GT
06-36
01-03
Pt4
Months after GT
06-24
01-03

Figure S3

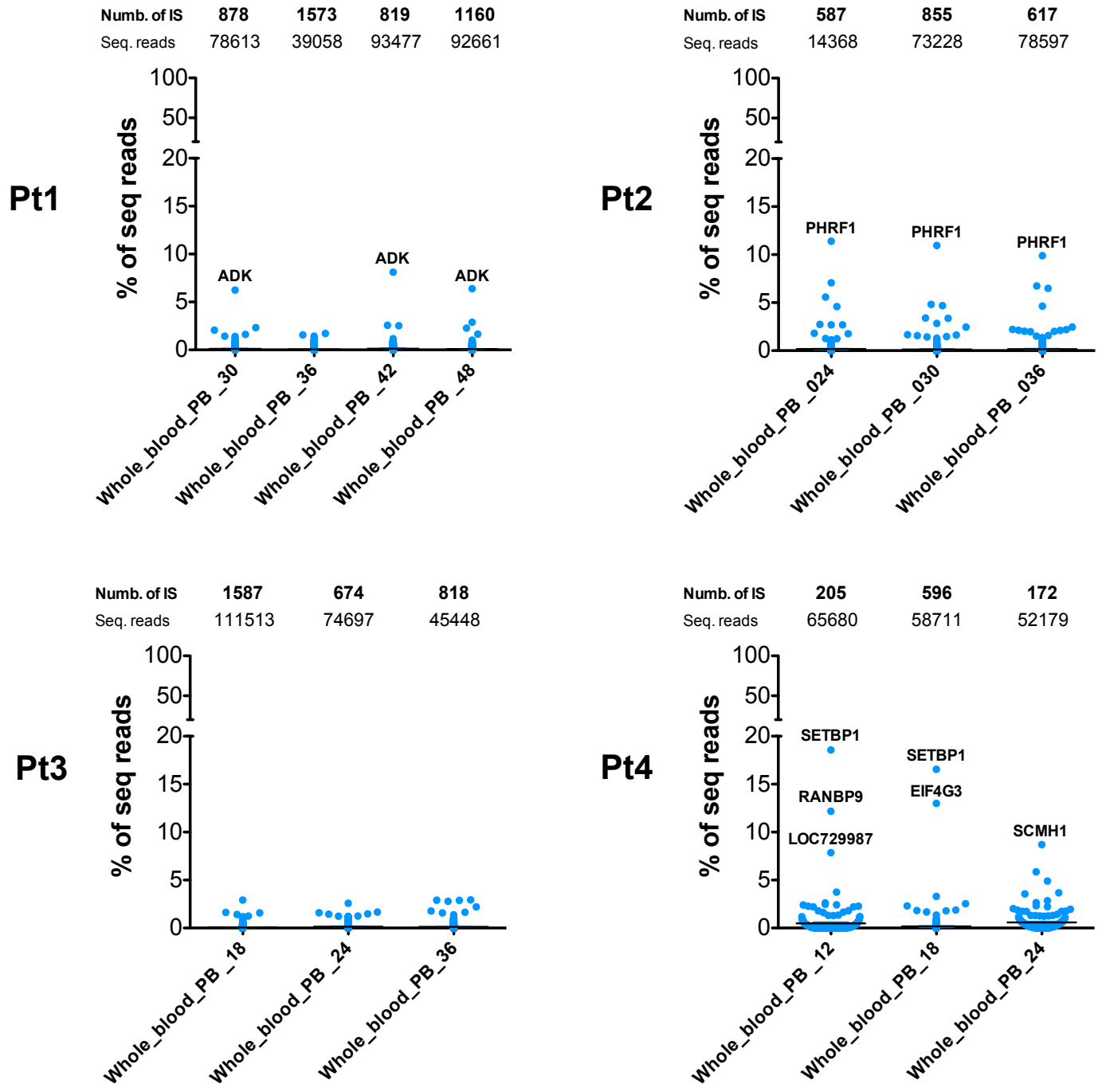
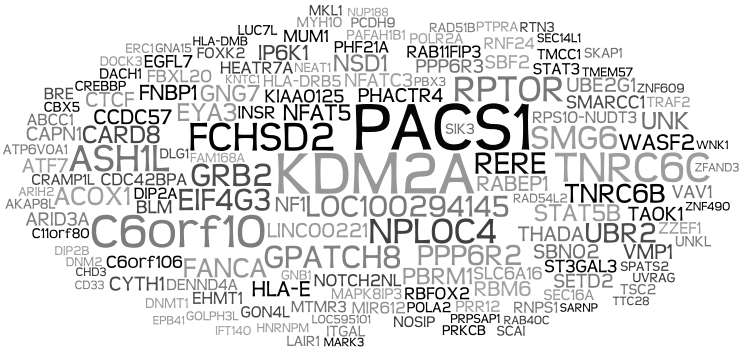
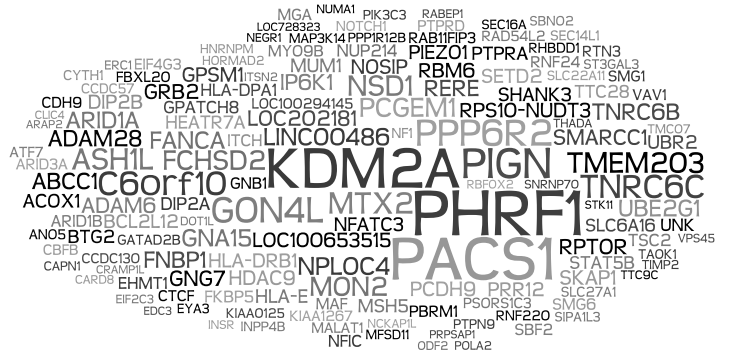

Pt1
Numb. of IS 878 1573 819 1160
Seq. reads 78613 39058 93477 92661
% of seq reads
100
50
20
15
10
5
0
ADK
ADK
ADK
Whole_blood_PB _30
Whole_blood_PB _36
Whole_blood_PB _42
Whole_blood_PB _48
Pt2
Numb. of IS 587 855 617
Seq. reads 14368 73228 78597
% of seq reads
PHRF1
PHRF1
PHRF1
Whole_blood_PB _024
Whole_blood_PB _030
Whole_blood_PB _036
Pt3
Numb. of IS 1587 674 818
Seq. reads 111513 74697 45448
% of seq reads
Whole_blood_PB _18
Whole_blood_PB _24
Whole_blood_PB_36
Pt4
Numb. of IS 205 596 172
Seq. reads 65680 58711 52179
% of seq reads
SETBP1
RANBP9
LOC729987
SETBP1
EIF4G3
SCMH1
Whole_blood_PB _12
Whole_blood_PB_18
Whole_blood_PB_24

Figure S4

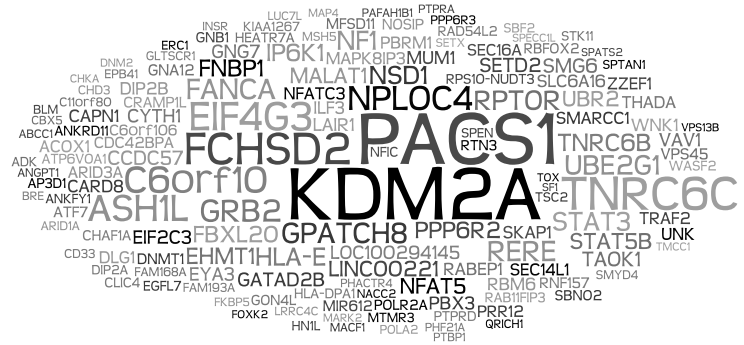
Pt1



Pt2



Pt3



Pt4

Table S1

IS from CFCs	*shared only with Myeloid cells*	*shared only with Lymphoid cells*	*bipotent*	*not shared*
Pt1_36mo	13.0	8.7	23.9	54.3
Pt2_24mo	28.0	12.0	16.0	44.0
Pt3_36mo	14.4	1.8	55.0	28.8
Pt4_24mo	14.3	7.1	53.6	25.0

Supplementary Figures Legends

Figure S1, related to Figure 1: Diversity index of different lineages and samples from BM and PB samples purified over time (left panel). Average diversity index of myeloid cells (orange line), lymphoid B and T cells (blue line), and BM CD34+ cells (gray line) over time (right panel).

Figure S2, related to Figure 1: Heatmaps showing pairwise positive associations of IS similarities among different lineages over time (see supplementary material for details). Red color intensity is proportional to increasing similarities. Right brackets summarize the most represented timepoints over the two main branches deriving from unsupervised clustering.

Figure S3, related to Figure 4: Dot plots showing the relative abundance of sequence counts (as percentage on the total) of IS retrieved from whole blood samples at different timepoints after GT (e.g. whole blood isolated from PB at 12 months after GT is reported as Whole_blood_PB_12). Number of IS and relative sequence counts are reported above for each sample/timepoint.

Figure S4, related to Figure 4: Word clouds showing the single closest gene to each integration site collected over the entire follow-up from the four WAS GT patients (top 150 hit genes). The size of the gene name is proportional to the number of IS detected in its proximity.

Table S1, related to Figure 2: Table showing the percentage of IS from CFC shared with only myeloid, only lymphoid and both myeloid and lymphoid lineages (bipotent) from the same timepoint (months after GT). The IS fractions detected only in CFC at each given time is labeled as “not shared”.

Supplemental Data File 1: Word file containing additional details of the technical procedures and protocols employed for the analyses shown in the main manuscript related to Figure 1-4 and to the experimental methods.