LETTER TO THE EDITOR

Expedited evaluation of hereditary hematopoietic malignancies in the setting of stem cell transplantation

Authors

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SUPPLEMENTARY MATERIALS FOR:

Expedited evaluation for hereditary hematopoietic malignancies in the setting of stem cell transplantation

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Figure S1.

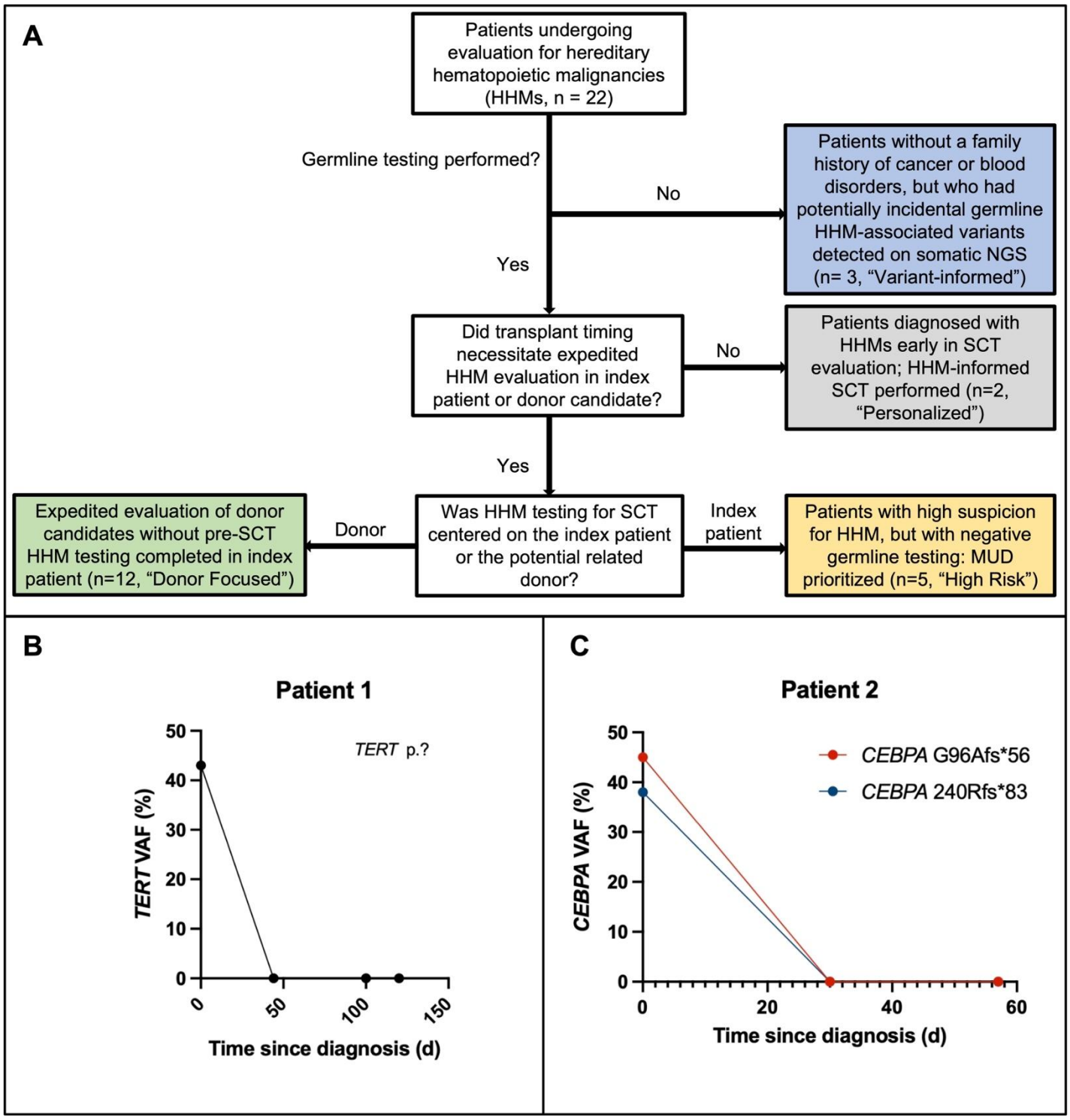

Figure S1. (A): Flow diagram for classification of patients and donor candidates undergoing expedited evaluation for hereditary hematopoietic malignancies in the setting of stem cell transplant. (B & C): longitudinal variant allele frequency (VAF) measurements for genes that raised suspicion for an HHM on diagnostic somatic tumor sequencing in patients 1 (B)

and 2 (B). These patients did not have high-risk family histories that were concerning for HHMs. The disappearance of detectable mutations with induction therapy strongly suggested these potentially incidental germline variants were of somatic origin. Therefore, transplantation was not delayed while formal HHM testing was performed. HHM: hereditary hematopoietic malignancy.

Table S1. Genes analyzed for donor-only sequencing.

Genes analyzed for donor-only sequencing.
AIP, ALK, ANKRD26, APC, APOA1, APOA2, ARID1A, ATM, AXIN2, BAP1, BARD1, BLM, BMPR1A, BRCA1, BRCA2, BRIP1, BTK, CARD11, CASP10, CASR, CBL, CD27, CD40LG, CD70, CDC73, CDH1, CDK4, CDKN1B, CDKN1C, CDKN2A, CEBPA, CHEK2, CSF3R, CST3, CTLA4, CTNNA1, CTPS1, DDX41, DICER1, DIS3, DIS3L2, DOCK8, EGFR, EPCAM, ERCC6L2, ETV6, FGA, FH, FLCN, GATA2, GPC3, GREM1, GSN, HOXB13, HRAS, IKZF1, ITK, JAK2, KDM1A, KIT, LYZ, MAGT1, MAX, MBD4, MECOM, MEN1, MET, MITF, MLH1, MPL, MRTFA, MSH2, MSH3, MSH6, MUTYH, NAF1, NBN, NF1, NF2, NPAT, NPM1, NTHL1, PALB2, PAX5, PDGFRA, PGM3, PHOX2B, PIK3CD, PMS2, POLD1, POLE, POT1, PRKAR1A, PTCH1, PTEN, PTPN11, RAD50, RAD51C, RAD51D, RASGRP1, RB1, RBBP6, RBM8A, RECQL4, RET, RTEL1, RUNX1, SAMD9, SAMD9L, SDHA, SDHAF2, SDHB, SDHC, SDHD, SH2B3, SMAD4, SMARCA4, SMARCB1, SMARCE1, SRP72, STAT3, STK11, SUFU, TERC, TERT, TET2, TMEM127, TNFRSF9, TP53, TSC1, TSC2, TTR, UNC13D, USP45, VHL, WAS, WRN, WT1

Table S2. Variants analyzed. Variants in HHM-related genes.

Patient	Variant	UChicago Interpretation	ClinVar Classification	dbSNP
Patient 1	*TERT* c.1951-1G>A, p.? NM_198253.3	P	N/A	N/A
Patient 2	*CEBPA* c.287_311del (p.G96Afs*56); c.707_713dup, (p.A240Rfs*83) NM_004364.3	P	N/A	N/A
Patient 3	*RECQL4* c.1132-1G>A, p.? NM_004260.3	LP	LP	rs751503394
Patient 4	*PALB2* c.466_467del, p.I156Ffs*11 NM_024675.4	P	P/LP	rs876659405
Patient 5	Unknown		N/A	N/A
Patient 6	*TP53* c.997dup, p.R333Pfs*4 NM_000546.6	P	N/A	N/A
Patient 7	Unknown		N/A	N/A
Patient 8	Unknown		N/A	N/A
Patient 9	*DDX41* c.571G>A, p.? NM_016222.4	P	N/A	N/A
Patient 10	*BRCA1* c.5329dup, p.Q1777Pfs*74 NM_007300.4	P	P	rs80357906
Patient 11	*BRCA2* c.7558C>T, p.Arg2520* NM_000059.3	P	P	rs80358981
Patient 12	*BRCA1* c.181T>G, p.C61G NM_007294.4	P	P	rs28897672
Patient 13	N/A	N/A	N/A	N/A
Patient 14	*CEBPA* p.Q312dup; p.V95fs*62 NM_004364.3	N/A	N/A	N/A
Patient 15	*DDX41* 2.4 kB deletion NM_016222.3	P	N/A	N/A
Patient 16	*PALB2* c.758dup, p.S254Ifs*3 NM_024675.4	P	P/LP	rs515726126
Patient 17	*FANCA* c.2738A>C , p.H913P NM_000135.4	P	P/LP	rs1302083447
Patient 18	*MLH1* c.1835_1837 (p.Val612del) NM_000249.3 *TP53 exon 1 deletion* NM_000546.5	LP / P	N/A	N/A
Patient 19	*CHEK2* c.470T>C, p.I157T NM_007194.4	LP	P/LP	rs17879961
Patient 20	*IKZF1* loss	P	N/A	N/A
Patient 21	*FANCE* c.1111C>T , p.Arg371Trp NM_021922.2	P (heterozygous)	P/LP	rs775076977
Patient 22	*HAVCR2* c.245 A>G, p.Tyr82Cys NM_032782.5	VUS	VUS	rs184868814