

### Supplementary table I

**Overview of forward (Fw) and reverse (Rv) primers used to confirm alleles on macaque and human KIR haplotypes.** To amplify different Mamu-KIR3DL07 alleles, a wobble had to be introduced in the forward primer sequence: adenine or thymine (W). The PCR product sizes were sufficient to distinguish alleles and confirm their presence.

Target	Fw / Rv	Exon	Primer sequence 5' - 3'	Product size
Mamu-KIR3DL05	Fw	4	TCTGCAAAGTGAGGTGACCTT	337 bp
	Rv	5	AAGCCTAAGTTCATGGGTCTCC	
Mamu-KIR3DL07	Fw	3	GACCTTCTTGWTTGCCCGGC	556 bp
	Rv	4	ACTGGGAGCTGACAACACATAGTC	
Mamu-KIR3DS02	Fw	3	GATCATACCCGCACTCCCCAA	319 bp
	Rv	4	TGGGAGTGAGTGACAGAACCA	
Mamu-KIR3DL20	Fw	5	CCAGAGCTCGTTTGACATTTACCG	183 bp
	Rv	5	GGGTGTGACCACACATAGGGCAG	
Mamu-KIR3DS05	Fw	5	GTGTCAACGGAACATTCCAGGA	109 bp
	Rv	5	CTCGGGTGTGACCACTTGTAGGA	
Human KIR2DL1	Fw	3	ACTTTGCGCCTCATTGGAGA	359 bp
	Rv	4	CCCAGAGGAAAGTCAGCCTG	
Human KIR2DL4	Fw	9	GCCCTTCTCAGAGGAGCAAG	116 bp
	Rv	9	CATCAAGGCCTGACTGTGGT	
Human KIR2DS4	Fw	4	GGTTCAGGCAGGAGAGAAT	111 / 133 bp
	Rv	4	CTGGAATGTTCCGTKGATG	

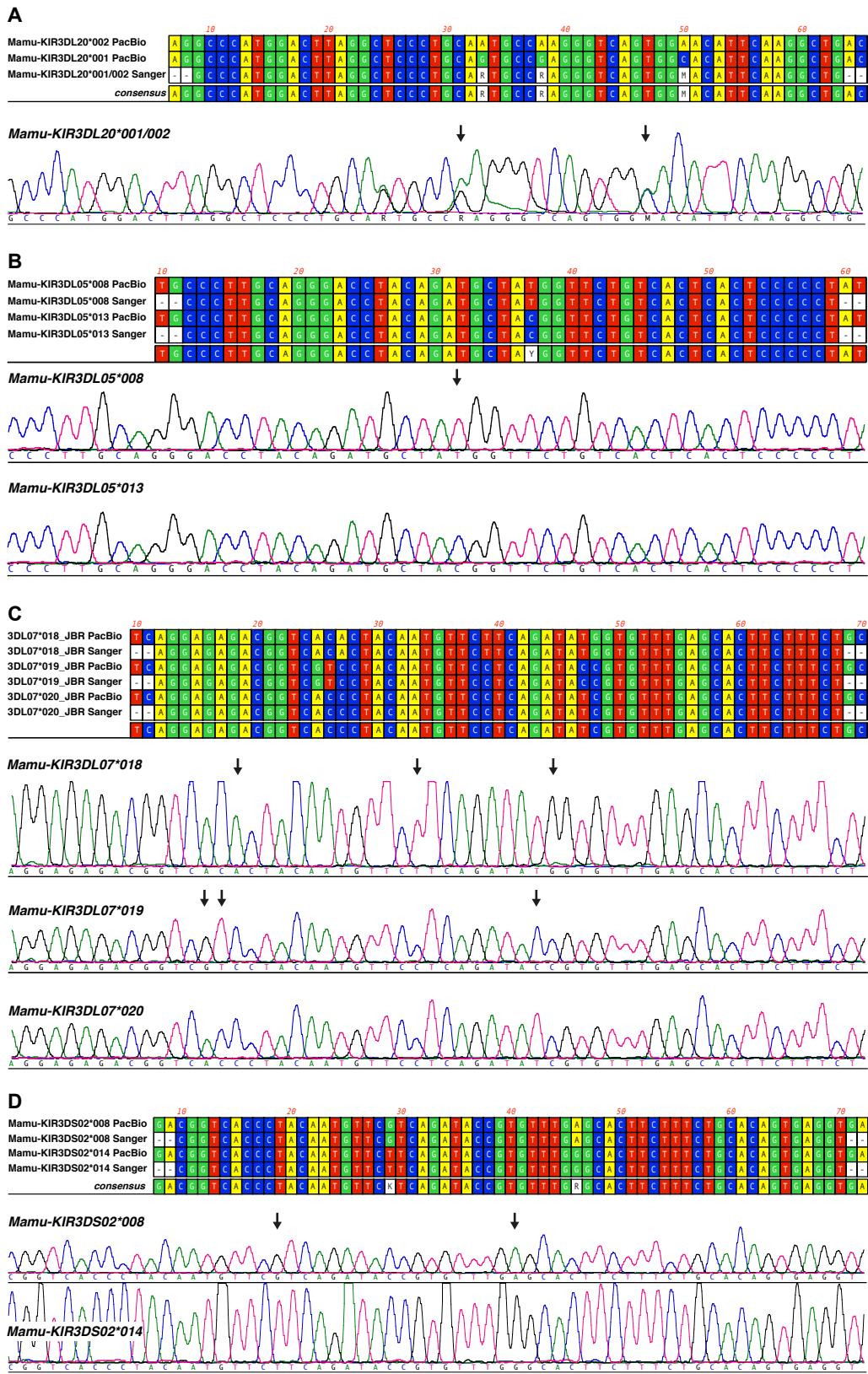


Supplementary table III

The *KIR* content of a human family with 15 members. The *KIR* gene system was characterized on both transcription and gDNA level. The *KIR* gene name is indicated on top of each column and the allele specification is provided per transcribed haplotype for each individual. The presence or absence of a *KIR* gene on gDNA is indicated with 'Pos' or 'Neg', respectively. Grey boxes were not amplified on transcription level. For individuals 08, 37, 39 and 82, no gDNA was available.

Individual		2DL1*	2DL2*	2DL3*	2DL4*	2DL5*	3DL1*	3DL2*	3DL3*	3DS1*	2DS1*	2DS2*	2DS3*	2DS4*	2DS5*	2DP1*	3DP1*	Fusion
00	H1	002:01	-	002:01	001:02		002	002:01		-	-	-	-	001:01	-	-	-	-
	H2	003:02	-	001:01	008:02		019	005:01		-	-	-	-	006:01	-	-	-	-
	gDNA	Pos	-	Pos	Pos	Neg	Pos	Pos	Pos	Neg	Neg	Neg	Neg	Pos	Neg	Pos	Pos	-
01	H3	004:01	001:01	-	008:01		009	011:01	Pos	-	-	-	001:01	001:03	003:01	-	-	-
	H4	-	-	005:01	-		-	-		-	-	-	-	-	-	-	-	2DL1/3DL2
	gDNA	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Neg	Neg	Pos	Pos	Pos	Neg	Pos	Pos	-
02	H1	002:01	001:01	002:01	001:02		002	002:01		-	-	-	-	001:01	-	-	-	-
	H3	004:01	001:01	-	008:01		009	011:01		-	-	001:01	001:03	003:01	-	-	-	-
	gDNA	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Neg	Neg	Pos	Pos	Pos	Neg	Pos	Pos	-
04	H1	002:01	-	002:01	001:02		002	002:01		-	-	-	-	001:01	-	-	-	-
	H4	-	-	005:01	-		-	-		-	-	-	-	-	-	-	-	2DL1/3DL2
	gDNA	Pos	Neg	Pos	Pos	Neg	Pos	Pos	Pos	Neg	Neg	Neg	Neg	Pos	Neg	Pos	Pos	-
06	H1	002:01	-	002:01	001:02		002	002:01		-	-	-	-	001:01	-	-	-	-
	H4	-	-	005:01	-		-	-		-	-	-	-	-	-	-	-	2DL1/3DL2
	gDNA	Pos	Neg	Pos	Pos	Neg	Pos	Pos	Pos	Neg	Neg	Neg	Neg	Pos	Neg	Pos	Pos	-
07	H2	003:02	-	001:01	008:02		019	005:01		-	-	-	-	006:01	-	-	-	-
	H3	004:01	001:01	-	008:01		009	011:01		-	-	001:01	001:03	003:01	-	-	-	-
	gDNA	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Neg	Neg	Pos	Pos	Pos	Neg	Pos	Pos	-
09	H1	002:01	-	002:01	001:02		002	002:01		-	-	-	-	001:01	-	-	-	-
	H4	-	-	005:01	-		-	-		-	-	-	-	-	-	-	-	2DL1/3DL2
	gDNA	Pos	Neg	Pos	Pos	Neg	Pos	Pos	Pos	Neg	Neg	Neg	Neg	Pos	Neg	Pos	Pos	-
38	H6	003:02	-	003	005:01		-	007:01		013:01	002:01	-	-	-	002:01	-	-	-
	H8	002:01	-	002:01	008:02		004:01	005:01		-	-	-	-	006:01	-	-	-	-
	gDNA	Pos	Neg	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Neg	Neg	Pos	Pos	Pos	Pos	-
72	H2	003:02	-	001:01	008:02		019	005:01		-	-	-	-	006:01	-	-	-	-
	H5	001	-	005:01	011		005:01	010:01		-	-	-	-	006:01	-	-	-	-
	gDNA	Pos	Neg	Pos	Pos	Neg	Pos	Pos	Pos	Neg	Neg	Neg	Neg	Pos	Neg	Pos	Pos	-
84	H1	002:01	-	002:01	001:02		002	002:01		-	-	-	-	001:01	-	-	-	-
	H6	003:02	-	003	005:01		-	007:01		013:01	002:01	-	-	-	002:01	-	-	-
	gDNA	Pos	Neg	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Neg	Neg	Pos	Pos	Pos	Pos	-
85	H1	002:01	-	002:01	001:02		002	002:01		-	-	-	-	001:01	-	-	-	-
	H7	002:01	-	002:01	006:02		007:01	008		-	-	-	-	004:01	-	-	-	-
	gDNA	Pos	Neg	Pos	Pos	Neg	Pos	Pos	Pos	Neg	Neg	Neg	Neg	Pos	Neg	Pos	Pos	-
08	H1	002:01	-	002:01	001:02		002	002:01		-	-	-	-	001:01	-	-	-	-
	H3	004:01	001:01	-	008:01		009	011:01		-	-	001:01	001:03	003:01	-	-	-	-
	gDNA	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	-
37	H5	001	-	005:01	011		005:01	010:01		-	-	-	-	006:01	-	-	-	-
	H9	003:02	-	001:01	008:01		001	001:01		-	-	-	-	003:01	-	-	-	-
	gDNA	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	-
39	H7	002:01	-	002:01	006:02		007:01	008		-	-	-	-	004:01	-	-	-	-
	H10	003:02	-	001:01	011		005:01	001		-	-	-	-	004:01	-	-	-	-
	gDNA	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	-
82	H3	004:01	001:01	-	008:01		009	011:01		-	-	001:01	001:03	003:01	-	-	-	-
	H6	003:02	-	003	005:01		-	007:01		013:01	002:01	-	-	-	002:01	-	-	-
	gDNA	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	-

**Figure S1**



**Supplementary Figure 1. Sequence confirmation by Sanger sequencing.**

Chromatograms and sequences obtained by Sanger sequencing to confirm results found by PacBio sequencing. Arrows in the chromatograms indicate sequence variation. Primers used for Sanger sequencing are listed in Supp. Table I. (A) Macaque haplotype H12 lacked informative offspring, and was therefore only identified in a single sire (95055). The haplotype was confirmed by multiple independent PCRs. Nonetheless, low PacBio read counts were obtained from the *Mamu-KIR3DL20* alleles, and therefore these alleles were confirmed by Sanger sequencing. The arrows indicate double peaks, illustrating the presence of *Mamu-KIR3DL20\*001* and *Mamu-KIR3DL20\*002* in sire 95055, which allowed us to assign the alleles to the specific haplotypes. (B) Two copies of the *Mamu-KIR3DL05* gene were found on macaque haplotype H9. One of these alleles was novel (*Mamu-KIR3DL05\*013*), whereas the other was reported previously (*Mamu-KIR3DL05\*008*). (C) Three copies of the *Mamu-KIR3DL07* gene were found on macaque haplotype H9. These alleles were all novelties, and confirmed by Sanger sequencing. (D) Two copies of the *Mamu-KIR3DS02* gene were found on macaque haplotype H9. One of these alleles was novel (*Mamu-KIR3DS02\*014*), whereas the other was reported previously (*Mamu-KIR3DS02\*008*).