

Supplementary Table 1 Univariable analysis for risk of 1-year relapse-related and all-cause mortality

Variable	Relapse-related mortality		All-cause mortality	
	sHR (95%CI)	p-Value	sHR (95%CI)	p-Value
Age at HCT	1.00 (1.00-1.01)	0.487	1.02 (1.01-1.02)	<0.001
Sex				
Female	1.00 (referent)	— <sup>b</sup>	1.00 (referent)	— <sup>b</sup>
Male	0.88 (0.63-1.22)	0.445	1.07 (0.83-1.38)	0.624
Race and ethnicity		0.102		0.241
Non-Hispanic White	1.00 (referent)	— <sup>b</sup>	1.00 (referent)	— <sup>b</sup>
Hispanic	1.01 (0.70-1.46)	0.954	1.15 (0.86-1.53)	0.343
Asian	1.49 (0.95-2.35)	0.085	1.47 (1.02-2.12)	0.041
Other	0.49 (0.20-1.24)	0.134	1.17 (0.71-1.91)	0.544
Insurance status at time of HCT		0.484		0.220
Private	1.00 (referent)	— <sup>b</sup>	1.00 (referent)	— <sup>b</sup>
Public	0.97 (0.68-1.37)	0.84	1.20 (0.93-1.55)	0.172
Uninsured or unknown	0.57 (0.23-1.42)	0.229	0.78 (0.40-1.44)	0.393
Diagnosis		0.776		0.001
Acute lymphoblastic leukemia	1.00 (referent)	— <sup>b</sup>	1.00 (referent)	— <sup>b</sup>
Acute myeloid leukemia	1.28 (0.83-1.96)	0.259	0.95 (0.68-1.32)	0.739
Lymphoma	1.18 (0.59-2.35)	0.650	0.80 (0.45-1.44)	0.459
Myelodysplastic syndrome	1.13 (0.66-1.93)	0.670	1.60 (1.12-2.28)	0.010
Other	0.97 (0.51-1.83)	0.919	0.63 (0.37-1.09)	0.096
Conditioning				
Myeloablative	1.00 (referent)	— <sup>b</sup>	1.00 (referent)	— <sup>b</sup>
Reduced intensity	1.05 (0.76-1.46)	0.761	1.35 (1.04-1.74)	0.022
Risk Relapse				
Low	1.00 (referent)	— <sup>b</sup>	1.00 (referent)	— <sup>b</sup>
High	2.04 (1.48-2.83)	<0.001	1.68 (1.31-2.16)	<0.001
GVHD prophylaxis		0.424		0.032
Tacrolimus/Sirolimus	1.00 (referent)	— <sup>b</sup>	1.00 (referent)	— <sup>b</sup>
Calcineurin inhibitor + MMF or MTX	1.04 (0.67-1.59)	0.873	1.27 (0.91-1.78)	0.166
Post-HCT cyclophosphamide	0.69 (0.42-1.12)	0.135	1.51 (1.12-2.04)	0.007
Other	0.54 (0.07-3.96)	0.545	0.40 (0.05-2.99)	0.370
Performance status <80	0.97 (0.95-0.99)	<0.001	0.97 (0.95-0.98)	<0.001
HCT-CI score	0.97 (0.89-1.05)	0.408	1.10 (1.04-1.17)	0.001
CMV status				
Negative	1.00 (referent)	— <sup>b</sup>	1.00 (referent)	— <sup>b</sup>
Positive	1.13 (0.69-1.84)	0.621	1.28 (0.86-1.90)	0.232
HLA Match		0.216		0.004
Matched	1.00 (referent)	— <sup>b</sup>	1.00 (referent)	— <sup>b</sup>
Haploididential	0.78 (0.44-1.36)	0.380	1.72 (1.24-2.38)	0.001
Mismatched	1.31 (0.87-1.97)	0.194	1.31 (0.94-1.81)	0.109
Distance to City of Hope	1.00 (1.00-1.00)	1.00	1.00 (1.00-1.00)	0.134
Overall SVI <sup>a</sup>	0.94 (0.67-1.31)	0.697	1.26 (0.98-1.63)	0.070
SVI socioeconomic status <sup>a</sup>	0.87 (0.61-1.25)	0.443	1.26 (0.97-1.62)	0.080
SVI household composition and disability <sup>a</sup>	0.88 (0.61-1.25)	0.467	1.24 (0.96-1.60)	0.096
SVI minority status and language <sup>a</sup>	0.82 (0.57-1.17)	0.269	1.24 (0.96-1.60)	0.100
SVI housing and transportation <sup>a</sup>	0.90 (0.63-1.28)	0.560	1.18 (0.91-1.52)	0.215

<sup>a</sup>Analysis conducted for highest tertile of SVI compared to lower two tertiles as referent groups<sup>b</sup>Not applicable

GVHD= graft-versus-host disease; MMF= mycophenolate mofetil; MTX= methotrexate; HCT-CI= hematopoietic cell transplantation-comorbidity index; CMV= cytomegalovirus; HLA= human leukocyte antigen; SVI= social vulnerability index; sHR= subdistribution hazard ratio; CI= confidence interval

Supplementary Table 2 Multivariable analysis for risk of 1-year relapse-related and all-cause mortality<sup>a</sup>

Covariable	sHR (95%CI)	p-Value
Relapse-related mortality		
Relapse Risk		
Low	1.00 (referent)	— <sup>d</sup>
High	1.54 (1.35-2.64)	<0.001
Performance status	0.97 (0.96-0.99)	<0.001
SVI overall(highest tertile) <sup>b,c</sup>	0.95 (0.67-1.33)	0.747
SVI socioeconomic status (highest tertile) <sup>b,c</sup>	0.88 (0.62-1.24)	0.876
SVI household composition and disability (highest tertile) <sup>b,c</sup>	0.89 (0.63-1.27)	0.892
SVI minority status and language (highest tertile) <sup>b,c</sup>	0.83 (0.59-1.19)	0.317
SVI housing and transportation (highest tertile) <sup>b,c</sup>	0.92 (0.65-1.31)	0.651
All-cause mortality		
Age at HCT	1.02 (1.01-1.02)	<0.001
Relapse Risk		
Low	1.00 (referent)	— <sup>d</sup>
High	1.53 (1.19-1.97)	0.001
Performance status	0.97 (0.96-0.98)	<0.001
HCT-CI score	1.09 (1.03-1.16)	0.005
HLA Match		
Matched	1.00 (referent)	— <sup>d</sup>
Haploididential	1.89 (1.36-2.63)	<0.001
Mismatched	1.50 (1.07-2.10)	0.019
SVI overall (highest tertile) <sup>b,c</sup>	1.37 (1.05-1.78)	0.022
SVI socioeconomic status (highest tertile) <sup>b,c</sup>	1.38 (1.06-1.81)	0.017
SVI household composition and disability (highest tertile) <sup>b,c</sup>	1.32 (1.02-1.72)	0.035
SVI minority status and language (highest tertile) <sup>b,c</sup>	1.33 (1.01-1.74)	0.040
SVI housing and transportation (highest tertile) <sup>b,c</sup>	1.25 (0.96-1.62)	0.097

<sup>a</sup>Each SVI component was added independently to the baseline clinical model<sup>b</sup>Reference: lower two SVI tertiles

HCT-CI= hematopoietic cell transplantation-comorbidity index; CMV= cytomegalovirus; HLA= human leukocyte antigen; SVI= social vulnerability index; sHR= subdistribution hazard ratio; CI= confidence interval

<sup>c</sup>SVI overall and SVI themes were each adjusted for the preceding non-SVI variables, but not for each other<sup>d</sup>Not applicable