

Table S1. STS mapping primers.

Gene		Primer sequence	Position	Size
3DL3	F	CACAGAAAACCTTCCCTCCTGGC	Exon 4	216
	R	GGTCCCTGCAAGGGCA TGTG (G)	Exon 4	
2DS2	F	GCACTTCCTTCTGCACAGAGAGGGGA CTA (G)	Exon 4	191
	R	TGTCCAGAGGGTCACTGGGAGC	Exon 4	
2DL3	F	CTTCCAG GTAACCCAGACACCTGCAT	Exon 7	132
	R	CTCTGCTTCGTAAGACTTAC TTTTTTTGT CGC (T)	Exon 7	
2DL2	F	CTCCTGGCCCACCCAGG ACG (T)	Exon 4	196
	R	CTGCAAGGTCTTGCATCA CGG (T)	Exon 4	
2DL5	F	GACCAAGAGCCTGC GGGG (C)	Exon 8	315
	R	TGCTTATGGGCAGGAGACAATGAT	Exon 9	
2DL5.2	F	TGTAAATCAATATCTGGCAGAGGAGTG GTA (A)	Intron 6	365
	R	GACCCCGCCAAACCTCACG	Intron 6	
2DL5.1	F	AATCAATATCTGGCAGAGGAGTG GTT (A)	Intron 6	361
	R	GACCCCGCCAAACCTCACG	Intron 6	
2DS3	F	ACTTTGCGCCTCATTGGAGAGCACAT	Exon 4	157
	R	CGATGTCCAGAGGGTCACTGGGAGCT CAA (G)	Exon 4	
2DS3/5	F	CGCCTCATTGGAGAGCACAT	Exon 4	148
	R	TGTCCAGAGGGTCACTGGGAGC	Exon 4	
2DP1 including exon3	F	CACAGAAAACCTTCCCTCCTGGC	Exon 4	270
	R	CACTGGGAGCTGACAACTG CTG (A)	Exon 4	
2DP1_hpltA including exon3	F	CACAGAAAACCTTCCCTCCTGGC	Exon 4	187
	R	CGATGGAGAAGTTGGCCTTG TAA (G)	Exon 4	
2DP1_hpltB including exon3	F	CTTCTGCACAGAGAGGGG CCA (A)	Exon 4	183
	R	TGTCCAGAGGGTCACTGGGAGC	Exon 4	
2DL1	F	TCCAAGGCCAACTTCTCCA ACA (T)	Exon 4	113
	R	AGAGGGTCACTGGGAGCTGA AAC (C)	Exon 4	
3DP1	F	TCTGCACAGAGAGGGGAAGTTT CAT (A)	Exon 4	182
	R	TGTCCAGAGGGTCACTGGGAGC	Exon 4	
2DL4A	F	CGGGCCCCACGGTT ACA (G)	Exon 5	171
	R	GGGTGGCAGGACCCAGAGG	Exon 5	
2DL4B	F	GGGGCCCCACGGTT ACG (G)	Exon 5	170
	R	GGGTGGCAGGACCCAGAGG	Exon 5	
3DL1A	F	TGCCTGGCCCAGCGCTGTGGT	Exon 3	154
	R	GCTCATGTTGAAGCTCTCCTGGAA AAA (T)	Exon 3	
3DL1B	F	TGCCTGGCCCAGCGCTGTGGT	Exon 3	133
	R	GAATATTCTGCCATGGAAGATGGG GAT (A)	Exon 3	
2DS5	F	TTGCGCCTCATTGGAGAGCACAT	Exon 4	147
	R	CAGAGGGTCACTGGGCGCT CAC (G)	Exon 4	
3DS1	F	AAGAGCCTGCAGGGAACAGAAGT	Exon 8	214
	R	GGGCGAGTGATTTTCTCTGTGTGA	Exon 9	
2DS4L	F	GCTCCTATGACATGTACCATCTATCCA	Exon 5	177
	R	AGTTTGACCACTCGTAGGG GGC (A)	Exon 5	
2DS4S deletion from (003, 004, 006, 007 and 009)	F	TGTCCTGCAGCTCCATCTATCCA	Exon 5	173
	R	AGTTTGACCACTCGTAGGG GGC (A)	Exon 5	
2DS1	F	CCAACTTCTCCATCAGTCGCAT CAA (G)	Exon 4	105
	R	GAGGGTCACTGGGAGCTGA GAA (C)	Exon 4	
3DL2	F	GCCCCACGGTTCAGGCAGG	Exon 5	222
	R	ACCACACGCAGGGCAGGG	Exon 5	

Sequence modification for specificity on PCR; Original sequence; Intron sequence

Table S2. Long range PCR and sequencing primers.

Gene		Primer sequence
3DL2-Fcar	F	GTAAGCACAGAATTCAATCACCTCATGTG
	R	TTTCCTTCCACAACAATCACAGTTTT
3DL3 (exon7)-2DL2 (exon5)	F	TCAGTGGTCATCATCCCCTTTGCT
	R	GTCTTCTCTCTGCATCTGTCCATGCTTA
3DS1-3DL2 hybrid	F	TTCTAGTGAGAGCAATTTCCAGGAAGCCATGC
	R	GCTAAGCAAAGGAGTGTGTTTTCTT
3DL1-3DL2 hybrid	F	GACGCGAGGTGTCAATTCTAGTGAGAG
	R	GGTGGGCAGGGGTCAAGTGAAATAGATAC
2DL4	F	GACGTAGAAGAAGCCTACCTATGTCCCCTTCA
	R	AGGCACCAGATTTGTGGTGTGAGGAAGAGT
3DL1-exon3-sequencing	F	CCAGGTGTGGTAGGAGCCTTAGAAA
	R	TTCAATCTCCCTTGACCCCAAATA
3DL1-exon4-sequencing	F	CATGGATGGGATGATAAAGAGAGA
	R	GAATCCCACACTTATCTTCCTCATG
3DL1-exon5-sequencing	F	AGGGGAGTGAGTTCTCAGCTCAGGT
	R	GCTAAGGATTTAGGATCATAGGACATG
3DL2-exon7-sequencing	F	AAGCTGGGTCTCCCGCCATCAGGC
	R	AGAAAGCCCTGCCTCTGTGGCTCCTC
3DL2-exon89-sequencing	F	TGAGTCTGGATGTTGGCAGCTGAAGA
	R	ACTGATGCCTTCAGATTCCAGCTGCTGGTT

Table S3. Frequency of KIR haplotypes in 4 ethnic groups.

Haplotype	AFA (%)	ASI (%)	HIS (%)	CAU (%)
cA01 tA01	51 (53.1)	58 (63.0)	57 (60.6)	57 (62.0)
cA01 tB01	4 (4.2)	16 (17.4)	16 (17.0)	10 (10.9)
cB01 tB01	2 (2.1)	1 (1.1)		4 (4.3)
cB02 tA01	6 (6.3)	4 (4.3)	8 (8.5)	14 (15.2)
cB01 tA01	15 (15.6)	3 (3.3)	8 (8.5)	5 (5.4)
cB02 tB01	2 (2.1)	5 (5.4)	3 (3.2)	1 (1.1)
cB03 tA01	2 (2.1)			
cA01 tB01-del7/8		1 (1.1)		
cA01 tA01-hybd1	4 (4.2)			
cA01 tA01-ins3	2 (2.1)			
cA01 tA01-ins5				1 (1.1)
cB01 tB01-del6	1 (1.0)			
cB02 tA01-hybd1	1 (1.0)			
cB01 tA01-del3	2 (2.1)			
cB01 tA01-ins4		1 (1.1)		
cB01 tA01-hybd1	2 (2.1)			
cB01 tA01-hybd2	1 (1.0)			
cB02 tB01-del6	1 (1.0)	3 (3.3)	2 (2.1)	