

Supplementary Tables

Table S1. The antibody information for FACS analysis

Marker	Fluorescence	Species	Brand	Clone	Item Number	RRID
CD45.1	V450	mouse	Invitrogen	A20	48-0453-82	AB_1272189
CD45.2	V500	mouse	BD	104	562130	AB_10897142
CD3	BV421	mouse	BioLegend	17A2	100228	AB_2562553
CD4	APC-H7	mouse	Biolegend	GK1.5	100414	AB_312699
CD8	BV650	mouse	BD	53-6.7	563234	AB_2738084
CD44	PE-CY7	mouse	Biolegend	IM7	103030	AB_830787
CD62L	PerCP-Cy5.5	mouse	BioLegend	MEL-14	104431	AB_2187123
Ly6C	BV570	mouse	BioLegend	HK1.4	128030	AB_2562617
CD61	AF488	mouse	Biolegend	2C9.G2	104311	AB_2128907
CD25	PE	mouse	BioLegend	A18246A	113703	AB_2927943
CD24	PE-Dazzle594	mouse	Biolegend	M1/69	101837	AB_2566731
Qa2	AF647	mouse	BioLegend	695H1-9-9	121707	AB_571988
Zombie yellow	-	mouse	BioLegend	-	423104	-
CD4	AF700	mouse	BioLegend	GK1.5	100430	AB_493699
CD69	BV421	mouse	Biolegend	H1.2F3	104545	AB_2686969
H-2B	PerCP-ef710	mouse	Invitrogen	AF6-88.5.5.3	46-5958-82	AB_2016714
TCR β	BV711	mouse	BioLegend	H57-597	109243	AB_2629564
CD3	AF700	human	Biolegend	OKT3	317340	AB_2563408
CD4	PerCP-Cy5.5	human	Biolegend	RPA-T4	300530	AB_893322
CD8	BV510	human	BioLegend	SK1	344732	AB_2564624

CD45RA	PE-CY7	human	BioLegend	HI100	304126	AB_10708879
CCR7	BV421	human	Biolegend	G043H7	353208	AB_11203894
CD31	APC	human	BioLegend	WM59	303116	AB_1877151
CD103	BV605	human	Biolegend	Ber-ACT8	350218	AB_2564283
CD38	PE-Dazzle594	human	Biolegend	HB-7	356630	AB_2650757
CD61	PE	human	Biolegend	VI-PL2	336405	AB_1227583

Table S2. The information of primer and probe sequences

Probe/Primer	Sequence
SJ TREC forward primer	5'-CAC ATC CCT TTC AAC CAT GCT-3'
SJ TREC reverse primer	5'-TGC AGG TGC CTA TGC ATC A-3'
SJ TREC Probe	5'-FAM-ACA CCT CTG GTT TTT GTA AAG GTG CCC ACT TAMRA-3'
The housekeeper gene TRAC forward primer	5'-TGG CCT AAC CCT GAT CCT CTT-3'
The housekeeper gene TRAC forward primer reverse primer	5'-GGA TTT AGA GTC TCT CAG CTG GTA CAC-3'
TRAC Probe	5'-FAM-TCC CAC AGA TAT CCA GAA CCC TGA CCC TAMRA-3'

Table S3. The gene information of the scoring gene dataset

Gene dataset	Genes
Mouse_Stemness_gene_signature	<i>Tcf7/Lef1/Id3/Klf2/Ilf7r/Sell/Ccr7/Cd27/Cd28</i> <i>/Slamf6/Foxo1/Bcl2/Bcl6/Sox4</i>
Mouse_RTE_gene_signature	<i>Cd24a/Cd38/Ccr9/Ikzf2/Pecam1/Dntt/Sell/</i> <i>H2-Q7/Ilf2ra/Cxcr3/Tox/Tcf7/Sox4</i>
Human_Stemness_gene_dataset	<i>Tcf7/Lef1/Id3/Klf2/Ilf7r/Sell/Ccr7/Cd27/Cd28</i> <i>/Slamf6/Foxo1/Bcl2/Bcl6/Sox4</i>
Human_Naïve T, RTE, and CD61-related signatures gene dataset	<i>CD3D/CD3E/CD4/CD8A/CD8B/CD27/CCR7/LEF1/SELL</i> <i>/IL7R/PTK7/PECAM1/CD38/ITGAE/ITGB3</i>
Human RTE_gene_dataset	<i>SOX4/IKZF2/TOX/CD38/PTK7/CR2/CR1/AOAH</i>

Table S4. Baseline characteristics and clinical outcomes of the post-HSCT validation cohort

Variables	Total (n = 54)	6-month cohort (n = 23)	12-month cohort (n = 31)	P
Recipient age, Median (IQR)	46.50 (36.00, 55.00)	51.00 (33.50, 54.00)	46.00 (36.00, 55.00)	0.930
Donor age , Median (IQR)[‡]	36.50 (28.75, 52.25)	32.00 (30.50, 36.50)	38.00 (28.00, 53.00)	0.560
TNC (×10⁸/kg), Median (IQR)	8.82 (7.78, 9.68)	9.20 (8.17, 9.96)	8.52 (7.45, 9.36)	0.059
CD34⁺ (×10⁶/kg), Median (IQR)	4.13 (2.75, 5.09)	4.19 (2.92, 6.12)	3.55 (2.67, 4.99)	0.421
Recipient gender, n (%)				0.784
<i>Female</i>	30 (55.56)	12 (52.17)	18 (58.06)	
<i>Male</i>	24 (44.44)	11 (47.83)	13 (41.94)	
Donor gender, n (%)				0.583
<i>Female</i>	23 (42.59)	11 (47.83)	12 (38.71)	
<i>Male</i>	31 (57.41)	12 (52.17)	19 (61.29)	
Gender match, n (%)				0.774
<i>No</i>	19 (35.19)	9 (39.13)	10 (32.26)	
<i>Yes</i>	35 (64.81)	14 (60.87)	21 (67.74)	
Diagnosis, n (%)				0.521
<i>AML</i>	37 (68.52)	15 (65.22)	22 (70.97)	
<i>MDS</i>	15 (27.78)	8 (34.78)	7 (22.58)	
<i>CMML</i>	1 (1.85)	0 (0.00)	1 (3.23)	
<i>MPAL</i>	1 (1.85)	0 (0.00)	1 (3.23)	
Donor type, n (%)				1.000
<i>Haploidentical</i>	43 (79.63)	18 (78.26)	25 (80.65)	
<i>Matched (sibling/unrelated)</i>	11 (20.37)	5 (21.74)	6 (19.35)	
DLI, n (%)				0.384
<i>No</i>	48 (88.89)	19 (82.61)	29 (93.55)	
<i>Yes</i>	6 (11.11)	4 (17.39)	2 (6.45)	
Acute GVHD, n (%)				0.139
<i>No aGVHD</i>	30 (55.56)	14 (60.87)	16 (51.61)	
<i>Grade I-II</i>	22 (40.74)	7 (30.43)	15 (48.39)	
<i>Grade III-IV</i>	2 (3.70)	2 (8.70)	0 (0.00)	
Chronic GVHD, n (%)				0.936

Variables	Total (n = 54)	6-month cohort (n = 23)	12-month cohort (n = 31)	P
<i>No cGVHD</i>	16 (29.63)	6 (26.09)	10 (32.26)	
<i>Mild</i>	17 (31.48)	7 (30.43)	10 (32.26)	
<i>Moderate</i>	15 (27.78)	7 (30.43)	8 (25.81)	
<i>Severe</i>	6 (11.11)	3 (13.04)	3 (9.68)	
Relapse, n (%)				1.000
<i>No</i>	38 (70.37)	16 (69.57)	22 (70.97)	
<i>Yes</i>	16 (29.63)	7 (30.43)	9 (29.03)	
<i>Time from HSCT to relapse, months; Median (Min, Max)*</i>	4.89 (2.79, 10.32)	3.01 (2.79, 6.70)	7.97 (2.89, 10.32)	0.020

* Time to relapse was calculable for 14/16 relapsed patients (2 patients with a second HSCT for prior relapse had ambiguous relapse dates relative to the current transplant and were excluded from this calculation).

‡ Donor age was available for 20/54 patients (3/23 in the 6-month cohort, 17/31 in the 12-month cohort).

TNC, total nucleated cell dose; DLI, donor lymphocyte infusion; GVHD, graft-versus-host disease; HSCT, hematopoietic stem cell transplantation.

P values: Mann-Whitney U test for continuous variables; chi-square or Fisher's exact test for categorical variables (6-month vs 12-month cohort).

The 6-month and 12-month cohorts were sampled cross-sectionally (not paired); only 3 of 54 patients contributed samples at both time points.