CORD BLOOD MATERNAL MICROCHIMERISM FOLLOWING UNRELATED CORD BLOOD TRANSPLANTATION

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This file contains supplementary information:

Supplementary Figures S1 to S3

Supplementary Table S1

A

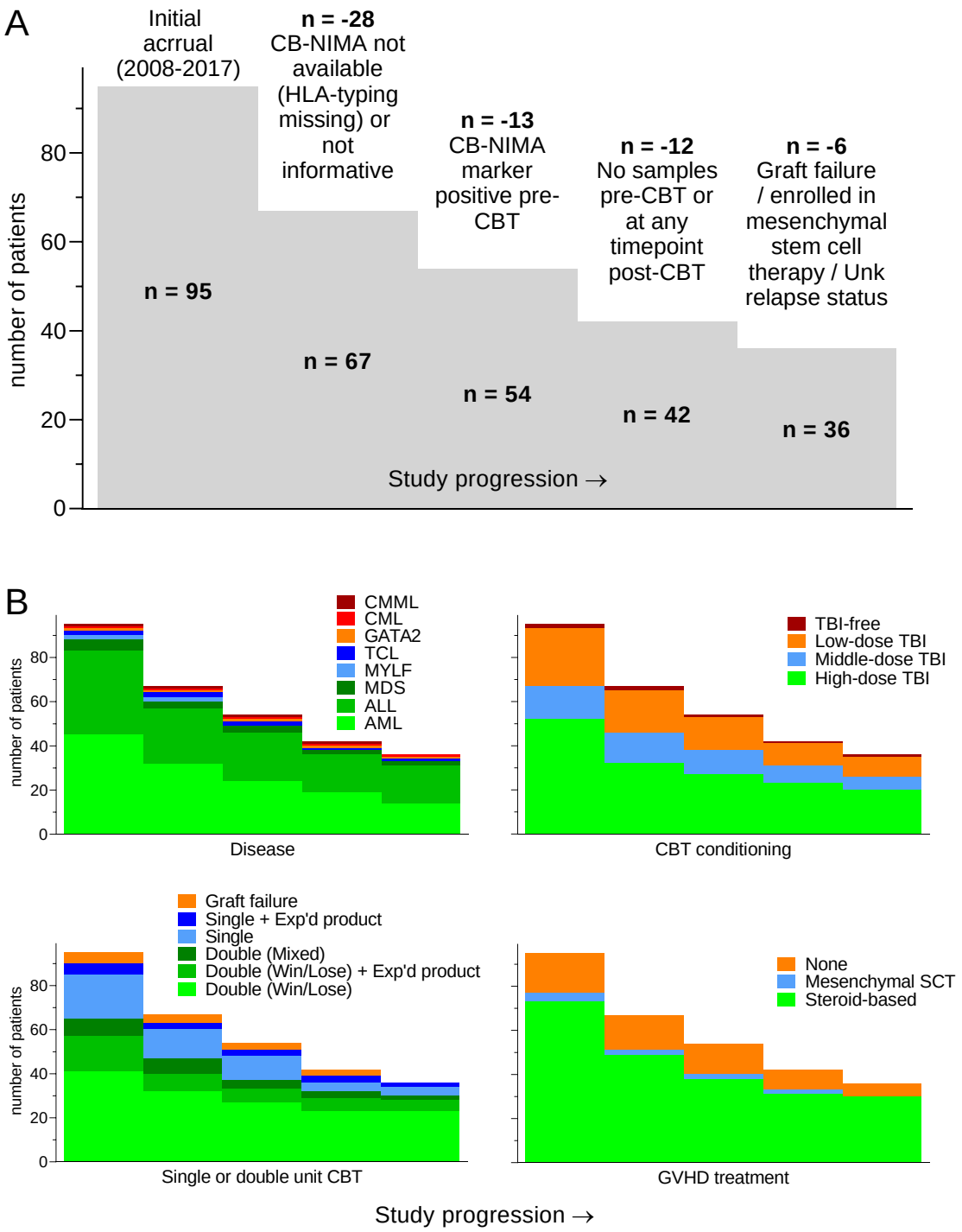
Microchimerism Panel of highly-sensitive HLA-specific qPCR-based assays			
*DRB1*01*	*DRB1*09*	*DQA1*03*	*QKRAA*
*DRB1*15/16*	*DRB1*10*	*DQA1*05*	*QRRAA*
*DRB1*03*	*DRB1*11:04*	*DQB1*02*	*DERAA*
*DRB1*04*	*DRB1*14*	*DQB1*03:01/4*	*B*44*
*DRB1*07*	*DRB4*	*DQB1*04*	*B*13*
*DRB1*08*	*DQA1*01*	*DQB1*06:02/3*	*A*30*

B

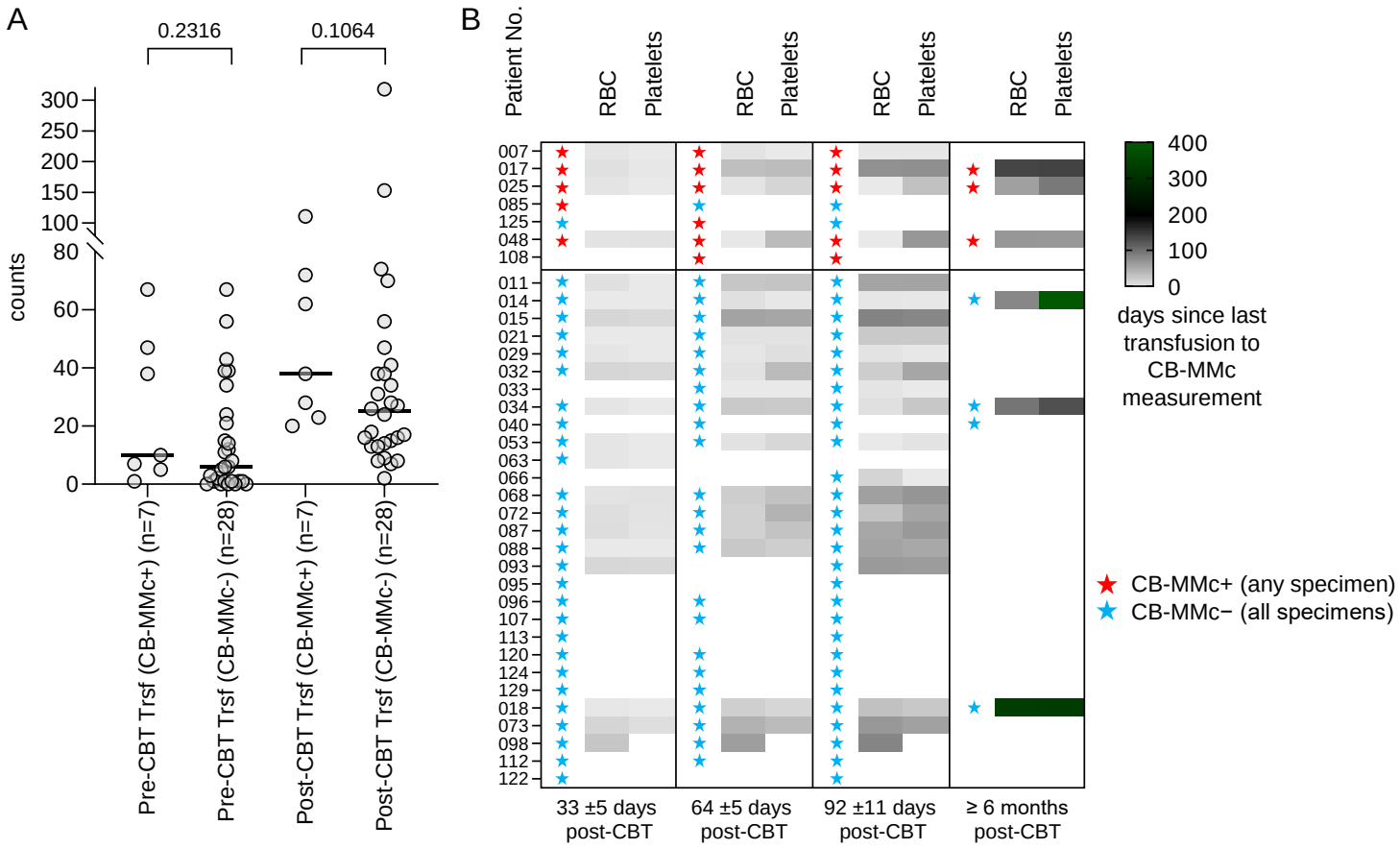
Marker unique to the mother of CB for which an HLA-specific assay is available
Marker unique to the mother of CB for which an HLA-specific assay is not available

	A*		B*		DRB1*		DQA1*		DQB1*	
Patient	03:01	01:01	52:01	51:01	14:01	11:01	NT	NT	05:03	03:01
CB_{Win}	03:01	01:01	07	51:01	07:01	11:01	NT	NT	NT	NT
CB_{Lose}	03:01	01:01	07	51:01	10:01	11:01	NT	NT	05:01	03:01
M-CB_{Win}	24:02	01:01	07:02	40:02	15:01	11:01	NT	NT	NT	NT
M-CB_{Lose}	32:01	01:01	49:01	51:01	04:05	11:01	NT	NT	03:02	03:01

Supplementary Figure S1. (**A**) The panel of highly sensitive quantitative PCR assays used in the current study to detect and quantify cord blood-origin maternal microchimerism (CB-MMc) with specificities to HLA class I and class II allelic families (e.g. DRB1*01 family of alleles) or group of alleles (e.g. the group of alleles encoding the DERAA amino-acid sequence, including some DRB1*11 and 13 alleles). (**B**) Example of the identification of a non-shared, non-inherited maternal HLA allele (NIMA) 'marker' in a patient; unique CB-NIMA markers were identified for both mothers of cord bloods (M-CB), and markers with available assays are depicted in green. When a patient did not have a unique CB-NIMA marker present for one of the mothers of a CB, or when an HLA-specific assay was not available for it (in grey), the patient was excluded from further analyses. NT, not typed.



Supplementary Figure S1. (A) Diagram showing patient exclusion criteria**. (B)** Summary of patients' characteristics at the time of inclusion and as study progressed (after exclusions). AML: acute myeloid leukemia; ALL: acute lymphoblastic leukemia; MDS: myelodysplastic syndrome; MYLF myelofibrosis; TCL: T cell lymphoma; GATA2: GATA2 haploinsufficiency; CML: chronic myeloid leukemia; CMML: chronic myelomonocytic leukemia; CBT: Cord blood transplantation; TBI: total body irradiation; Exp'd: non-engrafting non-HLA-matched ex-vivo expanded CB progenitor cell product; GVHD: graft-vs.-host disease; Mesenchymal SCT: mesenchymal stem cell therapy; NIMA: non-shared non-inherited maternal HLA allele.



Supplementary Figure S3. (**A**) Comparing the overall number of transfusions (red blood cells [RBC] and platelets) that patients received both pre- and post-cord blood transplantation (CBT), between patients with positive CB-maternal microchimerism (CB-MMc+) results vs. patients with CB-MMc−. *P*-values from the Mann-Whitney rank-sum test are represented. Bars represent the median. Records of transfusion counts were missing for one patient. (**B**) The transfusion state at each post-CBT timepoint category represents the number of days that passed since last transfusion to the day of specimen collection for CB-MMc measurement. Blank spots represent missing information; e.g. for patients 040, 085, 095, 096, and those with a number >107, records on the transfusion counts are available but without dates.

Patient No.	Specimen	TimePoint post-CBT	marker	**CB-MMc (losing)** and 95%CI of measurment, in gEq per 10^6 total gEq	marker	**CB-chimerism (losing)** and 95%CI of measurment, in gEq per 10^6 total gEq
017	BMA	33 ±5 days	DRB1*15	0.0 [0.0 - 35.9]	B*44 (also specific to losing CB mother)	
		64 ±5 days				
		92 ±11 days		0.0 [0.0 - 53.7]		0.0 [0.0 - 61.1]
		≥ 6 months		11.1 [2.0 - 63.4]		
	WB	33 ±5 days		85.7 [36.4 - 205.6]		0.0 [0.0 - 60.6]
		64 ±5 days		0.0 [0.0 - 40.4]		0.0 [0.0 - 77.4]
		92 ±11 days		31.7 [10.0 - 107.7]		0.0 [0.0 - 63.5]
		≥ 6 months				
	Neutrophils	33 ±5 days		9.8 [1.6 - 63.1]		48.2 [12.9 - 179.8]
		64 ±5 days		20.4 [5.4 - 79.6]		0.0 [0.0 - 33.5]
		92 ±11 days		0.0 [0.0 - 66.3]		0.0 [0.0 - 22.9]
		≥ 6 months				
	PBMC	33 ±5 days		12.7 [3.0 - 53.9]		0.0 [0.0 - 33.8]
		64 ±5 days		0.0 [0.0 - 35.6]		0.0 [0.0 - 26.8]
		92 ±11 days		0.0 [0.0 - 29.7]		0.0 [0.0 - 30.1]
		≥ 6 months		21.7 [3.8 - 123.3]		
025	BMA	33 ±5 days	DRB1*04	0.0 [0.0 - 204.8]	DRB1*10	0.0 [0.0 - 118.2]
		64 ±5 days				
		92 ±11 days				
		≥ 6 months		0.0 [0.0 - 65.4]		
	WB	33 ±5 days		43.4 [6.8 - 282.7]		0.0 [0.0 - 32.4]
		64 ±5 days				
		92 ±11 days				
		≥ 6 months				
	Neutrophils	33 ±5 days		0.0 [0.0 - 77.9]		
		64 ±5 days				
		92 ±11 days				
		≥ 6 months				
	PBMC	33 ±5 days		0.0 [0.0 - 44.1]		0.0 [0.0 - 33.6]
		64 ±5 days		13.3 [2.3 - 77.7]		0.0 [0.0 - 17.5]
		92 ±11 days		5.8 [0.8 - 46.1]		0.0 [0.0 - 17.5]
		≥ 6 months		0.0 [0.0 - 391.9]		
085	BMA	33 ±5 days	DQB1*06		DRB1*01 (also specific to losing CB mother)	
		64 ±5 days				
		92 ±11 days		0.0 [0.0 - 26.4]		989.9 [844.9 - 1159.7]
		≥ 6 months				
	WB	33 ±5 days		14.0 [2.1 - 95.9]		0.0 [0.0 - 37.6]
		64 ±5 days		0.0 [0.0 - 63.7]		0.0 [0.0 - 36.9]
		92 ±11 days				
		≥ 6 months				
	Neutrophils	33 ±5 days		0.0 [0.0 - 18.5]		0.0 [0.0 - 16.1]
		64 ±5 days		0.0 [0.0 - 12.3]		0.0 [0.0 - 17.0]
		92 ±11 days				
		≥ 6 months				
	PBMC	33 ±5 days		0.0 [0.0 - 35.6]		0.0 [0.0 - 25.1]
		64 ±5 days		0.0 [0.0 - 33.8]		0.0 [0.0 - 25.5]
		92 ±11 days		0.0 [0.0 - 25.6]		0.0 [0.0 - 25.0]
		≥ 6 months				

Supplementary Table S1. Comparing chimerism levels specific to the losing cord blood (CB) unit versus the mother of that losing CB unit in 3 patients who received double CB transplantation (CBT), who were positive for CB-Maternal microchimerism (CB-MMc) for multiple timepoints and specimens, and who had an informative HLA marker specific to the losing unit that we could target. Microchimerism concentrations are measured in human cell genome equivalent (gEq) of CB-MMc DNA per million gEq of total DNA from bone marrow aspirates (BMA), whole peripheral blood (WB), neutrophils, and peripheral blood mononuclear cells (PBMC). Each measurement is accompanied by a 95% confidence interval (95%CI) of the measured value, derived from the 'Wilson Score' without continuity correction. Blank spots are when a specimen at a timepoint was not available.