

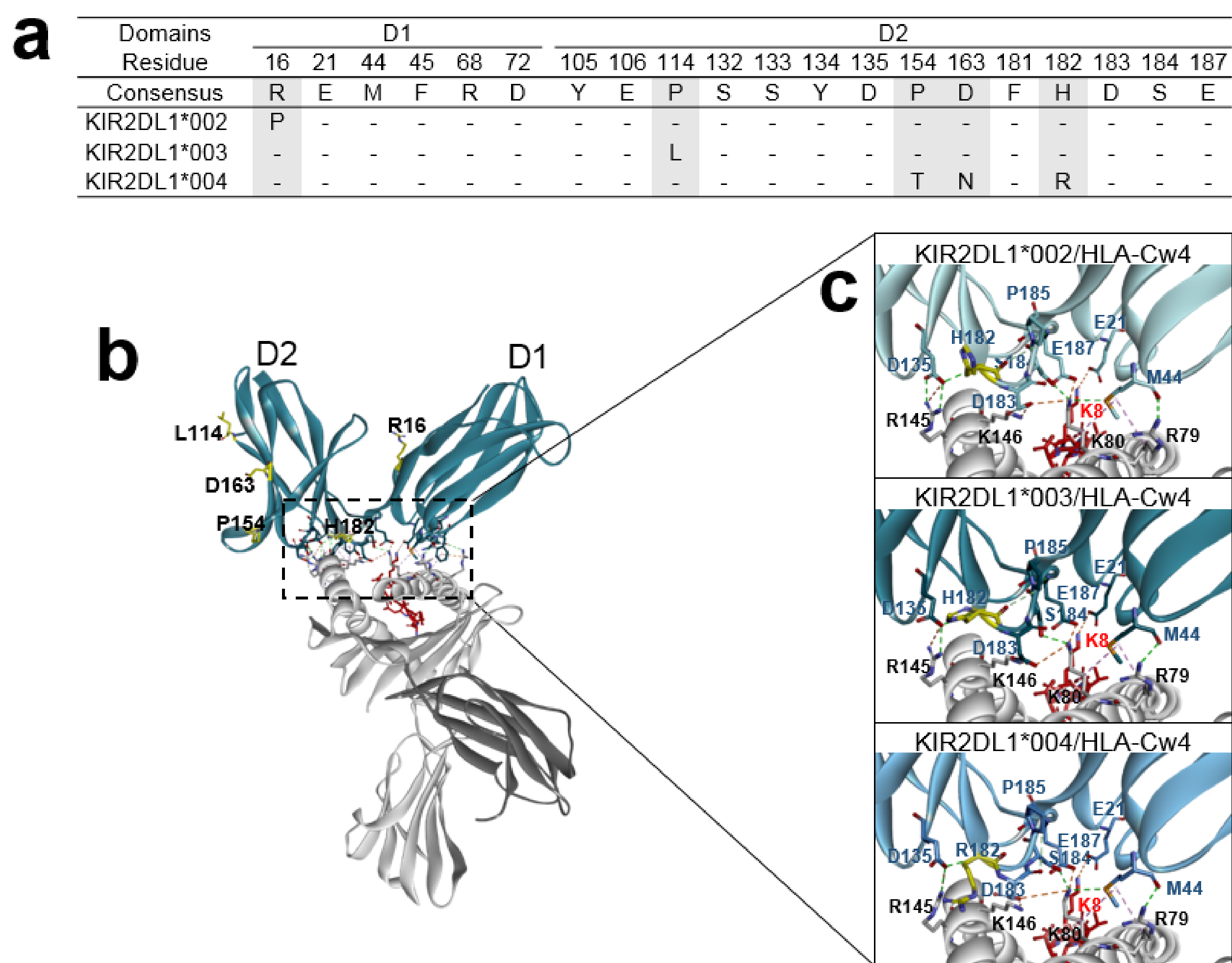


Figure S1. Structural model of KIR2DL1 allotypes complexed with HLA-Cw4 molecule. (a) Alignment of partial amino acid sequences of D1 and D2 domains for three KIR2DL1 allele-encoded receptors (allotypes). Identity with the consensus sequence is indicated by dashes “-”, the polymorphic residues are highlighted in grey and residues in contact with the HLA-Cw4 molecule are also shown. (b) Ribbon diagram of the KIR2DL1*003 allotype (in blue) bound to the HLA-Cw4 molecule (in grey) and in complex with its specific peptide (in red) (modelling based on the structure PDB 1IM9). The polymorphic residues are shown in yellow. (c) Details and comparison of the interaction network between three KIR2DL1 allotypes (in blue) and the HLA-Cw4 molecule (in grey) in complex with its specific peptide (in red), the polymorphic residue at position 182 of the KIR2DL1 allotypes is shown in yellow.

Table S1. Numerous KIR2DL1/2/3/S1/S2 allele combinations encountered in a cohort of French blood donors (N=108) depending on KIR gene motifs and HLA-Cw environment

	KIR allele typing										HLA-C environment				KIR motifs	
	2DS2	2DS2	2DL2	2DL2	2DL3	2DL3	2DL1	2DL1	2DS1	2DS1	N	C1C1	C1C2	C2C2	Cen	Tel
1	-		-		*001		*003		-		9	4	4	1	AA	AA
2	*001		*001		*001		*003	*004	*002		6	1	3	2	AB	AB/BB
3	-		-		*002	<i>*007</i>	*002		-		5	4	1		AA	AA
4	*001		*003		*002		*002		-		5	3		2	AB	AA
5	*001		*001		*002		*002	*004	*002		5	1	4		AB	AB/BB
6	-		-		+		*003		-		4	1	3		AA	AA
7	-		-		*002	*001	*002	*003	-		4	2		2	AA	AA
8	*001		*001		*002		*002	*004	-		4	4			AB	AA/AB
9	*001		*001		*002		*002		-		4	2	1	1	AB	AA/AB
10	*001		*003		*001		*003		-		3	2		1	AB	AA
11	*001		*001		*001		*003	*004	-		3		1	2	AB	AA/AB
12	*001		*003		*002		*002		*002		3	2	1		AB	AB/BB
13	-		-		*002	*005	*002	*001	-		2		1	1	AA	AA
14	-		-		*005	<i>*007</i>	*002		-		2		1	1	AA	AA
15	-		-		*001	<i>*002</i>	*003		-		2	1	1		AA	AA
16	*001		*001		*001		*003		*002		2		1	1	AB	AB/BB
17	*001		+		+		*003	*004	*002		2		1	1	AB	AB/BB
18	*001		*003	<i>*001</i>	-		*004		-		2	1		1	BB	AA
19	-		-		*001	*005	*003	*001	-		1	1			AA	AA
20	-		-		*002	<i>*015</i>	*003	*001	-		1		1		AA	AA
21	-		-		*002		*002		-		1	1			AA	AA
22	-		-		*002	<i>*001</i>	*002	<i>001/002/00</i>	-		1		1		AA	AA
23	-		-		*001		*003	<i>*001/002</i>	-		1	1			AA	AA
24	-		-		+		*003	<i>*001/002</i>	-		1		1		AA	AA
25	-		-		*001	<i>*002</i>	*003	<i>001/002/00</i>	-		1		1		AA	AA
26	-		-		*002		*002		*002		1		1		AA	AB
27	-		-		*002	<i>*007</i>	*002		*002	*003	1	1			AA	AB
28	-		-		*002	<i>*001</i>	*002	*004	*002		1			1	AA	AB
29	-		-		*001		*003		*002	*006	1	1			AA	AB
30	-		-		*001		*003		*002	*003	1		1		AA	AB
31	-		-		*003		*003		*002		1			1	AA	AB
32	-		-		*001		*003		*002		1	1			AA	AB
33	-		-		+		*003	<i>001/002/00</i>	*002		1		1		AA	AB
34	-		-		*001	<i>*005</i>	*003	<i>*001/002</i>	*002		1		1		AA	AB
35	-		-		*001	<i>*002</i>	*003		*002	*006	1	1			AA	AB
36	-		-		*001	<i>*002</i>	*003		*002		1			1	AA	BB
37	-		-		+		*003	*004	-		1		1		AA	nd
38	*001		*001		*005		*004	*001	-		1			1	AB	AA
39	*001		*001		*002		*002	<i>*007</i>	-		1		1		AB	AA
40	*001		+		+		*002	<i>*007</i>	-		1			1	AB	AA
41	*001		<i>*012</i>		*001		*003		-		1	1			AB	AA
42	*001		*001		*001		*003	<i>*004/006</i>	-		1	1			AB	AA
43	*001		*003		*002		*002		*002	*003	1		1		AB	AB
44	*001		*001		+		*002	*004	*002		1	1			AB	AB
45	*001		*008		*002		*002	*004	*002		1			1	AB	AB
46	-		+		*001		*003		*002		1	1			AB	AB
47	*001	<i>*002</i>	*001		*001		*003	*004	*002		1		1		AB	AB
48	*001		+		+		*003	*004	-		1		1		AB	AB
49	*001		+		+		*003	<i>*007</i>	*002		1	1			AB	BB
50	*001		*003		-		-		-		1		1		BB	AA
51	*001		*003	<i>*012</i>	-		-		-		1		1		BB	AA
52	*001		*003	<i>*012</i>	-		-		<i>*002/006</i>		1	1			BB	AB
53	*001	<i>*002</i>	*003	<i>*008</i>	-		*004		*002		1	1			BB	AB
54	*001		*001		-		*004		-		1			1	BB	AB
55	*001		*001	<i>*008</i>	-		*004		-		1			1	BB	AB
56	*001		*001	<i>*005</i>	-		*004		-		1		1		BB	AB
57	*001		*003		-		*004		*002		1		1		BB	AB
58	*001		+		-		<i>*007</i>	<i>*001/002</i>	*002		1		1		BB	AB
59	*001		+		-		<i>*007</i>		*002		1			1	BB	AB
N											108	42	41	25		

KIR2DL1/2/3/S1/S2 alleles were assigned using NGS and Profiler software. Main KIR2DL1/2/3 allele combinations were highlighted in bold or italics characters. Absence of a specific KIR gene was mentioned using "-". KIR2DL1/2/3 remaining allele ambiguities and non-assigned alleles were indicated using "/" and "+" respectively. KIR centromeric (Cen)/telomeric (Tel) motifs were defined. C1C1, C1C2 and C2C2 environment were defined depending on HLA-C allelic typing.

Table S2. Characteristics of patients

	All patients N=81	CenAA* donors N=39	CenAB.BB* donors N=42	P value
Gender: male	49 (60%)	26 (67%)	23 (55%)	0.36
Median age: years (range)	60 (24-71)	61 (24-71)	58 (32-71)	0.71
Disease				
AML/MDS	32/14 (57%)	17/6 (59%)	15/8 (55%)	0.82
ALL	5	1	4	
HD	4	2	2	
NHL	14	7	7	
CLL	4	3	1	
Myelofibrosis	4		4	
pDCs neoplasm	2	2		
CML	1		1	
Mycosis fungoides	1	1		
Myeloid/lymphoid	51(63%)/30(37%)	23(59%)/16(41%)	28(67%)/14(33%)	0.50
Status at treatment				
CR1/CR2/CR3	30/10/3 (53%)	13/4/1 (46%)	17/6/2 (60%)	0.27
PR1/PR2/PR3/PR5	5/5/4/4 (22%)	3/3/3/4 (33%)	2/2/1 (12%)	
Active	19 (24%)	7 (18%)	12 (28%)	
Aplasia	1 (1%)	1 (3%)		
Disease risk index				
Intermediate	34 (42%)	15 (38%)	19 (45%)	0.65
High	47 (58%)	24 (62%)	23 (55%)	
Previous allograft	12 (15%)	6 (15%)	6 (15%)	
Conditioning				
Baltimore	26 (32%)	11 (28%)	15 (36%)	0.49
Clo-Baltimore	27 (33%)	13 (33%)	14 (33%)	
CloB2A1	28 (35%)	15 (38%)	13 (31%)	
Haplo-donors				
Median age: years (range)	42 (20-72)	42 (22-71)	41 (20-72)	0.85
Sister/Brother	12/20 (40%)	9/7 (41%)	3/13 (38%)	0.83
Father/Mother	6/2 (10%)	4/1 (13%)	2/1 (7%)	
Son/Daughter	24/12 (44%)	11/4 (38%)	13/8 (50%)	
Nephew	5 (6%)	3 (8%)	2 (5%)	
Donor/recipient CMV status				
-/-	46 (57%)	20 (51%)	26 (62%)	0.37
-/+	16 (20%)	8 (21%)	8 (19%)	
+/-	8 (10%)	5 (13%)	3 (7%)	
+/+	11 (13%)	6 (15%)	5 (12%)	
ABO compatibility				
compatibility	53 (65%)	27 (70%)	26 (62%)	0.64
Minor inc	15 (19%)	6 (15%)	9 (21%)	
Major inc	13 (16%)	6 (15%)	7 (17%)	
Graft composition				
Median CD34 ⁺ cells: 10 ⁶ /kg	7.92 (2.88-19.94)	7.89 (3.10-15.16)	7.96 (2.88-19.94)	0.95
Median CD3 ⁺ T cells: 10 ⁷ /kg	26.61 (7.71-49.99)	25.02 (12.60-46.66)	24.27 (7.71-49.99)	0.94
Median CD45 ⁺ cells: 10 ⁸ /kg	8.57 (3.80-18.65)	8.04 (3.80-18.65)	9.07 (5.04-13.80)	0.80

Abbreviations: AML: acute myeloid leukemia; MDS: myelodysplastic syndrome; ALL: acute lymphoblastic leukemia; HD: Hodgkin disease; NHL: non-Hodgkin lymphoma; CLL: chronic lymphocytic leukemia; pDCs: plasmacytoid dendritic cells; CML: chronic myeloid leukemia; CR: complete remission; PR: partial remission; CMV: cytomegalovirus; inc: incompatibility. *CenAA donors are KIR2DL3+/2DL2-/S2- ; CenAB.BB donors are KIR2DL2/S2+ and KIR2DL3-/+