

Table S1. HLA-I allele frequencies in controls and patients.

HLA-allotype	Controls (n = 83)	Patients (n = 102)	B-ALL (n = 70)	T-ALL (n = 16)	AML (n = 16)
HLA-A *01	20 (24.1 %)	21 (21.6 %)	16 (24.6 %)	3 (18.8 %)	2 (12.5 %)
*02	29 (34.9 %)	37 (38.1 %)	29 (44.6 %)	4 (25.0 %)	4 (25.0 %)
*03	12 (14.5 %)	19 (19.6 %)	11 (16.9 %)	4 (25.0 %)	4 (25.0 %)
*11	11 (13.3 %)	14 (14.4 %)	12 (18.5 %)	0 (0 %)	2 (12.5 %)
*23	5 (6.0 %)	7 (7.2 %)	5 (7.7 %)	0 (0 %)	2 (12.5 %)
*24	18 (21.7 %)	21 (21.6 %)	14 (21.5 %)	4 (25.0 %)	3 (18.8 %)
*25	1 (1.2 %)	2 (2.1 %)	1 (1.5 %)	1 (6.3 %)	0 (0 %)
*26	9 (10.8 %)	8 (8.2 %)	7 (10.8 %)	0 (0 %)	1 (6.3 %)
*29	11 (13.3 %)	12 (12.4 %)	7 (10.8 %)	4 (25.0 %)	1 (6.3 %)
*30	13 (15.7 %)	11 (11.3 %)	5 (7.7 %)	2 (12.5 %)	4 (25.0 %)
*31	2 (2.4 %)	3 (3.1 %)	2 (3.1 %)	1 (6.3 %)	0 (0 %)
*32	5 (6.0 %)	5 (5.2 %)	3 (4.6 %)	0 (0 %)	2 (12.5 %)
*33	4 (4.8 %)	5 (5.2 %)	2 (3.1 %)	3 (18.8 %)	0 (0 %)
*68	12 (14.5 %)	11 (11.3 %)	6 (9.2 %)	1 (6.3 %)	4 (25.0 %)
HLA-B *07	9 (10.8 %)	11 (11.3 %)	6 (9.2 %)	3 (18.8 %)	2 (12.5 %)
*08	9 (10.8 %)	12 (12.4 %)	8 (12.3 %)	3 (18.8 %)	1 (6.3 %)
*14	8 (9.6 %)	11 (11.3 %)	7 (10.8 %)	3 (18.8 %)	1 (6.3 %)
*15	7 (8.4 %)	10 (10.3 %)	7 (10.8 %)	1 (6.3 %)	2 (12.5 %)
*18	17 (20.5 %)	12 (12.4 %)	8 (12.3 %)	1 (6.3 %)	3 (18.8 %)
*27	3 (3.6 %)	1 (1.0 %)	1 (1.5 %)	0 (0 %)	0 (0 %)
*35	10 (12.0 %)	33 (34.0 %)¹	23 (35.4 %)	4 (25.0 %)	6 (37.5 %)
*38	6 (7.2 %)	10 (10.3 %)	7 (10.8 %)	2 (12.5 %)	1 (6.3 %)
*39	5 (6.0 %)	10 (10.3 %)	7 (10.8 %)	1 (6.3 %)	2 (12.5 %)
*40	10 (12.0 %)	9 (9.3 %)	5 (7.7 %)	2 (12.5 %)	2 (12.5 %)
*44	19 (22.9 %)	19 (19.6 %)	14 (21.5 %)	4 (25.0 %)	1 (6.3 %)
*49	11 (13.3 %)	5 (5.2 %)	5 (7.7 %)	0 (0 %)	0 (0 %)
*50	5 (6.0 %)	7 (7.2 %)	5 (7.7 %)	1 (6.3 %)	1 (6.3 %)
*51	15 (18.1 %)	7 (7.2 %)	5 (7.7 %)	2 (12.5 %)	0 (0 %)
*52	0 (0 %)	4 (4.1 %)	3 (4.6 %)	0 (0 %)	1 (6.3 %)
*53	3 (3.6 %)	6 (6.2 %)	2 (3.1 %)	1 (6.3 %)	3 (18.8 %)
*57	5 (6.0 %)	5 (5.2 %)	3 (4.6 %)	2 (12.5 %)	0 (0 %)
*58	4 (4.8 %)	0 (0 %)	0 (0 %)	0 (0 %)	0 (0 %)
HLA-C*01	2 (2.4 %)	9 (8.8 %)	7 (10.0 %)	0 (0 %)	2 (12.5 %)
*02	7 (8.4 %)	6 (5.9 %)	3 (4.3 %)	1 (6.3 %)	2 (12.5 %)
*03	9 (10.8 %)	11 (10.8 %)	8 (11.4 %)	1 (6.3 %)	2 (12.5 %)
*04	17 (20.5 %)	34 (33.3 %)²	22 (31.4 %)	4 (25.0 %)	8 (50.0 %)
*05	20 (24.1 %)	20 (19.6 %)	15 (21.4 %)	2 (12.5 %)	3 (18.8 %)
*06	10 (12.0 %)	16 (15.7 %)	10 (14.3 %)	3 (18.8 %)	3 (18.8 %)
*07	35 (42.2 %)	34 (33.3 %)	25 (35.7 %)	6 (37.5 %)	3 (18.8 %)
*08	8 (9.6 %)	13 (12.7 %)	9 (12.9 %)	3 (18.8 %)	1 (6.3 %)
*12	11 (13.3 %)	23 (22.5 %)	17 (24.3 %)	4 (25.0 %)	2 (12.5 %)
*14	3 (3.6 %)	1 (1.0 %)	1 (1.4 %)	0 (0 %)	0 (0 %)
*15	10 (12.0 %)	7 (6.9 %)	3 (4.3 %)	1 (6.3 %)	3 (18.8 %)
*16	12 (14.5 %)	10 (9.8 %)	5 (7.1 %)	4 (25.0 %)	1 (6.3 %)
*17	6 (7.2 %)	1 (1.0 %)	1 (1.4 %)	0 (0 %)	0 (0 %)

¹ All patients vs. Controls, p=0.0005, Pc=0.009; ² All patients vs. Controls, p=0.037, Pc=0.185.

Supplementary Figure S1

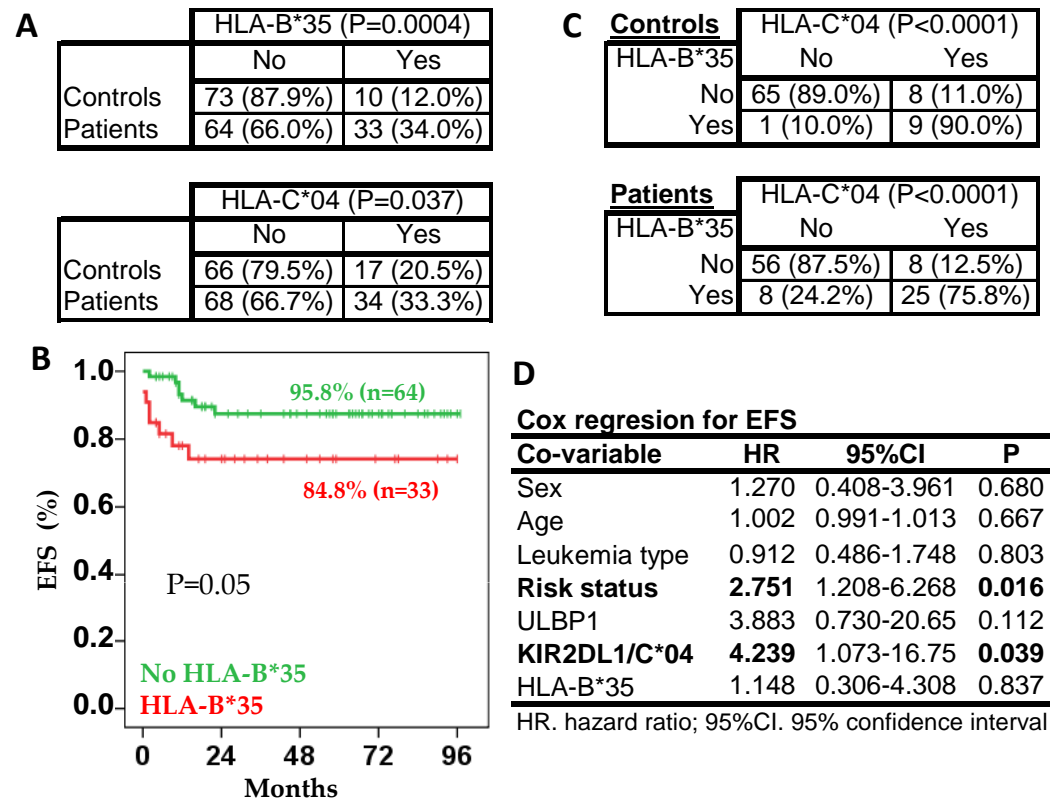


Figure S1. Reduced event-free survival (EFS) of acute leukemia patients associated with HLA-B*35 is due to its linkage disequilibrium with HLA-C*04. (a) Chi-squared test for HLA-B*35 or HLA-C*04 in controls and patients. Both HLA-B*35 and HLA-C*04 are significantly associated with acute leukemia. (b) Kaplan-Meier and Log-Rank tests for EFS of acute leukemia patients according to the presence of HLA-B*35. HLA-B*35 is associated with reduced EFS. (c) Chi-squared test for HLA-B*35 and HLA-C*04 in controls and patients. HLA-B*35 is in linkage disequilibrium with HLA-C*04 both in controls and in patients. KIR2DL1/HLA-C*04 interaction results in reduced EFS in HLA-B*35 patients. (d) Cox regression analysis for sex, age, leukemia type, ULBP expression on leukemic cells, KIR2DL1/HLA-C*04 interaction and HLA-B*35 allotype. KIR2DL1/HLA-C*04 interaction and risk-status are independent prognostic factors, whereas HLA-B*35 is not.

Supplementary Figure S2

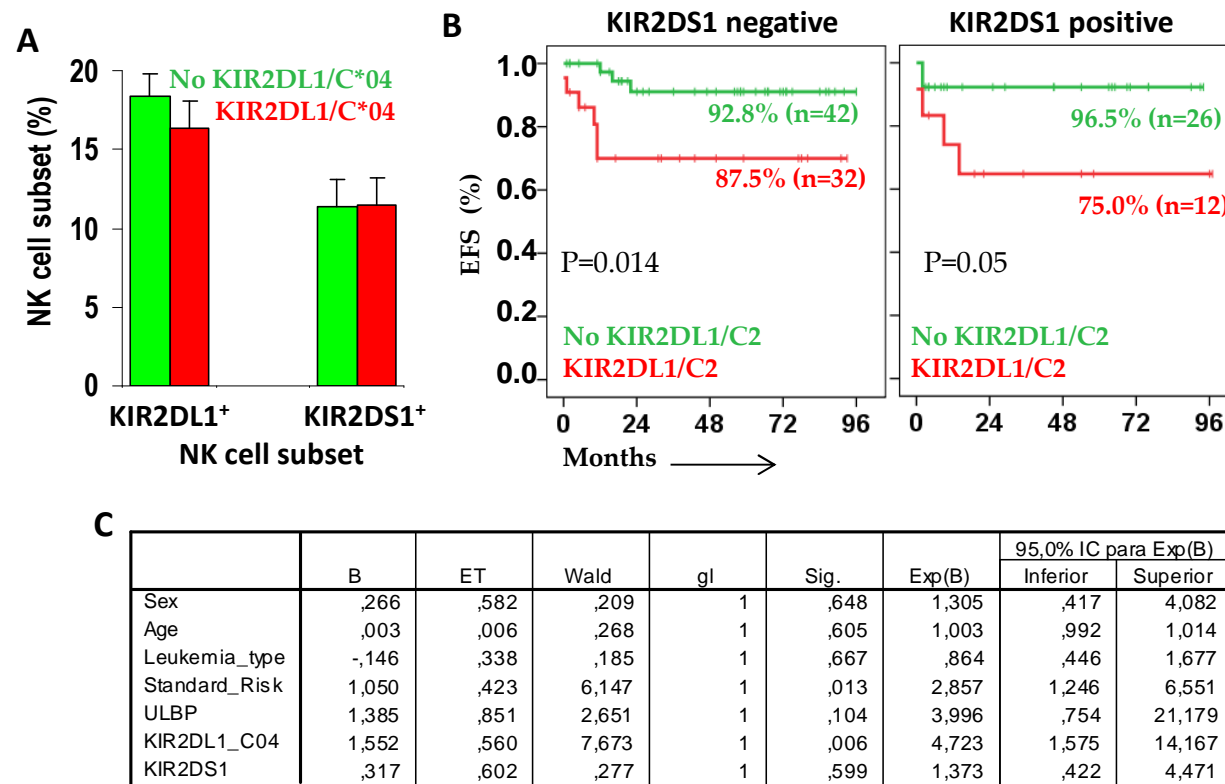


Figure S2. KIR2DS1 did not alter the event-free survival (EFS) curves of acute leukemia pediatric patients according to the presence of KIR2DL1/HLA-C*04 interaction. (a) Frequency of NK cells expressing KIR receptors for HLA C2-epitope (inhibitory KIR2DL1 and activating KIR2DS1) in the peripheral blood of pediatric acute leukemia patients according to the absence or presence of the KIR2DL1/HLA-C*04 interaction. (b) Kaplan-Meier and Log-Rank tests for EFS according to the presence of KIR2DL1/C*04 interaction in KIR2DS1 negative and positive patients. (c) Cox regression analysis for sex, age, leukemia type, ULBP expression on leukemic cells, KIR2DL1/HLA-C*04 interaction and presence of KIR2DS1 gene. The presence of KIR2DS1 gene did not alter the EFS curves according to the presence of KIR2DL1/HLA-C*04 interaction.

Patient Type Inclusion Relapse Death Months TPH A3 Bw4 C HLA- KIR KIR KIR KIR KIR KIR A3 Bw4 C HLA- D->R alloreactivity

Table-S2. Allogeneic stem cell transplantation performed in our series.

Patient Id	Type leukemia	Cause of Inclusion	Relapse	Death	OS months	HSCT Type	Receptor HLA-ligands				Donor KIR and HLA-ligands										D->R alloreactivity models ¹	
							A3	Bw4	C	HLA-C*04	KIR 2DL1	KIR 2DL2	KIR 2DL3	KIR 3DL1	KIR 3DL2	KIR 2DS1	A3	Bw4	C	HLA-C*04	Receptor ligand	Ligand incompatibility
p050	LMA	Relapse	Yes	Yes	11	Haplo	No	No	C1C2	Yes	1	0	1	1	1	0	No	Yes	C2C2	Yes	3DL1 & 3DL2	3DL1
p070	LMA	Relapse	Yes	Yes	29	Haplo	Yes	No	C2C2	Yes	1	1	1	1	1	0	Yes	No	C2C2	Yes	2DL2/L3 & 3DL1	None
p014	LLA-B	Relapse	No	Yes	1	UD	Yes	No	C1C2	Yes	1	1	1	1	1	0	Yes	No	C1C2	Yes	3DL1	None
p040	LLA-B	Relapse	No	Yes	11	UD	No	Yes	C2C2	Yes	1	0	1	1	1	0	No	Yes	C2C2	Yes	2DL3 & 3DL2	None
p056	LLA-B	Relapse	No	No	50	Haplo	No	No	C1C2	Yes	1	1	1	0	1	1	No	No	C1C2	Yes	3DL2 & 2DS1	2DS1
p002 ²	LMA	New diagnosis	Yes	No	26	UD	No	No	C1C2	No	1	1	1	1	1	1	No	No	C1C2	No	3DL1/L2 & 2DS1	2DS1
			Yes	Yes		Haplo					1	0	1	1	1	0	No	Yes	C1C2	No	3DL1 & 3DL2	3DL1
p007	LMA	New diagnosis	Yes	Yes	14	RD	Yes	No	C2C2	Yes	1	0	1	1	1	1	Yes	No	C2C2	Yes	2DL3 & 3DL1	None
p017	LLA-B	New diagnosis	Yes	No	86	Haplo	No	No	C1C2	No	1	0	1	1	1	1	No	No	C2C2	No	3DL1 & 3DL2	None
p030	LLA-T	New diagnosis	Yes	No	75	RD	No	No	C2C2	Yes	1	0	1	1	1	1	No	Yes	C2C2	Yes	2DL3 & 3DL1/L2	3DL1
p006	LMA	New diagnosis	No	No	94	UD	Yes	Yes	C1C2	No	1	0	1	1	1	0	Yes	Yes	C1C2	No	None	None
p009	LLA-T	New diagnosis	No	No	93	UD	No	Yes	C1C2	No	1	1	1	1	1	1	No	Yes	C1C2	No	3DL2 & 2DS1	2DS1
p010	LLA-B	New diagnosis	No	No	92	RD	No	Yes	C1C2	No	1	0	1	1	1	0	No	Yes	C1C2	No	3DL2	None
p049	LMA	New diagnosis	No	No	58	UD	No	No	C2C2	Yes	1	1	1	1	1	0	No	Yes	C2C2	Yes	2DL2/L3 & 3DL1/L2	3DL1
p063	LLA-B	New diagnosis	No	No	43	RD	Yes	No	C1C2	Yes	1	1	1	1	1	0	Yes	No	C1C2	Yes	3DL1	None
p068	LLA-T	New diagnosis	No	No	32	RD	No	Yes	C1C2	Yes	1	1	1	1	1	1	No	Yes	C1C2	Yes	3DL2 & 2DS1	2DS1
p078	LLA-B	New diagnosis	No	No	21	UD	No	No	C1C2	No	1	1	1	1	1	0	No	Yes	C1C2	No	3DL1 & 3DL2	3DL1
p084	LLA-B	New diagnosis	No	No	17	Haplo	No	No	C1C2	Yes	1	1	1	1	1	0	No	Yes	C1C1	No	3DL1 & 3DL2	3DL1
p086	LMA	New diagnosis	No	No	15	UD	No	No	C1C1	No	1	0	1	1	1	1	No	No	C1C1	No	2DL1 & 3DL1/L2	None

HSCT: stem cell transplantation; Haplo: haploidentical HSCT; RD: related donor; UD: unrelated donor; OS: overall survival.

¹ Symons HJ et cols. Biol Blood Marrow Transplant 2010;16(4):533-42. doi: 10.1016/j.bbmt.2009.11.022.

² This patient received UD-HSCT and Haplo-HSCT after relapsing.

Cumulative incidence

Models		Relapse	Death
Receptor Lig,	n	%	%
KIR2DL1	1	0%	0%
KIR2DS1	4	25%	0%
KIR3DL2	13	31%	23%
KIR3DL1	13	54%	38%
KIR2DL2/L3	4	50%	50%
Ligand incompatibility			
KIR2DS1	4	25%	0%
KIR3DL1	6	50%	33%
None	9	44%	44%

