LETTER TO THE EDITOR

αβT- and B-cell-depleted HLA-haploidentical hematopoietic stem cell transplantation in children with myelodysplastic syndromes

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Supplementary File

Supplementary Table 1: Germline and somatic variants identified in the cohort of patients.

Patient	Gene	Variante	VAF(%)	Ensembl (GRCh37)	Type of variant/ Effect	Origin/ Segregation	ACMG/AMP classification	ClinVAr /COSMIC classification	dbSNP	gnomAD	CADD score	OMIM ID	Inheritance	Reference
OPBG1	***GATA2***	c.414_417delCTCT	50	ENST00000341105.2	Frameshift / p.Ser139fs	Germline/ De Novo	Pathogenic	NR	NR	NR	32	#614286	AD	NR
OPBG2	***TP53***	c.1025G>T	50	ENST00000269305.4	Missense/ p.Arg342Leu	Germline/ Paternal	VUS	NR	NR	NR	18.39	#618165	AD	(1)
	TBXAS1	c.338C>T	50	ENST00000416849.2	Missense/ p.Ala113Val	Germline/ Maternal	VUS	NR	rs139976441	0.0018	12.96	#231095	AR	NR
	ERBB3	c.493C>G	50	ENST00000411731.2	Missense/ p.Pro165Ala	Germline/ Maternal	VUS	NR	rs772810438	0.0003	3.487	#133180	AD	NR
OPBG3	***ERCC6L2***	c.254C>T	50	ENST00000407474.3	Missense/ p.Ser85Leu	Germline/ Paternal	VUS	NR	rs372436741	0.0003	4.039	#615715	AR	NR
	RTEL1	c.1992T>G	50	ENST00000318100.4	Missense/ p.Asp664Glu	Germline/ Paternal	VUS	VUS	NR	NR	NR	#615190, #616373	AD, AR	NR
OPBG4	***KRAS***	c.540T>A	50	ENST00000256078.4	Nonsense/ p.Cys180*	Germline/ Maternal	Likely pathogenic	VUS	rs373169526	0.0002	40	#609942, #614470	AD	(2)
	LIG4	c.712A>G	50	ENST00000356922.4	Missense/ p.Ile238Val	Germline/ Maternal	VUS	VUS	rs149012859	0.0004	15.31	#606593	AR	NR
OPBG5	NO VARIANTS													
OPBG6	***PIK3R1***	c.347C>T	50	ENST00000396611.1	Missense/ p.Pro116Leu	Germline/ Maternal	VUS	VUS	rs774531250	0.0002	17.97	#616005	AD	NR
	SLX4	c.1448T>A	50	ENST00000294008.3	Missense/ p.Ile483Lys	Germline/ Maternal	VUS	NR	NR	NR	23.1	#613951	AR	NR
OPBG7	***DNAJC21***	c.214C>G	50	ENST00000382021.2	Missense/ p.Leu72Val	Germline/ Maternal	VUS	VUS	rs778723001	0.000008797	23.3	#617052	AR	NR
	CXCR4	c.1066A>G	50	ENST00000409817.1	Missense/ p.Ser356Gly	Germline/ Paternal	VUS	VUS	rs750756138	0.0000186	24.3	#193670	AD	NR
OPBG8	***GATA2***	c.1084C>T	50	ENST00000341105.2	Nonsense/ p.Arg362*	NA	Pathogenic	NR	NR	NR	41	#614286, #614038, #601626	AD	(3-6)
OPBG9	***PAX5***	c.77T>G	50	ENST00000358127.4	Missense/ p.Val26Gly	Germline/ Maternal	VUS	NR	rs926053251	0	28.1	#615545	AD	(7)
	ZBTB24	c.1394G>A	50	ENST00000230122.3	Missense/ p.Gly465Asp	Germline/ Maternal	VUS	VUS	NR	0.0000648	15.86	#614069	AR	NR
OPBG10	***SAMD9***	c.3570T>G	50	ENST00000379958.2	Missense/ p.Asp1190Glu	Germline/ Maternal	VUS	NR	NR	NR	0.088	#617053, #619041	AD	NR
	SAMD9L	c.505G>C	50	ENST00000318238.4	Missense/ p.Asp169His	Germline/ Maternal	VUS	VUS	rs144605831	0.0002	23.3	#159550, #252270	AD	NR
OPBG11	***SLX4***	c.193C>T	50	ENST00000294008.3	Missense/ p.His65Tyr	Germline/ Paternal	VUS	NR	rs145345695	0.00000879	18.03	# 613951	AR	NR
OPBG12	***RTEL1***	c.3218C>T	50	ENST00000318100.4	Missense/ p.Ser1073Phe	Germline/ Maternal	VUS	NR	NR	NR	22.3	#615190, # 616373	AD, AR	NR

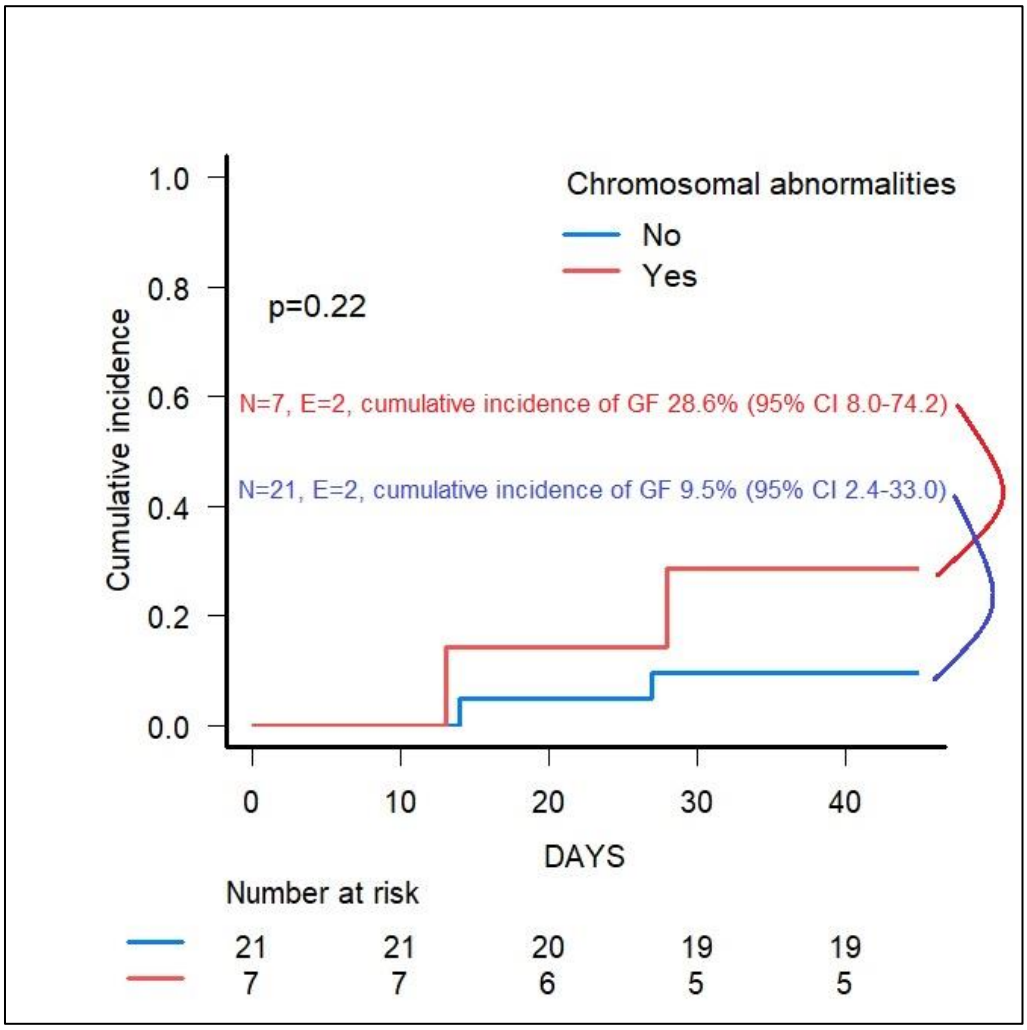
	MECOM	c.106G>T	50	ENST00000494292.1	Missense/ p.Ala36Ser	Germline/ Paternal	VUS	NR	rs781351398	0.0002	13.16	# 616738	AD	NR
	SLFN14	c.140G>A	50	ENST00000415846.3	Missense/ p.Arg47Gln	Germline/ Paternal	VUS	NR	rs372726659	0.0006	12.57	# 616913	AD	NR
	UNC13D	c.2363A>G	50	ENST00000412096.2	Missense/ p.Glu788Gly	Germline/ Paternal	VUS	NR	NR	NR	28.1	# 608898	AR	NR
OPBG13	***TBXAS1***	c.1036A>G	50	ENST00000416849.2	Missense/ p.Ile346Val	Germline/ Maternal	VUS	NR	NR	NR	6.357	# 231095	AR	NR
	CDAN1	c.1067A>G	50	ENST00000356231.3	Missense/ p.Glu356Gly	Germline/ Maternal	VUS	NR	rs770862298	0.000720721	20.5	# 224120	AR	NR
	DNAJC21	c.801G>T	50	ENST00000382021.2	Missense/ p.Glu267Asp	Germline/ Paternal	VUS	NR	NR	NR	24	# 617052	AR	NR
OPBG14	***RUNX1***	c.917G>C	50	ENST00000300305.3	Missense/ p.Arg306Pro	Germline/ Paternal	VUS	VUS	NR	0.00005437	25.9	# 601399	AD	NR
	ACTN1	c.2677G>A	50	ENST00000538545.2	Missense/ p.Asp893Asn	Germline/ Paternal	VUS	NR	NR	NR	24.4	# 615193	AD	NR
	ANK1	c.3409C>T	50	ENST00000396942.1	Missense/ p.Arg1137Trp	Germline/ Paternal	VUS	NR	NR	NR	22.8	# 182900	AD, AR	NR
OPBG15	***ANKRD26***	c.1416+3A>G	50	ENST00000436985.2	Splice regiont / ?	Germline/ Paternal	VUS	NR	rs770314193	0.000008878	16.31	#188000	AD	NR
	WRAP53	c.919C>T	50	ENST00000316024.5	Missense/ p.Arg307Trp	Germline/ Paternal	VUS	NR	rs149828392	0.0012	26.9	#613988	AR	NR
OPBG16	NO VARIANTS													
OPBG17	***PTPN11***	c.227A>C	36	ENST00000351677.2	Missense/ p.Glu76Ala	Somatic	Tier 1	Pathogenic/ Pathogenic	rs121918465	NR	27	#607785	somatic	(8)
	RPL11	c.424G>A	50	ENST00000374550.3	Missense/ p.Ala142Thr	Germline/ ?	VUS	VUS	NR	NR	23.8	#612562	AD	NR
OPBG18	***RUNX1***	c.320G>A	30	ENST00000300305.3	Missense/ p.Arg107His	Somatic	Tier 1	NR/ Pathogenic	NR	NR	33	#601626	somatic	(9)
	CBL	c.1111T>A	60	ENST00000264033.4	Missense/ p.Tyr371Asn	Somatic	Tier 1	Pathogenic/ Pathogenic	rs267606706	NR	32	#607785	somatic	NR
OPBG19	***GBA***	c.1448T>C	50	ENST00000327247.5	Missense/ p.Leu483Pro	Germline/ Maternal	Pathogenic	Pathogenic	rs421016	0.003507405	23.7	#230800, #230900, #231000, #231005	AR	(10)
PV7	NO VARIANTS													
PV8	NO VARIANTS													

AMP: Association for Molecular Pathology; ACMG: American College of Medical Genetics; AD: Autosomal Dominant; AR: Autosomal Recessive; CADD: Combined Annotation Dependent Depletion; NA, Not Available; NR: Not Reported; VAF: Variant allele frequency; VUS: Variant of Unknown Significance.

Supplementary Table 2. Comparison between patients with myelodysplastic syndromes (MDS) and severe aplastic anemia (SAA) (11) who underwent TCRαβ and CD19 B-cell depleted HLA-haploidentical HSCT

	MDS (n=28)	SAA (n=12)	p-value
Sex (F/M)	14/14	6/6	n.s.
Median (range) age at diagnosis, y	9.6 (1.3-17.5)	7.1 (1.4-14.2)	n.s.
Median (range) age at HSCT, y	10.2 (1.8-18.0)	8.4 (1.6-14.7)	n.s.
Median (range) time from diagnosis to, mo	7.7 (1.2-120.4)	11.4 (1.3-40.1)	n.s.
Previous HSCT	2	3	n.s.
Cell dose infused, median (range)			
CD34+ cells × 10^6/kg	14.7 (8.3-28.6)	20.0 (8.5-34.2)	0.04
αβ+ T cells × 10^6/kg	0.027 (0.008-0.098)	0.02 (0.005-0.09)	n.s.

Supplementary Figure 1. Cumulative incidence of graft failure (GF) in patients affected by myelodysplastic syndromes with or without chromosomal abnormalities at time of HSCT.



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