Number of interactions

INHIBITORY		ACTIVATING	
KIR	HLA	KIR	HLA
2DL1	C2	2DS1	C2
2DL2	C1	2DS2	C*16
2DL2	C2	2DS4	A*11
2DL3	C1	2DS4	C*01:02
3DL1	B-Bw4	2DS4	C*14:02
3DL1	A-Bw4	2DS4	C*16:01
3DL2	A*03	2DS4	C*02:02
3DL2	A*11	2DS4	C*05:01
		2DS4	C*04:01
		2DS5*003	C2
		2DS5*004	C2
		2DS5*005	C2
		2DS5*006	C2
		2DS5*007	C2
		2DS5*008	C2

Scoring matrix for counting number of interactions as previously described (21-23). HLA alleles were coded for their KIR ligand status (C1, C2, B-Bw4, A-Bw4) for those interactons involving only ligand status. For those with specific allotype designation, e.g. A*03, A*11, all alleles in those groups were counted. Homozygous interactions were counted twice.

Telomeric interactions

	KIR3DL1 group			
HLA	**K015**	**K001**	**K005**	**K004**
B*57:01	74.5	76.8	77.0	0
A*32:01	67.6	62.3	44.6	0
B*58:01	61.9	70.1	61.9	0
B*53:01	54.8	60.8	52.4	0
B*49:01	54.4	63.0	54.5	0
B*57:03	49.9	68.6	58.5	0
B*38:01	37.6	51.8	47.4	0
B*15:13	25.1	40.9	36.5	0
B*15:16	25.0	35.3	31.3	0
B*51:02	24.8	34.7	32.6	0
B*51:01	23.7	32.4	31.0	0
B*59:01	22.4	37.7	34.3	0
B*44:03	20.1	35.7	62.8	0
B*47:01	18.9	35.9	39.6	0
B*44:02	17.6	24.5	35.6	0
A*24:03	13.6	26.8	39.4	0
B*52:01	11.9	21.6	18.6	0
C*16:01	11.1	3.8	4.5	0
C*04:01	9.8	6.6	5.1	0
C*07:02	7.7	8.5	4.3	0
A*24:02	6.9	24.0	36.7	0
B*37:01	5.5	18.0	27.1	0
C*14:02	5.5	3.4	4.2	0
C*02:02	5.3	3.2	3.2	0
C*01:02	0.8	5.2	4.9	0
A*23:01	0.0	3.9	18.4	0
B*27:05	0.0	5.3	16.4	0
B*13:01	0.0	0.0	7.0	0

Cen and Tel interaction scores used the 'Telomeric Interactions' and 'Centromeric Interactions' scoring matrices. The results were summed for the composite interaction score. The centromeric interaction values were obtained from published binding studies where they were reported as absolute binding values. The values for low expressing allels were multiplied by 0.5 to account for the expression level difference. Telomeric interaction scores were taken from Saunders et al along with allele assignment to one of four groups (K001, K004, K005, K015). These values were reported as percent of maximum and were normalized to the centromeric values so that the 100% score of Saunders was equivalent to the maximum centromeric value. KIR and/or HLA of the donor and/or recipient were given the value of the closest allele if they did not appear in the matrix. In homozygous individuals the interaction was counted twice, once for each of the homozygous alleles.

Example calculation.
Donor KIR: 2DL2*003| 2DL3*002| 2DL1*002| 3DL1*001/009 (K001/K001)
Recipient HLA: A*01:01/03:01| B*07:02/44:03| C*07:02/16:01

Cen 19+7+12+0 = 38 Avg. = 38/4 = 9.5
Tel 35.7+35.7+8.5+8.5+3.8+3.8 = 98
Avg. = 98/6 = 16.33
Combined 38+98 = 136 Avg. = 136/10 = 13.6

Centromeric interactions

		C1									**C2**						
	Allotype	C*01:02	C*03:02	C*03:03	C*03:04	C*07:02	C*08:01	C*12:03	C*14:02	C*16:01	C*02:02	C*04:01	C*05:01	C*06:02	C*15:02	C*17:01	C*18:02
2DL2/3	2*001	20	28	44	50	22	34	14	18	12	17	7	14	17	30	9	20
	2*002	20	28	44	50	22	34	14	18	12	17	7	14	17	30	9	20
	2*003	17	21	26	38	19	23	12	13	7	1	1	2	4	14	3	8
	2*004	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	2*005	20	28	44	50	22	34	14	18	12	17	7	14	17	30	9	20
	2*006	13	21	27	37	15	21	10	11	4	4	2	2	3	12	1	4
	2*007	20	28	44	50	22	34	14	18	12	17	7	14	17	30	9	20
	2*008	10	14	22	25	11	17	7	9	6	8.5	3.5	7	8.5	15	4.5	10
	2*009	24	41	49	51	28	43	15	21	13	15	4	12	19	26	8	20
	2*010	10	14	22	25	11	17	7	9	6	8.5	3.5	7	8.5	15	4.5	10
	2*011	15	21	28	36	18	25	12	13	8	3	1	4	2	12	2	3
	3*001	7	21	27	30	12	21	1	3	0	3	1	1	2	2	2	3
	3*002	7	21	27	30	12	21	1	3	0	3	1	1	2	2	2	3
	3*003	7	21	27	30	12	21	1	3	0	3	1	1	2	2	2	3
	3*004	14	21	26	30	18	22	2	11	3	3	0	1	2	5	1	3
	3*005	14	21	26	30	18	22	2	11	3	3	0	1	2	5	1	3
	3*006	7	21	27	30	12	21	1	3	0	3	1	1	2	2	2	3
	3*007	7	21	27	30	12	21	1	3	0	3	1	1	2	2	2	3
	3*008N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	3*009	3	21	24	28	12	23	0	1	0	0	0	0	2	1	1	2
	3*010	14	21	26	30	18	22	2	11	3	3	0	1	2	5	1	3
	3*011	8	22	27	32	14	21	2	2	2	2	0	1	2	4	1	1
	3*012	7	21	27	30	12	21	1	3	0	3	1	1	2	2	2	3
	3*013	6	21	27	30	10	21	2	3	0	3	0	0	0	1	1	2
	3*014	24	41	49	54	29	41	17	22	14	1	0	4	2	9	2	3
	3*015	12	22	26	32	21	21	2	5	3	3	2	2	2	5	1	4
	3*016	24	41	50	57	33	42	16	21	17	4	1	2	5	15	3	12
	3*017	24	41	49	54	29	41	17	22	14	1	0	4	2	9	2	3
	3*018	24	41	49	54	29	41	17	22	14	1	0	4	2	9	2	3
2DL1	2DL1*022	34	35	54	57	27	44	24	22	18	0	0	0	0	0	0	0
	*001										39	9	38	47	65	25	53
	*002										39	9	38	47	65	25	53
	*003										38	8	37	46	63	25	53
	*004										15	3	15	18.5	25	10	21
	*005										38	8	37	46	63	25	53
	*006										19	4	18.5	23	31.5	12.5	26.5
	*007										15.5	3.5	15	18.5	25.5	10	21.5
	*008										8	2	7	9	13	5	11
	*009										38	8	37	46	63	25	53
	*010										30	6	30	37	50	20	42
	*011										15	3	15	18.5	25	10	21
	*012										36	8	35	44	59	23	50
	*014										1	0	1	1	1	0	1
	*020										50	11	48	61	77	33	66
	*021										24	2	25	25	44	17	39
	*023										46	9	45	58	74	31	67
	*024										14.5	3	14.5	18	24.5	9.5	20.5
	*025										21	4	20	25	34	14	29
	*026										0	0	0	0	0	0	0
	*035										15	3	15	18.5	25	10	21
	*036										39	9	38	47	65	25	53

Supplemental Figure1. Scoring matrices for calculating number of interactions (inset box) and interaction scores for centromeric and telomeric KIR.

			Centromeric (Cen)									Telomeric (Tel)								
Cen	**Tel**		**3DL3**	**2DS2**	**2DL2**	**2DL3**	**2DL5B**	**2DS3/5**	**2DP1**	**2DL1**	**3DP1**	**2DL4**	**3DL1**	**3DS1**	**2DL5A**	**2DS3/5**	**2DS1**	**2DS4**	**3DL2**	**N**
A/A	A/A		2			2			2	2	2	2	2					2	2	294
		DEL7	1			2			2	2	2	2	2					2	2	1
		DEL16	2			2			2	2	2	2	2					1	1	2
A/A	A/B		2			2			2	2	2	2	1	1	1	1	1	1	2	103
		DEL1	2			2			2	1	1	1	1				1	1	2	6
		DEL17	2			2			2	2	2	2	1	1	1	1		1	2	1
		DUP2	2			2			3	3	3	3	1	2	2	2	1	1	2	7
		DUP3	2			2			2	2	3	3	1	2	1	1	1	1	2	3
A/A	B/B		2			2			2	2	2	2		2	2	2	2		2	8
		DUP4	2			2			3	3	3	3		3	3	3	2		2	1
A/B01	A/A		2	1	1	1	1	1	2	2	2	2	2					2	2	56
		DEL8	2		1	1	1	1	2	2	2	2	2					2	2	2
A/B01	A/B		2	1	1	1	1	1	2	2	2	2	1	1	1	1	1	1	2	59
		DEL10	2	1	1	1			2	2	2	2	1	1	1	1	1	1	2	1
		DEL11	2	1		1	1	1	2	2	2	2	1	1	1	1	1	1	2	1
		DUP5	2	1	1	1	2	2	3	3	3	3	2	1				2	2	1
A/B01	B/B		2	1	1	1	1	1	2	2	2	2		2	2	2	2		2	9
A/B02	A/A		2	1	1	1			1	1	2	2	2					2	2	130
		DEL9	2	1		1			2	2	2	2	2					2	2	3
A/B02	A/B		2	1	1	1			1	1	2	2	1	1	1	1	1	1	2	65
		DEL2	2	1		1	1		1	1	1	1	1			1	1	1	2	1
		DEL3	2	1	1	1			1		1	1	1				1	1	2	1
		DEL4	2	1	1	1	1		1	1	1	1	1			1	1	1	2	10
		DUP6	2	1	1	1			1	1	3	3	2	1				2	2	1
		DUP7	2	1	1	1			2	2	3	3	2	1	1	1		2	2	9
		DUP8	2	1	1	1			1	1	3	3	1	2	1	1	1	1	2	1
		DUP9	2	1	1	1			2	2	3	3	1	2	2	2	1	1	2	2
A/B02	B/B		2	1	1	1			1	1	2	2		2	2	2	2		2	7
		DEL5	2	1	1	1	1		1	1	1	1		1	1	2	2		2	1
B01/B01	A/A		2	2	2		2	2	2	2	2	2	2					2	2	8
		DEL12	2	2	1		1	1	2	2	2	2	2					2	2	1
		DEL13	2	1	2		2	2	2	2	2	2	2					2	2	1
B01/B01	A/B		2	2	2		2	2	2	2	2	2	1	1	1	1	1	1	2	5
B01/B01	B/B		2	2	2		2	2	2	2	2	2		2	2	2	2		2	1
		DEL14	2	2	1		1	1	2	2	2	2		2	2	2	2		2	1
B01/B02	A/A		2	2	2		1	1	1	1	2	2	2					2	2	13
B01/B02	A/B		2	2	2		1	1	1	1	2	2	1	1	1	1	1	1	2	23
		DEL15	2	2	1				1	1	2	2	1	1	1	1	1	1	2	2
		DUP1	2	2	2				1	1	3	3	2	1	1	1		2	2	3
		DUP10	2	2	2		1	1	2	2	3	3	1	2	2	2	1	1	2	2
B01/B02	B/B		2	2	2		1	1	1	1	2	2		2	2	2	2		2	6
B02/B02	A/A		2	2	2						2	2	2					2	2	25
B02/B02	A/B		2	2	2						2	2	1	1	1	1	1	1	2	9
		DEL6	2	2	2		1				1	1	1			1	1	1	2	2
		DUP11	2	2	2						3	3	1	2	2	2	1	1	2	2
B02/B02	B/B		2	2	2						2	2		2	2	2	2		2	0

Supplemental Figure 2. This figure shows the genotypes of the cohort. Those that diverged from those predicted by the common structural types shown in Figure 2A are indicated as 'DEL' for deletion and 'DUP' for duplication. Gene presence is indicated by a shaded square and the number indicates the copy number of the gene. Black squares match the assigned genotype for the final analyses. Gray squares indicate genes with copy numbers different from expected. N are the number of observations of that genotype in the dataset. The individual genotypes are grouped with the genotype that they were assigned for the analyses.

FRAMEWORK

3DL2

3DL2 Allele	N (Allele)	Freq	N (Phenotypic)	Freq
Negative	2	0.001122334	2	0.002244669
*001	431	0.241863075	372	0.417508418
*002	348	0.195286195	305	0.342312009
*003	116	0.065095398	114	0.127946128
*005	106	0.059483726	104	0.116722783
*006	7	0.003928171	7	0.007856341
*007	325	0.182379349	297	0.333333333
*008	60	0.033670034	57	0.063973064
*009	139	0.078002245	133	0.149270483
*010	72	0.04040404	71	0.079685746
*011	79	0.044332211	75	0.084175084
*012	1	0.000561167	1	0.001122334
*013	9	0.005050505	9	0.01010101
*015	2	0.001122334	2	0.002244669
*017	1	0.000561167	1	0.001122334
*018	27	0.015151515	27	0.03030303
*019	16	0.008978676	16	0.017957351
*020	7	0.003928171	7	0.007856341
*021	1	0.000561167	1	0.001122334
*023	3	0.001683502	3	0.003367003
*026	1	0.000561167	1	0.001122334
*027	8	0.004489338	8	0.008978676
*029	1	0.000561167	1	0.001122334
*034	1	0.000561167	1	0.001122334
*038	1	0.000561167	1	0.001122334
*039	1	0.000561167	1	0.001122334
*040	2	0.001122334	2	0.002244669
*043	3	0.001683502	3	0.003367003
*047	1	0.000561167	1	0.001122334
*048	4	0.002244669	4	0.004489338
*076	4	0.002244669	4	0.004489338
*079	1	0.000561167	1	0.001122334
*098	2	0.001122334	2	0.002244669

2DL4

2DL4 Allele	N (Allele)	Freq	N (Phenotypic)	Freq
Negative	21	0.011576626	21	0.023569024
*001	506	0.278941566	419	0.470258137
*005	385	0.212238148	335	0.375982043
*006	56	0.030871003	54	0.060606061
*008	583	0.321389195	487	0.54657688
*009	3	0.001653804	3	0.003367003
*010	4	0.002205072	4	0.004489338
*011	244	0.134509372	222	0.249158249
*012	5	0.00275634	5	0.005611672
*014	1	0.000551268	1	0.001122334
*021	1	0.000551268	1	0.001122334
*022	3	0.001653804	3	0.003367003
*023	1	0.000551268	1	0.001122334
*029	1	0.000551268	1	0.001122334

TELOMERIC

3DL1/S1

3DL1/S1 Allele	N (Allele)	Freq	N (Phenotypic)	Freq
Negative	21	0.011576626	21	0.023569024
L1*001	298	0.164277839	266	0.298540965
L1*002	201	0.110804851	187	0.209876543
L1*004	244	0.134509372	231	0.259259259
L1*005	235	0.12954796	213	0.239057239
L1*007	54	0.029768467	54	0.060606061
L1*008	99	0.054575524	95	0.106621773
L1*009	25	0.013781698	25	0.028058361
L1*015	151	0.083241455	138	0.154882155
L1*016	1	0.000551268	1	0.001122334
L1*017	6	0.003307607	6	0.006734007
L1*019	8	0.004410143	8	0.008978676
L1*020	37	0.020396913	37	0.041526375
L1*021	1	0.000551268	1	0.001122334
L1*022	3	0.001653804	3	0.003367003
L1*028	1	0.000551268	1	0.001122334
L1*029	9	0.004961411	7	0.007856341
L1*031	6	0.003307607	6	0.006734007
L1*033	7	0.003858875	6	0.006734007
L1*034	1	0.000551268	1	0.001122334
L1*035	1	0.000551268	1	0.001122334
L1*039	1	0.000551268	1	0.001122334
L1*051	1	0.000551268	1	0.001122334
L1*052	6	0.003307607	6	0.006734007
L1*053	6	0.003307607	6	0.006734007
L1*059	2	0.001102536	2	0.002244669
L1*072	1	0.000551268	1	0.001122334
L1*075	1	0.000551268	1	0.001122334
L1*109	1	0.000551268	1	0.001122334
S1*013	375	0.206725469	326	0.365881033
S1*049N	11	0.006063947	11	0.012345679

2DS4

2DS4 Allele	N (Allele)	Freq	N (Phenotypic)	Freq
Negative	377	0.211560045	343	0.384960718
*001	412	0.231200898	352	0.395061728
*003	428	0.240179574	373	0.418630752
*004	61	0.034231201	58	0.065095398
*006	257	0.144219978	243	0.272727273
*008	1	0.000561167	1	0.001122334
*009	4	0.002244669	4	0.004489338
*010	242	0.135802469	220	0.24691358

2DL5A

2DL5A Allele	N (Allele)	Freq	N (Phenotypic)	Freq
Negative	1402	0.786756453	845	0.948372615
A*001	290	0.162738496	267	0.2996633
A*005	89	0.049943883	85	0.095398429
A*014	1	0.000561167	1	0.001122334

2DS3/5 as single locus

2DS3/5 Allele	N (Allele)	Freq	N (Phenotypic)	Freq
Negative	1209	0.66869469	746	0.837261504
3*001	226	0.125	217	0.243546577
3*002	51	0.028207965	51	0.057239057
3*003N	14	0.007743363	14	0.015712682
5*002	302	0.167035398	285	0.31986532
5*003	1	0.000553097	1	0.001122334
5*005	1	0.000553097	1	0.001122334
5*007	3	0.001659292	3	0.003367003
5*009	1	0.000553097	1	0.001122334

CENTROMERIC

2DL2/3

2DL2/3 Allele	N (Allele)	Freq	N (Phenotypic)	Freq
Negative	10	0.005611672	10	0.011223345
2*001	287	0.161054994	258	0.28956229
2*003	265	0.148709315	243	0.272727273
2*004	1	0.000561167	1	0.001122334
2*006	3	0.001683502	3	0.003367003
2*009	1	0.000561167	1	0.001122334
2*012	1	0.000561167	1	0.001122334
3*001	708	0.397306397	551	0.618406285
3*002	404	0.22671156	358	0.401795735
3*003	11	0.00617284	11	0.012345679
3*005	79	0.044332211	78	0.087542088
3*006	2	0.001122334	2	0.002244669
3*009	5	0.002805836	5	0.005611672
3*011	1	0.000561167	1	0.001122334
3*012	1	0.000561167	1	0.001122334
3*015	1	0.000561167	1	0.001122334
3*022	1	0.000561167	1	0.001122334
3*026	1	0.000561167	1	0.001122334

2DL1

2DL1 Allele	N (Allele)	Freq	N (Phenotypic)	Freq
Negative	347	0.19374651	308	0.345679012
*001	74	0.0413177	73	0.081930415
*002	395	0.22054718	351	0.393939394
*003	703	0.392518146	554	0.621773288
*004	217	0.121161362	200	0.224466891
*006	2	0.001116695	2	0.002244669
*007	21	0.011725293	21	0.023569024
*008	9	0.005025126	9	0.01010101
*010	2	0.001116695	2	0.002244669
*011	1	0.000558347	1	0.001122334
*012	3	0.001675042	3	0.003367003
*014	2	0.001116695	2	0.002244669
*020	3	0.001675042	3	0.003367003
*021	1	0.000558347	1	0.001122334
*032N	10	0.005583473	10	0.011223345
*034	1	0.000558347	1	0.001122334

2DL5B

2DL5B Allele	N (Allele)	Freq	N (Phenotypic)	Freq
Negative	1563	0.877104377	876	0.983164983
B*002	197	0.110549944	187	0.209876543
B*003	1	0.000561167	1	0.001122334
B*006	6	0.003367003	6	0.006734007
B*008	9	0.005050505	9	0.01010101
B*010	3	0.001683502	3	0.003367003
B*011	1	0.000561167	1	0.001122334
B*017	2	0.001122334	1	0.001122334

2DS3/5 as two loci

2DS3/5 Allele	N (Allele)	Freq	N (Phenotypic)	Freq
Negative	2991	0.833147632	1713	0.961279461
3*001	226	0.062952646	217	0.121773288
3*002	51	0.014206128	51	0.028619529
3*003N	14	0.003899721	14	0.007856341
5*002	302	0.084122563	285	0.15993266
5*003	1	0.000278552	1	0.000561167
5*005	1	0.000278552	1	0.000561167
5*007	3	0.000835655	3	0.001683502
5*009	1	0.000278552	1	0.000561167

2DS3 and 2DS5 can be found at two positions in the KIR region. The frequencies have been calculated as both a single allelic series and as a two locus series. This changes the count of negatives as an allele and the calculated phenotypic frequencies

Supplemental Figure 3. Shown are the allele and phenotypic frequencies for genes for which alleles were determined. 'Negative' has been included as an allele and its frequency includes its presence in both the homozygous and heterozygous state. A difference exists between N (Allele) and N (Phenotypic) indicates the presence of individuals homozygous for absence of the gene.

CONTINUOUS

Factor	Level	Count	HRatio	HR_Low	HR_Up	Pvalue
Cen genotype v1	*overall	857	0.79	0.71	0.87	<.0001
Cen genotype v2	*overall	857	0.78	0.71	0.87	<.0001
B segment count	*overall	857	0.78	0.69	0.88	0.0001
Inhibitory interactions (D:R)	*overall	853	1.01	0.94	1.09	0.7607
Inhibitory interactions (D:D)	*overall	849	1.01	0.94	1.08	0.8315
Cen interaction score (D:R)	*overall	857	1	1	1	0.3275
Avg. Cen interaction score (D:R)	*overall	857	0.99	0.97	1.01	0.3667
Tel interaction score (D:R)	*overall	857	1	1	1	0.549
Avg. Tel interaction score (D:R)	*overall	857	0.99	0.98	1	0.1534
Total interaction score (D:R)	*overall	857	1	1	1	0.966
Avg. Total interaction score (D:R)	*overall	857	0.98	0.96	1	0.1104
Cen interaction score (D:D)	*overall	857	1	1	1.01	0.2091
Avg. Cen interaction score (D:D)	*overall	857	0.99	0.97	1.02	0.5206
Tel interaction score (D:D)	*overall	857	1	1	1	0.4636
Avg. Tel interaction score (D:D)	*overall	857	0.99	0.98	1	0.1146
Total interaction score (D:D)	*overall	857	1	1	1	0.923
Avg. Total interaction score (D:D)	*overall	857	0.98	0.96	1	0.1045

CATEGORICAL

Factor	Level	COUNT	HRatio	HR_Low	HR_Up	Pvalue
Cen genotype v1	*overall	.	.	.	.	0.0009
	A/A	408	1	.	.	.
	A/B01	125	1	0.72	1.41	0.98
	A/B02	222	0.77	0.58	1.04	0.0891
	B01/B01	17	0.29	0.07	1.18	0.0832
	B01/B02	45	0.23	0.09	0.56	0.0012
	B02/B02	40	0.23	0.07	0.73	0.0122
Cen genotype v2	*overall	.	.	.	.	0.0003
	A/A	408	1	.	.	.
	A/B01	125	1	0.72	1.41	0.9807
	A/B02	222	0.77	0.58	1.04	0.0892
	B01/Bx	62	0.24	0.11	0.52	0.0003
	B02/B02	40	0.23	0.07	0.73	0.0122
Tel genotype	*overall	.	.	.	.	0.1005
	A/A	516	1	.	.	.
	A/B	309	0.77	0.59	0.99	0.0448
	B/B	32	0.7	0.34	1.42	0.3214
2DS4 expressed	*overall	.	.	.	.	0.7647
	expressed	521	1	.	.	.
	absent	336	1.04	0.81	1.34	0.7647
3DL1 expressed	*overall	.	.	.	.	0.7134
	expressed	105	1	.	.	.
	absent	752	0.93	0.65	1.34	0.7134
B segment count v1	*overall	.	.	.	.	0.0015
	0	284	1	.	.	.
	1	292	1.01	0.77	1.33	0.9443
	2	195	0.53	0.37	0.77	0.0007
	3	71	0.55	0.33	0.93	0.0246
	4	15	0	0	2.20E+247	0.9645
B segment count v2	*overall	.	.	.	.	0.0001
	0	284	1	.	.	.
	1	292	1.01	0.77	1.33	0.946
	2	195	0.53	0.37	0.77	0.0007
	< 3	86	0.46	0.27	0.77	0.0029
3DL1:Bw4(recipient)	*overall	.	.	.	.	0.6655
	none	418	1	.	.	.
	weak	226	0.94	0.7	1.26	0.6587
	strong	213	1.09	0.82	1.46	0.5593
3DL1:Bw4(donor)	*overall	.	.	.	.	0.6564
	none	411	1	.	.	.
	weak	238	0.96	0.72	1.28	0.7755
	strong	208	1.11	0.83	1.49	0.4778
Inhibitory interactions (D:R)	*overall	.	.	.	.	0.6154
donor KIR: recipient HLA	10	53	0.83	0.45	1.54	0.5551
	4	156	1	.	.	.
	5	102	0.81	0.5	1.33	0.4089
	6	262	1.22	0.85	1.74	0.2816
	7	88	1.09	0.68	1.74	0.7163
	8	164	1.14	0.77	1.69	0.5194
	9	28	1.16	0.56	2.38	0.6946

CATEGORICAL (continued)

Factor	Level	COUNT	HRatio	HR_Low	HR_Up	Pvalue
Activating interactions (D:R) v1	*overall	.	.	.	.	0.6701
donor KIR: recipient HLA	0	502	1	.	.	.
	1	193	1.19	0.9	1.59	0.2243
	2	123	0.95	0.66	1.37	0.7939
	3	16	0.98	0.31	3.12	0.9787
	4	20	0.72	0.26	1.95	0.5144
Activating interactions (D:R) v2	*overall	.	.	.	.	0.5442
donor KIR: recipient HLA	0	502	1	.	.	.
	1 or more	355	1.08	0.84	1.38	0.5442
Inhibitory interactions (D:D)	*overall	.	.	.	.	0.171
donor KIR: donor HLA	10	46	0.59	0.28	1.26	0.173
	4	159	1	.	.	.
	5	107	0.87	0.53	1.42	0.5783
	6	254	1.27	0.88	1.82	0.1987
	7	90	1.44	0.92	2.25	0.1078
	8	165	1.17	0.78	1.74	0.4481
	9	28	1.35	0.67	2.7	0.4008
Activating interactions (D:D) v1	*overall	.	.	.	.	0.2218
donor KIR: donor HLA	0	491	1	.	.	.
	1	207	1.34	1.01	1.77	0.0415
	2	125	0.93	0.65	1.35	0.7106
	3	16	1.12	0.41	3.04	0.82
	4	15	0.67	0.21	2.12	0.4934
Activating interactions (D:D) v2	*overall	.	.	.	.	0.2554
donor KIR: donor HLA	0	491	1	.	.	.
	1 or more	366	1.15	0.9	1.47	0.2554
Cen interaction score (D:R)	*overall	.	.	.	.	0.4526
donor KIR: recipient HLA	0	271	1	.	.	.
tertiles	1	296	0.83	0.61	1.12	0.2215
	2	290	0.94	0.7	1.27	0.704
Avg. Cen interaction score (D:R)	*overall	.	.	.	.	0.2547
donor KIR: recipient HLA	0	285	1	.	.	.
tertiles	1	284	0.79	0.59	1.06	0.1098
	2	288	0.85	0.63	1.14	0.2664
Tel interaction score (D:R)	*overall	.	.	.	.	0.6839
donor KIR: recipient HLA	0	286	1	.	.	.
tertiles	1	286	0.88	0.66	1.18	0.3912
	2	285	0.96	0.71	1.29	0.7809
Avg. TelInteraction score (D:R)	*overall	.	.	.	.	0.3365
donor KIR: recipient HLA	0	287	1	.	.	.
tertiles	1	284	0.88	0.66	1.17	0.3809
	2	286	0.8	0.59	1.08	0.1453
Total interaction score (D:R)	*overall	.	.	.	.	0.5445
donor KIR: recipient HLA	0	287	1	.	.	.
tertiles	1	284	0.85	0.63	1.16	0.3129
	2	286	0.99	0.74	1.32	0.9209
Avg. Total interaction score (D:R)	*overall	.	.	.	.	0.7497
donor KIR: recipient HLA	0	287	1	.	.	.
tertiles	1	287	0.98	0.73	1.32	0.8835
	2	283	0.9	0.67	1.2	0.4703
Cen interaction score (D:D)	*overall	.	.	.	.	0.5967
donor KIR: donor HLA	0	281	1	.	.	.
tertiles	1	293	0.87	0.65	1.18	0.3677
	2	283	0.99	0.74	1.33	0.9537
Avg. Cen interaction score (D:D)	*overall	.	.	.	.	0.6677
donor KIR: donor HLA	0	284	1	.	.	.
tertiles	1	284	0.89	0.67	1.19	0.4311
	2	289	0.89	0.66	1.2	0.4504
Tel interaction score (D:D)	*overall	.	.	.	.	0.7427
donor KIR: donor HLA	0	277	1	.	.	.
tertiles	1	297	0.9	0.67	1.21	0.4824
	2	283	0.99	0.73	1.33	0.9371
Avg. Tel interaction score (D:D)	*overall	.	.	.	.	0.5458
donor KIR: donor HLA	0	278	1	.	.	.
tertiles	1	296	0.9	0.67	1.21	0.4949
	2	283	0.85	0.63	1.14	0.2785
Total interaction score (D:D)	*overall	.	.	.	.	0.8315
donor KIR: donor HLA	0	289	1	.	.	.
tertiles	1	283	0.91	0.68	1.23	0.5438
	2	285	0.96	0.71	1.29	0.7833
Avg. Total interaction score (D:D)	*overall	.	.	.	.	0.375
donor KIR: donor HLA	0	289	1	.	.	.
tertiles	1	287	0.81	0.6	1.09	0.1643
	2	281	0.89	0.66	1.19	0.4318

Supplemental Figure 4. Results of statistical analyses with the endpoint of relapse. Significant overall results are highlighted in gold. The telomeric, centromeric and total interaction scores were analyzed as both continuous variables and discrtized into tertiles and analyzed as categorical variables.