LETTER TO THE EDITOR

TET2 mutation does not impact the prognosis of adult acute myeloid leukemia patients receiving a hematopoietic stem cell transplantation in first remission: similar outcome following matched sibling and unrelated *versus* haploidentical donor transplants in a multi-center retrospective analysis from the Global Committee and the Acute Leukemia Working Party of the European Society for Blood and Marrow Transplantation

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Table S1 Characteristics of the patients *TET2* unmutated and mutated.

Variables	**Modalities**	**N=755**	**Neg (N=632)**	**Pos (N=123)**	**p value**
Year of HSCT	median [IQR]	2019 [2018-2021]	2019 [2018-2021]	2019 [2018-2021]	0.14
	(range)	(2013-2022)	(2013-2022)	(2015-2022)	
Age at HSCT	median [IQR]	55.2 [43.5-61.9]	54 [42.8-61.4]	59.5 [47.9-65.1]	< 0.001
	(range)	(18.2-75.1)	(18.5-75.1)	(18.2-74.9)	
Patient sex	Female, N(%)	380 (50.3)	322 (50.9)	58 (47.2)	0.44
	Male, N(%)	375 (49.7)	310 (49.1)	65 (52.8)	
Karnofsky score	< 90, N(%)	142 (19.8)	111 (18.4)	31 (27.4)	0.03
	>= 90, N(%)	574 (80.2)	492 (81.6)	82 (72.6)	
	missing, N	39	29	10	
AML type	de novo, N(%)	658 (87.4)	556 (88.1)	102 (83.6)	0.17
	secAML, N(%)	95 (12.6)	75 (11.9)	20 (16.4)	
	missing, N	2	1	1	
MRD	Negative, N(%)	272 (65.4)	222 (63.1)	50 (78.1)	0.02
	Positive, N(%)	144 (34.6)	130 (36.9)	14 (21.9)	
	missing, N	339	280	59	
Number of *TET2* mutations	1, N(%)			96 (78)	Not done
	2, N(%)			21 (17.1)	
	3, N(%)			4 (3.3)	
	4, N(%)			2 (1.6)	
TET2 max VAF	median [IQR]			47 [42-51]	Not done
	(range)			(1-100)	
	missing, N			30	
Chromosomal analysis	Abnormal, N(%)	363 (51.4)	314 (52.8)	49 (44.1)	0.09
	Normal, N(%)	343 (48.6)	281 (47.2)	62 (55.9)	

	missing, N	49	37	12	
ELN2022 cytogenetic	Favorable, N(%)	33 (4.7)	28 (4.8)	5 (4.6)	0.32
	Intermediate, N(%)	487 (70.1)	405 (69)	82 (75.9)	
	Adverse, N(%)	175 (25.2)	154 (26.2)	21 (19.4)	
	missing, N	60	45	15	
NPM1	Negative, N(%)	573 (78.4)	494 (79.7)	79 (71.2)	0.04
	Positive, N(%)	158 (21.6)	126 (20.3)	32 (28.8)	
	missing, N	24	12	12	
FLT3-ITD	Negative, N(%)	528 (74.6)	451 (74.5)	77 (74.8)	0.96
	Positive, N(%)	180 (25.4)	154 (25.5)	26 (25.2)	
	missing, N	47	27	20	
DNMT3A	Negative, N(%)	569 (76.8)	484 (77.6)	85 (72.6)	0.25
	Positive, N(%)	172 (23.2)	140 (22.4)	32 (27.4)	
	missing, N	14	8	6	
CEBPA	Negative, N(%)	554 (93.6)	458 (93.7)	96 (93.2)	0.86
	Positive, N(%)	38 (6.4)	31 (6.3)	7 (6.8)	
	missing, N	163	143	20	
RUNX1	Negative, N(%)	632 (83.8)	528 (83.7)	104 (84.6)	0.81
	Positive, N(%)	122 (16.2)	103 (16.3)	19 (15.4)	
	missing, N	1	1	0	
ASXL1	Negative, N(%)	679 (89.9)	576 (91.1)	103 (83.7)	< 0.001
	Positive, N(%)	76 (10.1)	56 (8.9)	20 (16.3)	
SRSF2	Negative, N(%)	673 (90.2)	570 (91.2)	103 (85.1)	0.04
	Positive, N(%)	73 (9.8)	55 (8.8)	18 (14.9)	
	missing, N	9	7	2	
TP53	Negative, N(%)	689 (93.2)	577 (93.2)	112 (93.3)	0.96

	Positive, N(%)	50 (6.8)	42 (6.8)	8 (6.7)	
	missing, N	16	13	3	
BCOR	Negative, N(%)	490 (91.8)	409 (91.7)	81 (92)	0.92
	Positive, N(%)	44 (8.2)	37 (8.3)	7 (8)	
	missing, N	221	186	35	
EZH2	Negative, N(%)	638 (96.2)	537 (97.3)	101 (91)	0.004
	Positive, N(%)	25 (3.8)	15 (2.7)	10 (9)	
	missing, N	92	80	12	
SF3B1	Negative, N(%)	714 (95.7)	594 (95)	120 (99.2)	0.04
	Positive, N(%)	32 (4.3)	31 (5)	1 (0.8)	
	missing, N	9	7	2	
STAG2	Negative, N(%)	464 (92.6)	387 (93)	77 (90.6)	0.43
	Positive, N(%)	37 (7.4)	29 (7)	8 (9.4)	
	missing, N	254	216	38	
U2AF1	Negative, N(%)	691 (96.9)	579 (96.7)	112 (98.2)	0.56
	Positive, N(%)	22 (3.1)	20 (3.3)	2 (1.8)	
	missing, N	42	33	9	
ZRSR2	Negative, N(%)	563 (98.3)	458 (98.3)	105 (98.1)	1
	Positive, N(%)	10 (1.7)	8 (1.7)	2 (1.9)	
	missing, N	182	166	16	
Source of cells	PB, N(%)	705 (93.4)	595 (94.1)	110 (89.4)	Not done
	BM, N(%)	41 (5.4)	30 (4.7)	11 (8.9)	
	BM+PB, N(%)	1 (0.1)	1 (0.2)	0 (0)	
	CB, N(%)	7 (0.9)	5 (0.8)	2 (1.6)	
	Double CB, N(%)	1 (0.1)	1 (0.2)	0 (0)	
Donor type	Matched sibling donor,	242 (32.1)	208 (33)	34 (27.6)	Not done

	N(%)				
	Matched other relative, N(%)	21 (2.8)	20 (3.2)	1 (0.8)	
	Syngeneic, N(%)	2 (0.3)	1 (0.2)	1 (0.8)	
	Haplo, N(%)	143 (19)	111 (17.6)	32 (26)	
	MMR (missing HLA), N(%)	2 (0.3)	2 (0.3)	0 (0)	
	MMR 1 locus, N(%)	5 (0.7)	4 (0.6)	1 (0.8)	
	UD 10/10, N(%)	256 (34)	218 (34.6)	38 (30.9)	
	UD 9/10, N(%)	43 (5.7)	33 (5.2)	10 (8.1)	
	UD <=8/10, N(%)	3 (0.4)	2 (0.3)	1 (0.8)	
	UD (missing HLA), N(%)	29 (3.9)	26 (4.1)	3 (2.4)	
	UCB 5/6, N(%)	1 (0.1)	1 (0.2)	0 (0)	
	UCB <=4/6, N(%)	3 (0.4)	2 (0.3)	1 (0.8)	
	UCB (missing HLA), N(%)	2 (0.3)	1 (0.2)	1 (0.8)	
	Double UCB, N(%)	1 (0.1)	1 (0.2)	0 (0)	
	missing, N	2	2	0	
Donor type	Matched relative, N(%)	265 (35.2)	229 (36.3)	36 (29.3)	Not done
	Mismatched relative, N(%)	150 (19.9)	117 (18.6)	33 (26.8)	
	UD 10/10, N(%)	256 (34)	218 (34.6)	38 (30.9)	
	UD<=9/10, N(%)	44 (5.8)	35 (5.6)	9 (7.3)	
	UD (missing HLA), N(%)	31 (4.1)	26 (4.1)	5 (4.1)	
	UCB, N(%)	7 (0.9)	5 (0.8)	2 (1.6)	
	missing, N	2	2	0	
Female to male	No, N(%)	640 (84.8)	533 (84.3)	107 (87)	0.45
	Yes, N(%)	115 (15.2)	99 (15.7)	16 (13)	
Patient CMV	Negative, N(%)	195 (26.5)	171 (27.5)	24 (21.2)	0.17

	Positive, N(%)	540 (73.5)	451 (72.5)	89 (78.8)	
	missing, N	20	10	10	
CMV donor to patient	Neg to Neg, N(%)	130 (17.8)	112 (18.1)	18 (16.2)	0.16
	Neg to Pos, N(%)	164 (22.4)	140 (22.6)	24 (21.6)	
	Pos to Neg, N(%)	62 (8.5)	58 (9.4)	4 (3.6)	
	Pos to Pos, N(%)	375 (51.3)	310 (50)	65 (58.6)	
	missing, N	24	12	12	
Conditioning regien	BuCy based, N(%)	78 (10.4)	67 (10.6)	11 (8.9)	Not done
	BuFlu based, N(%)	250 (33.2)	215 (34.1)	35 (28.5)	
	BuFluThio based, N(%)	212 (28.2)	162 (25.7)	50 (40.7)	
	FluMel based, N(%)	67 (8.9)	61 (9.7)	6 (4.9)	
	TBI based, N(%)	87 (11.6)	76 (12.1)	11 (8.9)	
	TreoFlu based, N(%)	50 (6.6)	40 (6.3)	10 (8.1)	
	Other, N(%)	9 (1.2)	9 (1.4)	0 (0)	
	missing, N	2	2	0	
Myeloablativity	No, N(%)	401 (54.3)	334 (53.5)	67 (58.8)	0.3
	Yes, N(%)	337 (45.7)	290 (46.5)	47 (41.2)	
	missing, N	17	8	9	
Invivo TCD	No, N(%)	331 (44.2)	277 (44.1)	54 (44.6)	0.92
	Yes, N(%)	418 (55.8)	351 (55.9)	67 (55.4)	
	missing, N	6	4	2	
Use of PTCy	No, N(%)	495 (66.3)	423 (67.6)	72 (59.5)	0.09
	Yes, N(%)	252 (33.7)	203 (32.4)	49 (40.5)	
	missing, N	8	6	2	
GVHD prevention	CSA+/-SIRO/TACRO, N(%)	71 (9.5)	60 (9.6)	11 (9.1)	Not done
	CSA+MMF+/-SIRO/TACRO,	222 (29.6)	169 (26.9)	53 (43.8)	

	N(%)				
	CSA+MTX+/-SIRO/TACRO, N(%)	172 (23)	154 (24.5)	18 (14.9)	
	MMF+/-SIRO/TACRO, N(%)	201 (26.8)	182 (29)	19 (15.7)	
	MTX+/-SIRO/TACRO, N(%)	20 (2.7)	17 (2.7)	3 (2.5)	
	MTX+MMF+TACRO, N(%)	21 (2.8)	17 (2.7)	4 (3.3)	
	SIRO/TACRO, N(%)	17 (2.3)	15 (2.4)	2 (1.7)	
	Other, N(%)	25 (3.3)	14 (2.2)	11 (9.1)	
	missing, N	6	4	2	

Abbreviations: Neg, negative; Pos, positive; HSCT, hematopoietic stem cell transplantation; IQR, interquartile range; AML, acute myeloid leukemia; MRD, measurable residual disease; PB, peripheral blood; CB, cord blood; BM, bone marrow; CB, cord blood; MSD, matched sibling donor; Haplo, haploidentical donor; UD, unrelated donor; MMR, mismatched relative donor; UCB, unrelated cord blood; CMV, cytomegalovirus; BU, busulfan; Cy, cyclophosphamide; Flu, fludarabine; Thio, thiotepa; Mel, melphalan; TBI, total body irradiation; Treo, treosulfan; TCD, T-cell depletion; PTCY, post-transplant cyclophosphamide; GVHD, graft-versus-host disease; CSA, cyclosporine A; SIRO, sirolimus; TACRO, tacrolimus; MMF, mycophenolate mofetil; MTX, methotrexate.

Table S2 Characteristics of the two pair-matched groups *TET2* unmutated and mutated.

Variables	**Modalities**	**N=436**	**Neg (N=320)**	**Pos (N=116)**	**p value**
Chromosomal analysis	Abnormal, N(%)	207 (51.1)	162 (54)	45 (42.9)	0.049
	Normal, N(%)	198 (48.9)	138 (46)	60 (57.1)	
	missing, N	31	20	11	
NPM1	Negative, N(%)	330 (77.8)	255 (80.2)	75 (70.8)	0.04
	Positive, N(%)	94 (22.2)	63 (19.8)	31 (29.2)	
	missing, N	12	2	10	
FLT3-ITD	Negative, N(%)	298 (72.7)	225 (72.3)	73 (73.7)	0.79

	Positive, N(%)	112 (27.3)	86 (27.7)	26 (26.3)	
	missing, N	26	9	17	
DNMT3A	Negative, N(%)	311 (72.3)	231 (72.4)	80 (72.1)	0.94
	Positive, N(%)	119 (27.7)	88 (27.6)	31 (27.9)	
	missing, N	6	1	5	
CEBPA	Negative, N(%)	327 (95.1)	235 (95.5)	92 (93.9)	0.58
	Positive, N(%)	17 (4.9)	11 (4.5)	6 (6.1)	
	missing, N	92	74	18	
RUNX1	Negative, N(%)	364 (83.7)	267 (83.7)	97 (83.6)	0.98
	Positive, N(%)	71 (16.3)	52 (16.3)	19 (16.4)	
	missing, N	1	1	0	
ASXL1	Negative, N(%)	386 (88.5)	288 (90)	98 (84.5)	0.11
	Positive, N(%)	50 (11.5)	32 (10)	18 (15.5)	
SRSF2	Negative, N(%)	380 (88.4)	283 (89.6)	97 (85.1)	0.2
	Positive, N(%)	50 (11.6)	33 (10.4)	17 (14.9)	
	missing, N	6	4	2	
TP53	Negative, N(%)	391 (92)	286 (91.7)	105 (92.9)	0.67
	Positive, N(%)	34 (8)	26 (8.3)	8 (7.1)	
	missing, N	11	8	3	
BCOR	Negative, N(%)	295 (91.9)	218 (92)	77 (91.7)	0.93
	Positive, N(%)	26 (8.1)	19 (8)	7 (8.3)	
	missing, N	115	83	32	
EZH2	Negative, N(%)	368 (94.8)	272 (96.5)	96 (90.6)	0.02
	Positive, N(%)	20 (5.2)	10 (3.5)	10 (9.4)	
	missing, N	48	38	10	
SF3B1	Negative, N(%)	414 (96.3)	301 (95.3)	113 (99.1)	0.08

	Positive, N(%)	16 (3.7)	15 (4.7)	1 (0.9)	
	missing, N	6	4	2	
STAG2	Negative, N(%)	280 (92.7)	206 (93.2)	74 (91.4)	0.58
	Positive, N(%)	22 (7.3)	15 (6.8)	7 (8.6)	
	missing, N	134	99	35	
U2AF1	Negative, N(%)	398 (96.8)	291 (96.4)	107 (98.2)	0.52
	Positive, N(%)	13 (3.2)	11 (3.6)	2 (1.8)	
	missing, N	25	18	7	
ZRSR2	Negative, N(%)	335 (98.5)	236 (98.7)	99 (98)	0.64
	Positive, N(%)	5 (1.5)	3 (1.3)	2 (2)	
	missing, N	96	81	15	
Patient CMV	Negative, N(%)	108 (25.7)	86 (27.3)	22 (20.8)	0.18
	Positive, N(%)	313 (74.3)	229 (72.7)	84 (79.2)	
	missing, N	15	5	10	
Conditioning regimen	BuCy based, N(%)	31 (7.1)	20 (6.2)	11 (9.5)	Not done
	BuFlu based, N(%)	150 (34.4)	116 (36.2)	34 (29.3)	
	BuFluThio based, N(%)	130 (29.8)	85 (26.6)	45 (38.8)	
	FluMel based, N(%)	43 (9.9)	37 (11.6)	6 (5.2)	
	TBI based, N(%)	43 (9.9)	33 (10.3)	10 (8.6)	
	TreoFlu based, N(%)	36 (8.3)	26 (8.1)	10 (8.6)	
	Other, N(%)	3 (0.7)	3 (0.9)	0 (0)	
GVHD prevention	CSA+/-SIRO/TACRO, N(%)	39 (9)	28 (8.8)	11 (9.6)	Not done
	CSA+MMF+/-SIRO/TACRO, N(%)	133 (30.6)	85 (26.6)	48 (42.1)	
	CSA+MTX+/-SIRO/TACRO, N(%)	98 (22.6)	80 (25)	18 (15.8)	

MMF+/-SIRO/TACRO, N(%)	118 (27.2)	101 (31.6)	17 (14.9)
MTX+/-SIRO/TACRO, N(%)	12 (2.8)	9 (2.8)	3 (2.6)
MTX+MMF+TACRO, N(%)	10 (2.3)	6 (1.9)	4 (3.5)
SIRO/TACRO, N(%)	8 (1.8)	6 (1.9)	2 (1.8)
Other, N(%)	16 (3.7)	5 (1.6)	11 (9.6)
missing, N	2	0	2

Abbreviations: Neg, negative; Pos, positive; MSD, matched sibling donor; Haplo, haploidentical donor; UD, unrelated donor; MMR, mismatched relative donor; UCB, unrelated cord blood; CMV, cytomegalovirus; BU, busulfan; Cy, cyclophosphamide; Flu, fludarabine; Thio, thiotepa; Mel, melphalan; TBI, total body irradiation; Treo, treosulfan; TCD, T-cell depletion; PTCY, post-transplant cyclophosphamide; GVHD, graft-versus-host disease; CSA, cyclosporine A; SIRO, sirolimus; TACRO, tacrolimus; MMF, mycophenolate mofetil; MTX, methotrexate.

Table S3 Characteristics of 644 adult acute myeloid leukemia patients with *TET2* mutations

Variables	**Modalities**	**N=644**	**MSD (N=149)**	**Haplo (N=176)**	**UD 10/10 (N=268)**	**UD 9/10 (N=51)**	**p value**
Year of HSCT	median [IQR]	2020 [2018-2021]	2019 [2018-2021]	2020 [2018-2021]	2020 [2019-2021]	2020 [2019-2021]	0.03
	(range)	(2013-2022)	(2014-2022)	(2016-2022)	(2013-2022)	(2016-2022)	
Age at HSCT	median [IQR]	59.4 [48.4-65.9]	57.5 [47.6-62.5]	52.8 [42.6-62.2]	62.2 [55.6-68]	60.7 [49.1-64.9]	< 0.001
	(range)	(18.1-86.3)	(22.7-73.7)	(20-86.3)	(18.1-74.9)	(25.7-73.5)	
Age at diagnosis	median [IQR]	58.9 [47.8-65.4]	57 [47.1-62]	52.2 [42.1-61.3]	61.7 [55.2-67.6]	60.3 [48.7-64.4]	< 0.001
	(range)	(17.5-85.9)	(22.4-73.2)	(19.5-85.9)	(17.5-74.7)	(25.2-73)	
Months between diagnosis and HSCT	median [IQR]	4.9 [3.8-6.2]	4.4 [3.6-5.5]	5.2 [4.1-6.9]	5.1 [3.9-6.2]	5 [3.9-6.1]	0.005
	(range)	(0.9-89.9)	(0.9-71.6)	(2-89.9)	(1.6-37.7)	(2.1-10.4)	
AML type	de novo, N(%)	556 (86.3)	130 (87.2)	161 (91.5)	225 (84)	40 (78.4)	0.045

	secAML, N(%)	88 (13.7)	19 (12.8)	15 (8.5)	43 (16)	11 (21.6)	
MRD	Negative, N(%)	181 (54.4)	38 (56.7)	42 (60)	87 (49.7)	14 (66.7)	0.28
	Positive, N(%)	152 (45.6)	29 (43.3)	28 (40)	88 (50.3)	7 (33.3)	
	missing, N	311	82	106	93	30	
Cytogenetic classification	Fav/Interm, N(%)	498 (83.7)	115 (84.6)	130 (82.3)	214 (84.9)	39 (79.6)	0.76
	Adverse, N(%)	97 (16.3)	21 (15.4)	28 (17.7)	38 (15.1)	10 (20.4)	
	missing, N	49	13	18	16	2	
Cytogenetic abnormality	t(8;21) , N(%)	16 (2.7)	5 (3.7)	6 (3.8)	5 (2)	0 (0)	Not done
	inv(16) , N(%)	6 (1)	1 (0.7)	4 (2.5)	1 (0.4)	0 (0)	
	t(15;17) , N(%)	1 (0.2)	1 (0.7)	0 (0)	0 (0)	0 (0)	
	Normal K, N(%)	355 (59.7)	89 (65.4)	94 (59.5)	149 (59.1)	23 (46.9)	
	t(9;11) , N(%)	4 (0.7)	1 (0.7)	1 (0.6)	2 (0.8)	0 (0)	
	Other interm abnormality, N(%)	116 (19.5)	18 (13.2)	25 (15.8)	57 (22.6)	16 (32.7)	
	monosomal/complex, N(%)	39 (6.6)	12 (8.8)	10 (6.3)	13 (5.2)	4 (8.2)	
	mono(7) , N(%)	20 (3.4)	2 (1.5)	7 (4.4)	10 (4)	1 (2)	
	mono(5)/del(5q) , N(%)	14 (2.4)	3 (2.2)	4 (2.5) 3 (1.9) 2 (1.3)	5 (2)	2 (4.1)	
	11q23 not t(9;11) , N(%)	12 (2)	3 (2.2)		5 (2)	1 (2)	
	abn(17p) , N(%)	6 (1)	1 (0.7)		1 (0.4)	2 (4.1)	

	abn(3q) , N(%)	3 (0.5)	0 (0)	1 (0.6)	2 (0.8)	0 (0)	
	t(6;9) , N(%)	2 (0.3)	0 (0)	1 (0.6)	1 (0.4)	0 (0)	
	t(9;22) , N(%)	1 (0.2)	0 (0)	0 (0)	1 (0.4)	0 (0)	
	missing, N	49	13	18	16	2	
Patient sex	Female, N(%)	275 (42.8)	63 (42.6)	73 (41.5)	114 (42.5)	25 (50)	0.75
	Male, N(%)	367 (57.2)	85 (57.4)	103 (58.5)	154 (57.5)	25 (50)	
	missing, N	2	1	0	0	1	
Donor sex	Female, N(%)	209 (32.5)	61 (40.9)	68 (38.6)	66 (24.7)	14 (27.5)	0.001
	Male, N(%)	434 (67.5)	88 (59.1)	108 (61.4)	201 (75.3)	37 (72.5)	
	missing, N	1	0	0	1	0	
Female donor to Male recipient	No, N(%)	536 (83.6)	114 (77)	137 (77.8)	241 (90.3)	44 (88)	< 0.001
	Yes, N(%)	105 (16.4)	34 (23)	39 (22.2)	26 (9.7)	6 (12)	
	missing, N	3	1	0	1	1	
CMV patient	Negative, N(%)	233 (40)	45 (32.8)	79 (57.7)	93 (35.5)	16 (34.8)	< 0.001
	Positive, N(%)	349 (60)	92 (67.2)	58 (42.3)	169 (64.5)	30 (65.2)	
	missing, N	62	12	39	6	5	
CMV donor	Negative, N(%)	313 (53.8)	64 (47.1)	103 (75.2)	123 (46.9)	23 (48.9)	< 0.001
	Positive, N(%)	269 (46.2)	72 (52.9)	34 (24.8)	139 (53.1)	24 (51.1)	
	missing, N	62	13	39	6	4	
CMV donor to patient	Neg to Neg, N(%)	194 (33.7)	41 (30.1)	76 (56.7)	66 (25.4)	11 (23.9)	Not done
	Neg to Pos, N(%)	115 (20)	23 (16.9)	24 (17.9)	56 (21.5)	12 (26.1)	
	Pos to Neg, N(%)	35 (6.1)	3 (2.2)	2 (1.5)	25 (9.6)	5 (10.9)	
	Pos to Pos, N(%)	232 (40.3)	69 (50.7)	32 (23.9)	113 (43.5)	18 (39.1)	
	missing, N	68	13	42	8	5	

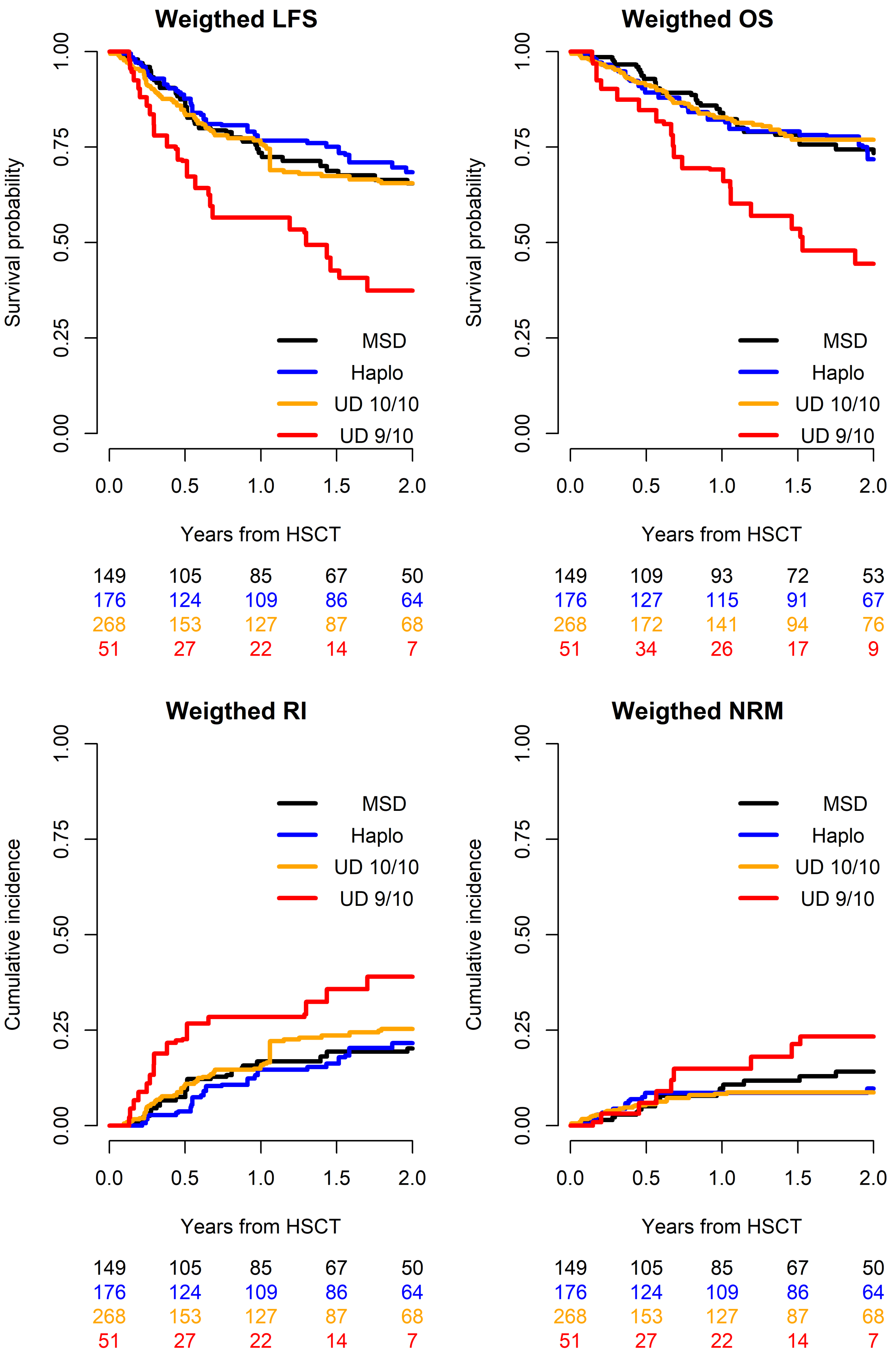
Source of cells	PB alone, N(%)	546 (84.8)	141 (94.6)	97 (55.1)	260 (97)	48 (94.1)	< 0.001
	Other, N(%)	98 (15.2)	8 (5.4)	79 (44.9)	8 (3)	3 (5.9)	
Myeloablative regimen	No, N(%)	314 (53.3)	69 (50.4)	65 (45.8)	148 (56.5)	32 (66.7)	0.04
	Yes, N(%)	275 (46.7)	68 (49.6)	77 (54.2)	114 (43.5)	16 (33.3)	
	missing, N	55	12	34	6	3	
Conditioning regimen	BuFlu based, N(%)	194 (30.2)	58 (38.9)	17 (9.8)	100 (37.3)	19 (37.3)	Not done
	BuFluThio based, N(%)	53 (8.3)	7 (4.7)	32 (18.4)	12 (4.5)	2 (3.9)	
	BuCy+Arac based, N(%)	97 (15.1)	20 (13.4)	73 (42)	3 (1.1)	1 (2)	
	BuCy based, N(%)	39 (6.1)	15 (10.1)	12 (6.9)	7 (2.6)	5 (9.8)	
	TreoFlu based, N(%)	101 (15.7)	20 (13.4)	7 (4)	65 (24.3)	9 (17.6)	
	TBI based, N(%)	81 (12.6)	10 (6.7)	25 (14.4)	41 (15.3)	5 (9.8)	
	FluMel based, N(%)	53 (8.3)	16 (10.7)	5 (2.9)	25 (9.3)	7 (13.7)	
	Other, N(%)	24 (3.7)	3 (2)	3 (1.7)	15 (5.6)	3 (5.9)	
	missing, N	2	0	2	0	0	
GVHD prophylaxis	CSA+MMF, N(%)	206 (32.3)	36 (24.3)	41 (23.8)	105 (39.3)	24 (47.1)	Not done
	CSA+MTX, N(%)	160 (25.1)	54 (36.5)	1 (0.6)	93 (34.8)	12 (23.5)	
	CSA+MTX+MM	110 (17.2)	12 (8.1)	91 (52.9)	3 (1.1)	4 (7.8)	

	F, N(%)						
	CSA, N(%)	50 (7.8)	19 (12.8)	3 (1.7)	23 (8.6)	5 (9.8)	
	MMF+TACRO/SIRO, N(%)	73 (11.4)	14 (9.5)	31 (18)	25 (9.4)	3 (5.9)	
	Other, N(%)	39 (6.1)	13 (8.8)	5 (2.9)	18 (6.7)	3 (5.9)	
	missing, N	6	1	4	1	0	
Invivo TCD	No, N(%)	200 (31.3)	74 (50)	67 (39)	46 (17.2)	13 (25.5)	< 0.001
	Yes, N(%)	438 (68.7)	74 (50)	105 (61)	221 (82.8)	38 (74.5)	
	missing, N	6	1	4	1	0	
PTCY	No, N(%)	526 (82.4)	136 (91.9)	101 (58.7)	246 (92.1)	43 (84.3)	< 0.001
	Yes, N(%)	112 (17.6)	12 (8.1)	71 (41.3)	21 (7.9)	8 (15.7)	
	missing, N	6	1	4	1	0	
Combination invivo TCD and PTCy	No invivo TCD; No PTCy, N(%)	100 (15.7)	63 (42.6)	7 (4.1)	25 (9.4)	5 (9.8)	Not done
	ATG, N(%)	405 (63.5)	66 (44.6)	94 (54.7)	212 (79.4)	33 (64.7)	
	Campath, N(%)	21 (3.3)	7 (4.7)	0 (0)	9 (3.4)	5 (9.8)	
	PTCy, N(%)	100 (15.7)	11 (7.4)	60 (34.9)	21 (7.9)	8 (15.7)	
	ATG+PTCy, N(%)	12 (1.9)	1 (0.7)	11 (6.4)	0 (0)	0 (0)	
	missing, N	6	1	4	1	0	

Abbreviations: MSD, matched sibling donor; Haplo, haploidentical donor; UD, unrelated donor; HSCT, hematopoietic stem cell transplantation; IQR, interquartile range; AML, acute myeloid leukemia; MRD, measurable residual disease; CMV, cytomegalovirus; Neg, negative; Pos, positive; PB, peripheral blood; BU, busulfan; Flu, fludarabine; Thio, thiotepa; Cy, cyclophosphamide; Arac, cytarabine ; Treo, treosulfan; TBI, total body irradiation; Mel, melphalan; GVHD, graft-versus-host disease; CSA, cyclosporine A; MMF, mycophenolate mofetil; MTX, methotrexate; TACRO, tacrolimus; SIRO, sirolimus; PTCY, post-transplant cyclophosphamide; TCD, T-cell depletion; ATG, antithymocyte globulin.

Figure legend

Figure S1: Transplant outcomes across different donor types: matched sibling, haploidentical, 9/10 and 10/10 unrelated donors. (A) Leukemia free survival (LFS). (B) Overall survival (OS). (C) Relapse incidence (RI). (D) Non relapse mortality (NRM).


Weigthed LFS
Survival probability
1.00
0.75
0.50
0.25
0.00
MSD
Haplo
UD 10/10
UD 9/10
0.0
0.5
1.0
1.5
2.0
Years from HSCT
149 105 85 67 50
176 124 109 86 64
268 153 127 87 68
51 27 22 14 7
Weigthed OS
Survival probability
1.00
0.75
0.50
0.25
0.00
MSD
Haplo
UD 10/10
UD 9/10
0.0
0.5
1.0
1.5
2.0
Years from HSCT
149 109 93 72 53
176 127 115 91 67
268 172 141 94 76
51 34 26 17 9
Weigthed RI
Cumulative incidence
1.00
0.75
0.50
0.25
0.00
MSD
Haplo
UD 10/10
UD 9/10
0.0
0.5
1.0
1.5
2.0
Years from HSCT
149 105 85 67 50
176 124 109 86 64
268 153 127 87 68
51 27 22 14 7
Weigthed NRM
Cumulative incidence
1.00
0.75
0.50
0.25
0.00
MSD
Haplo
UD 10/10
UD 9/10
0.0
0.5
1.0
1.5
2.0
Years from HSCT
149 105 85 67 50
176 124 109 86 64
268 153 127 87 68
51 27 22 14 7