Nomenclature report for killer-cell immunoglobulin-like receptors (KIR) in macaque species: new genes/alleles, renaming recombinant entities and IPD-NHKIR updates

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Abstract
The Killer-cell Immunoglobulin-like Receptors (KIR) are encoded by a diverse group of genes, which are characterized by allelic polymorphism, gene duplications, and recombinations, which may generate recombinant entities. The number of reported macaque KIR sequences is steadily increasing, and these data illustrate a gene system that may match or exceed the complexity of the human KIR cluster. This report lists the names of quality controlled and annotated KIR genes/alleles with all the relevant references for two different macaque species: rhesus and cynomolgus macaques. Numerous recombinant KIR genes in these species necessitate a revision of some of the earlier-published nomenclature guidelines. In addition, this report summarizes the latest information on the Immuno Polymorphism Database (IPD)-NHKIR Database, which contains annotated KIR sequences from four non-human primate species.

Keywords Killer-cell immunoglobulin-like receptors · Nomenclature · Macaque species · Rhesus · Cynomolgus · Recombinants

Introduction
Over the last two decades, the number of human Killer-cell Immunoglobulin-like Receptor (KIR) sequences and haplotypes has increased substantially. These data shed light on a plastic gene cluster of higher primates that is characterized by allelic polymorphism and variable gene content, and that involves complex recombinations and high levels of alternative splicing (Trowsdale et al. 2001; Hsu et al. 2002; Parham 2004; Hammond et al. 2016; Bruijnesteijn et al. 2018a, b; Bruijnesteijn et al. 2018a, b). The system of nomenclature for human KIR genes (Marsh et al. 2003) accounts for the number of domains (2D or 3D), as well as for the activating (S) or inhibitory (L) signalling potential of the intracellular
Following the D, whereas "KIR" genes are differentiated by numbers. For example, KIR3DL1*001 defines the first allele of a gene encoding a receptor that has three extracellular domains and a long cytoplasmic tail. For non-human primate species (NHP) such as macaques, chimpanzees, and orangutans, the human KIR nomenclature rules have been applied, and when these have not been sufficient, species-specific adaptations have been added to the guidelines for the nomenclature (Robinson et al. 2018).

Among the human KIR characterized, only a few intragenic recombinations have been reported (Roe et al. 2017; Bruijnesteijn et al. 2018a, b), although the number of such recombinant KIR could be underestimated, because family studies have not been a focus of the work, and might be missed by studies that mainly involved unrelated individuals. A recent study of the KIR gene transcriptome in families of rhesus (Macaca mulatta, Mamu) and cynomolgus (Macaca fascicularis, Mafa) macaques has identified numerous intragenic recombinant KIR (Bruijnesteijn et al., unpublished data). In this report on KIR nomenclature, we build on the previously reported human and NHP guidelines (Robinson et al. 2018) to focus on macaques, because in these species the number of genes/alleles reported has significantly increased.

**General nomenclature guidelines for macaque KIR genes**

The naming of macaque KIR genes follows the general principles that have been previously described (Marsh et al. 2003; Robinson et al. 2018). In brief, the first digit following the KIR abbreviation gives the number of immunoglobulin-like domains (denoted as “D”). In macaques, genes that encode KIR1D, KIR2D, and KIR3D structures are found (Hershberger et al. 2001). Either a long or short cytoplasmic tail, which are characteristic of inhibitory and activating receptors, respectively, is specified with an “L” or an “S” following the D, whereas “P” denotes a pseudogene. Genes considered to be novel but that lack sufficient confirmation—at the genomic DNA level—to define a gene or lineage, are denoted by a “W” for “Workshop”, which follows the designation of the cytoplasmic tail. Different KIR genes are distinguished by sequential two-digit numbering. Non-synonymous KIR alleles are distinguished by three-digit numbers that are separated from the gene digits by an asterisk. Synonymous polymorphisms in the coding sequence of a KIR gene are distinguished by a second set of two digits, which is separated from the non-synonymous three-digit number by a colon (e.g., Mamu-KIR3DL01*012:02). A third set of digits, separated from the synonymous two-digit number by a colon, define substitutions in the introns. Optional suffixes indicating the expression status of alleles can be provided, and these include indicators of no expression, referred to as “Null” alleles (“N”), low cell surface expression (“L”), soluble and secreted gene products (“S”), and cytoplasmic expression (“C”). The “A” suffix is used when there is doubt as to whether a protein is expressed, whereas “Q” indicates alleles for which the expression is “Questionable” based on the study of previously reported mutations that do affect the level of expression.

**KIR genes in the various species of macaque**

More than 20 species of macaque have been distinguished (Anandam et al. 2013). At present, characterization of the KIR genes has concentrated on rhesus and cynomolgus macaques (Khakoo et al. 2000; Grendell et al. 2001; Hershberger et al. 2001; Rajalingam et al. 2001; Guethlein et al. 2002; Andersen et al. 2004; Sambrook et al. 2005; Guethlein et al. 2007; Bimber et al. 2008; Blokhuis et al. 2009a, b; Blokhuis et al. 2009a, b; Bostik et al. 2009; Abi-Rached et al. 2010; Blokhuis et al. 2010; Chaichompoo et al. 2010; Kruse et al. 2010; Colantonio et al. 2011; Hellmann et al. 2011; Moreland et al. 2011; Bimber and Evans 2015; Prall et al. 2017). Up to now, knowledge regarding the organization of KIR genes in macaque is sparse, with only two genomic assemblies of the macaque KIR region available (Sambrook et al. 2005; Graves 2019). Consequently, KIR genes that are highly similar based on phylogenetic clustering and sequence homology are considered to define a single gene or locus that is common to both species of macaque, and are therefore designated as orthologs and given matching gene names: for example, Mamu-KIR3DL01 and Mafa-KIR3DL01. In contrast, species-specific KIR genes are given different numbers in the order in which they are distinguished. To give an example, KIR3DLW13 has only been detected in cynomolgus macaques (Mafa-KIR3DLW13). At the allele level, sequences are numbered in sequence according to the order in which they were defined. This procedure was applied independently to the different macaque species, without taking shared KIR alleles into account. In total, 58 and 59 rhesus and cynomolgus macaque KIR genes have been defined, and these represent 576 and 334 KIR alleles, respectively (Tables 1 and 2).

These guidelines for naming KIR sequences will be applied to other macaque species, but will be distinguished by the use of species-specific prefixes (Table 3).

**Nomenclature for recombinant macaque KIR genes**

Study of rhesus and cynomolgus macaque KIR from different geographical origins has identified many recombinant KIR that are composed of segments derived from two or more different KIR genes, which were confirmed by independent PCRs or segregation analysis. According to the previous
Table 1  List of rhesus macaque KIR genes, their previous names, and the number of reported alleles per gene

| KIR gene     | Previous designations | Number of reported alleles |
|--------------|-----------------------|---------------------------|
| Mamu-KIR1D   | KIR1D                 | 12                        |
| Mamu-KIR2DL04| 2DL501NK, 2DL503NK, KIR2DL4, KIR2DL4.1, MmKIR2DL4 | 49                        |
| Mamu-KIR3DL20| KIR3DL20, KIR3DL20_variant_2, KIR3DL06, KIR2DL5 | 64                        |
| Mamu-KIR3DL01| 2DL426NK, 3DL4, KIR3DL, KIR3DL-like_1, KIR3DL1, KIR3DL1-like1, KIR3DL12, KIR3DL13, KIR3DL14, KIR3DL15, KIR3DL19, KIR3DL1_variant_2, KIR3DL2, KIR3DL2-old, KIR3DL3, KIR3DL4, KIR3DL5 | 63                        |
| Mamu-KIR3DL02| KIR3DL-like_3, KIR3DL2, KIR3DL21, KIR3DL21-like1 | 16                        |
| Mamu-KIR3DL03| KIR3DL-4, KIR3DL-5, KIR3DL-like1-BNB, KIR3DL21 | 15                        |
| Mamu-KIR3DL04| KIR3DL11               | 4                         |
| Mamu-KIR3DL05| 3DL7b-3DL40, KIR3DL, KIR3DL-3, KIR3DL16, KIR3DL7, KIR3DL7-like2, KIR3DL07 | 33                        |
| Mamu-KIR3DL06| KIR3DL6                | 8                         |
| Mamu-KIR3DL07| 2DL420, KIR3DL, KIR3DL18, KIR3DL7, KIR3DL7-like1, KIR3DL7-like3, KIR3DL03 | 67                        |
| Mamu-KIR3DL08| KIR3DL, KIR3DL-like_2, KIR3DL17, KIR3DL8, KIR3DL8, Mamu-KIR3DL04, Mamu-KIR3DL4 | 27                        |
| Mamu-KIR3DL10| 3DL10-2DL501, 3DL3NK, KIR3DL, KIR3DL10, KIR3DL9, Mamu-KIR3DL05 | 6                         |
| Mamu-KIR3DL11| KIR3DL, KIR3DL-1, KIR3DL-6, KIR3DL-7, KIR3DL11 | 19                        |
| Mamu-KIR3DL12| Newly identified in Chinese rhesus macaques | 2                         |
| Mamu-KIR3DL14| Newly identified in Indian and Chinese rhesus macaques | 3                         |
| Mamu-KIR3DL17| Newly identified in Burmese and Chinese rhesus macaques | 3                         |
| Mamu-KIR3DL18| Newly identified in Burmese rhesus macaques | 2                         |
| Mamu-KIR3DL25| Newly identified in Burmese rhesus macaques | 1                         |
| Mamu-KIR3DL31| Renamed Mamu-KIR3DL02 fusion alleles | 4                         |
| Mamu-KIR3DL32| Renamed Mamu-KIR3DL02 fusion alleles, Mamu-KIR3DL10A/3DL02 | 2                         |
| Mamu-KIR3DL33| Renamed Mamu-KIR3DL02 fusion allele, Mamu-KIR3DL10B/3DL02 | 1                         |
| Mamu-KIR3DL34| Renamed Mamu-KIR3DL03 fusion alleles | 9                         |
| Mamu-KIR3DL35| Renamed Mamu-KIR3DL03 fusion allele | 1                         |
| Mamu-KIR3DL36| Renamed Mamu-KIR3DL05 fusion alleles | 3                         |
| Mamu-KIR3DL37| Renamed Mamu-KIR3DL05 alleles | 2                         |
| Mamu-KIR3DL38| Renamed Mamu-KIR3DL07 fusion allele | 1                         |
| Mamu-KIR3DL39| Renamed Mamu-KIR3DL07 fusion allele | 1                         |
| Mamu-KIR3DL40| Renamed Mamu-KIR3DL07 fusion allele | 1                         |
| Mamu-KIR3DL41| Renamed Mamu-KIR3DL07 fusion allele | 1                         |
| Mamu-KIR3DL42| Renamed Mamu-KIR3DL07 fusion allele | 1                         |
| Mamu-KIR3DL43| Renamed Mamu-KIR3DL08 fusion alleles | 3                         |
| Mamu-KIR3DL44| Renamed Mamu-KIR3DL08 fusion allele | 1                         |
| Mamu-KIR3DL45| Renamed Mamu-KIR3DL10 fusion alleles | 7                         |
| Mamu-KIR3DL46| Renamed Mamu-KIR3DS04 fusion allele | 1                         |
| Mamu-KIR3DS01| KIR3DH-7, KIR3DH1, KIR3DH5, Mamu-KIR3DS01-JHB-HEFGH | 10                        |
| Mamu-KIR3DS02| 3DH2, 3DH42, KIR3DH-like_5, KIR3DH-like_6, KIR3DH10, KIR3DH12, KIR3DH13, KIR3DH14, KIR3DH15, KIR3DH16, KIR3DH2 | 32                        |
| Mamu-KIR3DS03| KIR3DH3, KIR3DH8, KIR3DH9 | 6                         |
| Mamu-KIR3DS04| KIR3DH-1, KIR3DH4, KIR3DH6 | 11                        |
| Mamu-KIR3DS05| KIR3DH1, KIR3DM-1, KIR3DM1, KIR3DM6, KIR Partial_Sequence_1 | 10                        |
| Mamu-KIR3DS06| KIR3DH-4, KIR3DH-like8, KIR3DH-like_7, KIR3DH18 | 22                        |
| Mamu-KIR3DS07| KIR3DH-5, KIR3DH7, Mamu-KIR3DS07-JHB-HO | 5                         |
| Mamu-KIR3DS08| KIR3DH-2, KIR3DH-3, KIR3DH-4, KIR3DH-5, KIR3DH-like_1, KIR3DH-like_2, KIR3DH-like_3, KIR3DH-like_4, KIR3DH21 | 7                         |
| Mamu-KIR3DS09| KIR3DH-8, KIR3DH20, KIR3DH5, KIR3DH5-like1, mmKIR3DH1 | 8                         |
| Mamu-KIR3DS10| Newly identified in Burmese rhesus macaques | 1                         |
| Mamu-KIR3DS16| Newly identified in Burmese rhesus macaques | 1                         |
nomenclature guidelines (Robinson et al. 2018), the recombinant rhesus macaque KIR were named after alleles of the gene that contributed the longest gene segment. From experience we have learned that this criterion can result in confusing allele names. For example, *Mamu-KIR3DS04* *011* (acc. nr. LR694568) comprises the first 5 exons of *Mamu-KIR3DS04*, joined to exons encoding the transmembrane region and cytoplasmic tail that are similar to those of *Mamu-KIR3DL07*. Because the activating gene parent makes the larger contribution, this recombinant was originally named as an allele of *Mamu-KIR3DS04*, although the cytoplasmic tail derived from *Mamu-KIR3DL07* predicts that the receptor has an inhibitory signalling function. To prevent confusion, such hybrid KIR genes have been renamed, and are indicated by the workshop status (Table 4). In the future, newly discovered recombinant sequences will be assigned sequential gene (workshop) numbers. Previous designations of renamed alleles and genes will be retained and marked as deleted.

An exception is made for recombinant KIR genes in the centromeric region and that involve the macaque framework gene *KIR3DL20*. The physical location of these recombinant genes has been established (Sambrook et al. 2005), which contrasts with those of the recombinant lineage II KIR genes. Recombinant sequences derived from the centromeric region are still assigned as *KIR3DL20* alleles, but are shown to be “Recombinant” with a novel suffix “R” subsequent to the allele designation. For example, *Mamu-KIR3DL20* *030R* (acc. nr. LR694489) and *Mamu-KIR3DL20* *044R* (acc. nr. LR694507) are recombinants that consist of the first seven exons of *Mamu-KIR3DL20*, and of the intracellular domains of *Mamu-KIR2DL04* and *Mamu-KIR1D*, respectively.

Most recombinant KIR genes of cynomolgus macaques have been assigned novel workshop numbers (Bruijnesteijn et al., unpublished data). Three additional KIR sequence groups have been renamed based on their recombinant nature (Table 5).

### Renaming other macaque KIR genes

Several rhesus and cynomolgus macaque KIR sequences that were not obvious recombinants have been renamed based on sequence comparison and phylogenetic analysis (Tables 4 and 5). For example, 13 *Mamu-KIR3DSW08* alleles are readily distinguished from the other KIR3DSW08 alleles, and have been renamed as alleles of *Mamu-KIR3DSW39* (Table 4).

We should stress that *Mamu-KIR3DL07* and *Mamu-KIR3DL11* alleles group phylogenetically into three and two clusters, respectively, and that some KIR haplotypes contain several copies of these genes (Blokhuys et al. 2010; Bruijnesteijn et al. 2018a, b). Although an argument can be made for giving these paralogous genes unique gene names, sequence comparison has yet to indicate distinctive functions, and for this reason these genes have not been renamed.

### The IPD-NHKIR Database

Knowledge regarding the KIR repertoire in various NHP species has increased steadily over the past decade, escalating the need

| KIR gene | Previous designations | Number of reported alleles |
|----------|-----------------------|---------------------------|
| *Mamu-KIR3DSW18* | Newly identified in Burmese rhesus macaques | 1 |
| *Mamu-KIR3DSW20* | Newly identified in Burmese rhesus macaques | 1 |
| *Mamu-KIR3DSW21* | Newly identified in Burmese and Chinese rhesus macaques | 4 |
| *Mamu-KIR3DSW32* | Newly identified in Chinese rhesus macaques | 1 |
| *Mamu-KIR3DSW34* | Newly identified in Burmese rhesus macaques | 1 |
| *Mamu-KIR3DSW35* | Renamed *Mamu-KIR3DS02* fusion alleles | 2 |
| *Mamu-KIR3DSW36* | Renamed *Mamu-KIR3DS04* allele | 1 |
| *Mamu-KIR3DSW37* | Renamed *Mamu-KIR3DS04* allele | 1 |
| *Mamu-KIR3DSW38* | Renamed *Mamu-KIR3DS06* fusion allele | 1 |
| *Mamu-KIR3DSW39* | Renamed *Mamu-KIR3DSW08* alleles | 13 |
| *Mamu-KIR3DSW40* | Renamed *Mamu-KIR3DSW09* fusion allele | 1 |
| *Mamu-KIR3DSW41* | Renamed *Mamu-KIR3DSW09* fusion alleles | 2 |
| *Mamu-KIRDX1* | *KIR3DL0* | 1 |
| Total | | 576 |
Table 2  List of cynomolgus macaque KIR genes, their previous names, and the number of reported alleles per gene

| KIR gene     | Previous designations                  | Number of reported alleles |
|--------------|---------------------------------------|----------------------------|
| Mafa-KIR1D   | KIR1D                                  | 35                         |
| Mafa-KIR2DL04| KIR2DL04                               | 41                         |
| Mafa-KIR3DL20| —                                     | 36                         |
| Mafa-KIR3DL01| KIR3DL1                                | 17                         |
| Mafa-KIR3DLW03| —                                     | 4                          |
| Mafa-KIR3DL05| —                                     | 5                          |
| Mafa-KIR3DL06| —                                     | 1                          |
| Mafa-KIR3DL07| —                                     | 21                         |
| Mafa-KIR3DL11| —                                     | 18                         |
| Mafa-KIR3DLW12| Alleles of Mafa-KIR3DL2, Mafa-KIR2DL02 | 15                         |
| Mafa-KIR3DLW13| Alleles of Mafa-KIR3DL11 Alleles of Mafa-KIR3DL11 | 10                         |
| Mafa-KIR3DLW14| Alleles of Mafa-KIR3DL11              | 8                          |
| Mafa-KIR3DLW15| Alleles of Mafa-KIR3DL07              | 4                          |
| Mafa-KIR3DLW16| Alleles of Mafa-KIR3DL07              | 4                          |
| Mafa-KIR3DLW17| —                                     | 3                          |
| Mafa-KIR3DLW18| —                                     | 1                          |
| Mafa-KIR3DLW19| Alleles of Mafa-KIR3DL21 (EU419080.11)| 2                          |
| Mafa-KIR3DLW21| —                                     | 1                          |
| Mafa-KIR3DLW22| —                                     | 1                          |
| Mafa-KIR3DLW23| —                                     | 1                          |
| Mafa-KIR3DLW24| Alleles of Mafa-KIR3DL21 (EU419100.1) | 1                          |
| Mafa-KIR3DLW25| Alleles of Mafa-KIR3DL2               | 4                          |
| Mafa-KIR3DLW26| Alleles of Mafa-KIR3DL02              | 1                          |
| Mafa-KIR3DLW27| —                                     | 1                          |
| Mafa-KIR3DLW28| Mafa-KIR3DL07a                        | 1                          |
| Mafa-KIR3DL29| —                                     | 1                          |
| Mafa-KIR3DL30| —                                     | 1                          |
| Mafa-KIR3DLW47| Mafa-KIR3DL05*001                      | 1                          |
| Mafa-KIR3DLW48| Alleles of Mafa-KIR3DL05              | 2                          |
| Mafa-KIR3DS02| —                                     | 2                          |
| Mafa-KIR3DS04| —                                     | 1                          |
| Mafa-KIR3DS06| —                                     | 3                          |
| Mafa-KIR3DSW07| —                                     | 3                          |
| Mafa-KIR3DSW08| —                                     | 3                          |
| Mafa-KIR3DSW09| Mafa-KIR3DSW11*004                    | 1                          |
| Mafa-KIR3DSW10| Alleles of Mafa-KIR3DS                | 5                          |
| Mafa-KIR3DSW11| —                                     | 5                          |
| Mafa-KIR3DSW12| Alleles of Mafa-KIR3DS                | 11                         |
| Mafa-KIR3DSW13| Alleles of Mafa-KIR3DS                | 2                          |
| Mafa-KIR3DSW14| —                                     | 2                          |
| Mafa-KIR3DSW15| —                                     | 9                          |
| Mafa-KIR3DSW16| —                                     | 3                          |
| Mafa-KIR3DSW17| Alleles of Mafa-KIR3DS, Mafa-KIR3DH   | 4                          |
| Mafa-KIR3DSW18| —                                     | 2                          |
| Mafa-KIR3DSW19| —                                     | 2                          |
| Mafa-KIR3DSW20| Alleles of Mafa-KIR3DS                | 4                          |
| Mafa-KIR3DSW21| Alleles of Mafa-KIR3DS                | 7                          |
| Mafa-KIR3DSW22| Mafa-KIR3DL07b                        | 3                          |
| Mafa-KIR3DSW23| —                                     | 1                          |
for a centralized database with annotated sequences and a standard nomenclature. In July 2018, the IPD-NHKIR Database (https://www.ebi.ac.uk/ipd/nhkir/) was launched, and is now part of the Immuno Polymorphism Database (IPD) platform (https://www.ebi.ac.uk/ipd/) (Maccari et al. 2017). The database provides a centralized repository for non-human KIR (NHKIR) sequences, and currently archives data for four different NHP species as well as for cattle. The NHP species represented in the database are chimpanzee (Pan troglodytes, Patr), Sumatran orangutan (Pongo abelii, Poab), Bornean orangutan (Pongo pygmaeus, Popy), and rhesus monkey (Macaca mulatta, Mamu). For these four species, 266 annotated alleles representing various KIR genes are archived (Table 6), and comprise data submitted or published by several different research groups (Khakoo et al. 2000; Grendell et al. 2001; Hershberger et al. 2001; Rajalingam et al. 2001; Guethlein et al. 2002; Andersen et al. 2004; Sambrook et al. 2005; Guethlein et al. 2007; Blokhuis et al. 2009a, b; Bostik et al. 2009; Abi-Rached et al. 2010; Blokhuis et al. 2010; Chaichompoo et al. 2010; Kruse et al. 2010; Colantonio et al. 2011; Hellmann et al. 2011; Moreland et al. 2011). The KIR genes identified in cynomolgus macaques (Bimber et al. 2008; Prall et al. 2017) (Bruijnesteijn et al., unpublished data) have now been named, meaning that the KIR data from a fifth non-human primate species should soon be available. The current version of the IPD-NHKIR Database can host genomic sequences, and contains a multiple sequence alignment tool (Maccari et al. 2017). This tool allows for single gene alignments (nucleotide or protein) as well as inter- and intra-species gene alignments from all groups within the IPD-NHKIR Database. For each allele, a nomenclature table is accessible with additional information (for example: previous designations, GenBank/ENA/DDBJ accession number, and publications).

The curators of the IPD-NHKIR Database are responsible for assembling, categorizing, and providing official designations for newly identified alleles. For the NHP part of the IPD-NHKIR Database, the research group of Prof. Dr. R.E. Bontrop (Rijswijk, The Netherlands) is responsible for curation of the KIR sequences of macaque species, and for these species currently only full-length sequences are accepted for annotation, whereas curation for all other non-human primate species is the responsibility of Dr. L. A. Guethlein and Prof. Dr. P. Parham (Stanford, USA). Sequences/alleles can be submitted using the online submission tool, which is available from the IPD-NHKIR Database homepage (https://www.ebi.ac.uk/ipd/nhkir/). Submitted sequences must meet the criteria described above and have a GenBank/ENA/DDBJ accession number. In addition to newly identified KIR sequences, we urge and encourage all scientists working in the field of non-human primate KIR to submit all the sequences determined in their cohorts that are identical to published KIR alleles. This latter approach will provide an additional and valuable quality control tool for the database of archived KIR sequences. Although at present, only one KIR sequence at a time can be submitted, we are currently developing a bulk submission tool. The IPD-NHKIR Database provides a data release twice a year, which updates the website with all novel NHP KIR sequences that have become public, and relates them to the previously deposited sequences.

Table 3  Official names of macaque species. The abbreviation of the scientific name is used as suffix for the KIR designation

| Species name | Scientific name | KIR designation |
|--------------|-----------------|-----------------|
| Stump-tailed macaque | Macaca arctoides | Maar |
| Crab-eating macaque* | Macaca fascicularis | Mafa |
| Japanese macaque | Macaca fuscata | Mafu |
| Rhesus macaque | Macaca mulatta | Mumu |
| Southern pig-tailed macaque | Macaca nemestrina | Mane |
| Lion-tailed macaque | Macaca silenus | Masi |
| Milne-Edwards’s macaque | Macaca thibetana | Math |

*Other common names of this species are long-tailed and cynomolgus macaque
| Previous designation | New designation | Recombination segments |
|----------------------|----------------|-----------------------|
| Gene | Allele | Gene | Allele | Segment 1 | Segment 2 | Accession number | Reference |
| Mamu-KIR3DL02 | Mamu-KIR3DL02*005 | Mamu-KIR3DLW31 | Mamu-KIR3DLW31*001 | Mamu-KIR3DL02 | Mamu-KIR3DL02 | EU419054 | Moreland et al., BMC Genomics 2001 |
| Mamu-KIR3DL02 | Mamu-KIR3DL02*006 | Mamu-KIR3DLW31 | Mamu-KIR3DLW31*002 | Mamu-KIR3DL02 | Mamu-KIR3DL02 | EU688989 | Moreland et al., BMC Genomics 2001 |
| Mamu-KIR3DL02 | Mamu-KIR3DL02*010 | Mamu-KIR3DLW31 | Mamu-KIR3DLW31*003 | Mamu-KIR3DL02 | Mamu-KIR3DL02 | LS997661 | D. O’Connor 24-10-2017 |
| Mamu-KIR3DL02 | Mamu-KIR3DL02*011 | Mamu-KIR3DLW31 | Mamu-KIR3DLW31*004 | Mamu-KIR3DL02 | Mamu-KIR3DL02 | LS997662 | D. O’Connor 24-10-2017 |
| Mamu-KIR3DL02 | Mamu-KIR3DL02*016 | Mamu-KIR3DLW32 | Mamu-KIR3DLW32*001 | Mamu-KIR3DL10 | Mamu-KIR3DL02 | LR94230 | Bruijnesteijn et al., unpublished data |
| Mamu-KIR3DL10A/3DL02 | Mamu-KIR3DLW32 | Mamu-KIR3DLW32*002 | Mamu-KIR3DL10 | Mamu-KIR3DL02 | LT907840 | Bruijnesteijn et al., Journal of Immunology 2018 |
| Mamu-KIR3DL10B/3DL02 | Mamu-KIR3DLW33 | Mamu-KIR3DLW33*001 | Mamu-KIR3DL05 | Mamu-KIR3DL02 | LT907841 | Bruijnesteijn et al., Journal of Immunology 2018 |
| Mamu-KIR3DLW03 | Mamu-KIR3DLW03*001 | Mamu-KIR3DLW34 | Mamu-KIR3DLW34*001 | Mamu-KIR3DLW03 | Mamu-KIR3DLW03 | EU419051 | Moreland et al., BMC Genomics 2001 |
| Mamu-KIR3DLW03 | Mamu-KIR3DLW03*003 | Mamu-KIR3DLW34 | Mamu-KIR3DLW34*002 | Mamu-KIR3DLW03 | Mamu-KIR3DLW03 | EU419031 | Moreland et al., BMC Genomics 2001 |
| Mamu-KIR3DLW03 | Mamu-KIR3DLW03*004 | Mamu-KIR3DLW34 | Mamu-KIR3DLW34*003 | Mamu-KIR3DLW03 | Mamu-KIR3DLW03 | FN424253 | Kruse et al., Immunogenetics 2010 |
| Mamu-KIR3DLW03 | Mamu-KIR3DLW03*005 | Mamu-KIR3DLW34 | Mamu-KIR3DLW34*004 | Mamu-KIR3DLW03 | Mamu-KIR3DLW03 | FN424256 | Kruse et al., Immunogenetics 2010 |
| Mamu-KIR3DLW03 | Mamu-KIR3DLW03*009 | Mamu-KIR3DLW34 | Mamu-KIR3DLW34*005 | Mamu-KIR3DLW03 | Mamu-KIR3DLW03 | LS997651 | Bruijnesteijn et al., unpublished data |
| Mamu-KIR3DLW03 | Mamu-KIR3DLW03*014 | Mamu-KIR3DLW34 | Mamu-KIR3DLW34*006 | Mamu-KIR3DLW03 | Mamu-KIR3DLW03 | LR694237 | Bruijnesteijn et al., unpublished data |
| Mamu-KIR3DLW03 | Mamu-KIR3DLW03*016 | Mamu-KIR3DLW34 | Mamu-KIR3DLW34*007 | Mamu-KIR3DLW03 | Mamu-KIR3DLW03 | LR694239 | Bruijnesteijn et al., unpublished data |
| Mamu-KIR3DLW03 | Mamu-KIR3DLW03*017 | Mamu-KIR3DLW34 | Mamu-KIR3DLW34*008 | Mamu-KIR3DLW03 | Mamu-KIR3DLW03 | LR694240 | Bruijnesteijn et al., unpublished data |
| Mamu-KIR3DLW03 | Mamu-KIR3DLW03*018 | Mamu-KIR3DLW34 | Mamu-KIR3DLW34*009 | Mamu-KIR3DLW03 | Mamu-KIR3DLW03 | LR694241 | Bruijnesteijn et al., unpublished data |
| Mamu-KIR3DLW03 | Mamu-KIR3DLW03*023 | Mamu-KIR3DLW35 | Mamu-KIR3DLW35*001 | Mamu-KIR3DLW03 | Mamu-KIR3DLW03 | LR694248 | Bruijnesteijn et al., unpublished data |
| Mamu-KIR3DL05 | Mamu-KIR3DL05*001 | Mamu-KIR3DLW36 | Mamu-KIR3DLW36*001 | Mamu-KIR3DL05 | Mamu-KIR3DL05 | EU419045 | Moreland et al., BMC Genomics 2001 |
| Mamu-KIR3DL05 | Mamu-KIR3DL05*011 | Mamu-KIR3DLW36 | Mamu-KIR3DLW36*002 | Mamu-KIR3DL05 | Mamu-KIR3DL05 | FJS2121 | Bosik et al., J Immunology 2009 |
| Mamu-KIR3DL05 | Mamu-KIR3DL05*017 | Mamu-KIR3DLW36 | Mamu-KIR3DLW36*003 | Mamu-KIR3DL05 | Mamu-KIR3DL05 | LS997639 | D. O’Connor 24-10-2017 |
| Mamu-KIR3DL05 | Mamu-KIR3DL05*003 | Mamu-KIR3DLW37 | Mamu-KIR3DLW37*001 | Mamu-KIR3DL05 | Mamu-KIR3DL05 | EU419069 | Moreland et al., BMC Genomics 2001 |
| Mamu-KIR3DL05 | Mamu-KIR3DL05*009 | Mamu-KIR3DLW37 | Mamu-KIR3DLW37*002 | Mamu-KIR3DL05 | Mamu-KIR3DL05 | GU113210 | Blokhuis et al., Immunogenetics 2010 |
| Mamu-KIR3DL07 | Mamu-KIR3DL07*042 | Mamu-KIR3DLW38 | Mamu-KIR3DLW38*001 | Mamu-KIR3DL07 | Mamu-KIR3DL07 | LR694456 | Bruijnesteijn et al., unpublished data |
| Mamu-KIR3DL07 | Mamu-KIR3DL07*045 | Mamu-KIR3DLW39 | Mamu-KIR3DLW39*001 | Mamu-KIR3DL07 | Mamu-KIR3DL07 | LR694459 | Bruijnesteijn et al., unpublished data |
| Mamu-KIR3DL07 | Mamu-KIR3DL07*056 | Mamu-KIR3DLW40 | Mamu-KIR3DLW40*001 | Mamu-KIR3DL05 | Mamu-KIR3DL07 | LR694470 | Bruijnesteijn et al., unpublished data |
| Mamu-KIR3DL07 | Mamu-KIR3DL07*064 | Mamu-KIR3DLW41 | Mamu-KIR3DLW41*001 | Mamu-KIR3DL05 | Mamu-KIR3DL07 | LR694479 | Bruijnesteijn et al., unpublished data |
| Mamu-KIR3DL07*065 | Mamu-KIR3DLW42 | Mamu-KIR3DLW42*001 | Unknown donor | Mamu-KIR3DL07 | LR694480 Bruijnesteijn et al., unpublished data |
| Mamu-KIR3DL08 | Mamu-KIR3DLW43 | Mamu-KIR3DLW43*001 | Mamu-KIR3DL02 | Mamu-KIR3DL08 | LT907838 Bruijnesteijn et al., Journal of Immunology 2018 |
| Mamu-KIR3DL08*019Mamu-KIR3DL02/3DL08 | Mamu-KIR3DLW43*002 | Unknown donor | Mamu-KIR3DL07 | LR694480 Bruijnesteijn et al., unpublished data |
| Mamu-KIR3DL08*020 | Mamu-KIR3DLW43*003 | Mamu-KIR3DL02/3DL08A | Mamu-KIR3DL02/3DL08B | Mamu-KIR3DL08 | LR694519 Bruijnesteijn et al., unpublished data |
| Mamu-KIR3DL10 | Mamu-KIR3DLW45 | Mamu-KIR3DLW45*001 | Mamu-KIR3DL05 | Mamu-KIR3DL10 | LT907839 Bruijnesteijn et al., Journal of Immunology 2018 |
| Mamu-KIR3DL10*001 | Mamu-KIR3DLW45*002 | Mamu-KIR3DL05 | Mamu-KIR3DL07 | LR694480 Bruijnesteijn et al., unpublished data |
| Mamu-KIR3DL10*003 | Mamu-KIR3DLW45*003 | Mamu-KIR3DL07 | Mamu-KIR3DL07 | LR694480 Bruijnesteijn et al., unpublished data |
| Mamu-KIR3DL10*004 | Mamu-KIR3DLW45*004 | Mamu-KIR3DL07 | Mamu-KIR3DL07 | LR694480 Bruijnesteijn et al., unpublished data |
| Mamu-KIR3DL10*005:01 | Mamu-KIR3DLW45*004:01 | Mamu-KIR3DL07 | Mamu-KIR3DL07 | LR694480 Bruijnesteijn et al., unpublished data |
| Mamu-KIR3DL10*005:02 | Mamu-KIR3DLW45*004:02 | Mamu-KIR3DL07 | Mamu-KIR3DL07 | LR694480 Bruijnesteijn et al., unpublished data |
| Mamu-KIR3DL10*006 | Mamu-KIR3DLW45*005 | Mamu-KIR3DL07 | Mamu-KIR3DL07 | LR694480 Bruijnesteijn et al., unpublished data |
| Mamu-KIR3DL20 | Mamu-KIR3DL20*030 | Mamu-KIR3DL20 | Mamu-KIR3DL20 | Mamu-KIR3DL04 | LR694489 Bruijnesteijn et al., unpublished data |
| Mamu-KIR3DL20*044 | Mamu-KIR3DL20*044R | Mamu-KIR3DL20 | Mamu-KIR3DL04 | LR694489 Bruijnesteijn et al., unpublished data |
| Mamu-KIR3DS02 | Mamu-KIR3DSW35 | Mamu-KIR3DSW35*001 | Mamu-KIR3DS02 | Mamu-KIR3DS09 | JN613291 Hellmann et al., PLoS Pathogen 2011 |
| Mamu-KIR3DS02*029 | Mamu-KIR3DSW35*002 | Mamu-KIR3DS02 | Mamu-KIR3DS09 | JN613291 Hellmann et al., PLoS Pathogen 2011 |
| Mamu-KIR3DS04 | Mamu-KIR3DSW36 | Mamu-KIR3DSW36*001 | Mamu-KIR3DS04 | Mamu-KIR3DS07 | LR694564 Bruijnesteijn et al., unpublished data |
| Mamu-KIR3DS04*008 | Mamu-KIR3DSW36 | Mamu-KIR3DSW36*001 | Mamu-KIR3DS04 | Mamu-KIR3DS07 | LR694564 Bruijnesteijn et al., unpublished data |
| Mamu-KIR3DS04*011 | Mamu-KIR3DSW46 | Mamu-KIR3DSW46*001 | Mamu-KIR3DS04 | Mamu-KIR3DS07 | LR694564 Bruijnesteijn et al., unpublished data |
| Mamu-KIR3DS04*012 | Mamu-KIR3DSW37 | Mamu-KIR3DSW37*001 | Mamu-KIR3DS04 | Mamu-KIR3DS07 | LR694564 Bruijnesteijn et al., unpublished data |
| Mamu-KIR3DS06 | Mamu-KIR3DSW38 | Mamu-KIR3DSW38*001 | Mamu-KIR3DS06 | Mamu-KIR3DS06 | LR694573 Bruijnesteijn et al., unpublished data |
| Mamu-KIR3DS06*019 | Mamu-KIR3DSW38 | Mamu-KIR3DSW38*001 | Mamu-KIR3DS06 | Mamu-KIR3DS06 | LR694573 Bruijnesteijn et al., unpublished data |
| Mamu-KIR3DS08 | Mamu-KIR3DSW39 | Mamu-KIR3DSW39*001 | Mamu-KIR3DS08 | Mamu-KIR3DS08 | EU702467 Blokhuis et al., Mol Immunology 2009 |
| Mamu-KIR3DS08*005 | Mamu-KIR3DSW39 | Mamu-KIR3DSW39*001 | Mamu-KIR3DS08 | Mamu-KIR3DS08 | EU702467 Blokhuis et al., Mol Immunology 2009 |
| Mamu-KIR3DS08*006 | Mamu-KIR3DSW39*002 | Mamu-KIR3DS08 | Mamu-KIR3DS08 | Mamu-KIR3DS08 | EU702467 Blokhuis et al., Mol Immunology 2009 |
| Mamu-KIR3DS08*007 | Mamu-KIR3DSW39*003 | Mamu-KIR3DS08 | Mamu-KIR3DS08 | Mamu-KIR3DS08 | EU702467 Blokhuis et al., Mol Immunology 2009 |
| Mamu-KIR3DS08*008 | Mamu-KIR3DSW39*004 | Mamu-KIR3DS08 | Mamu-KIR3DS08 | Mamu-KIR3DS08 | EU702467 Blokhuis et al., Mol Immunology 2009 |
| Mamu-KIR3DS08*010:01 | Mamu-KIR3DSW39*005:01 | Mamu-KIR3DS08 | Mamu-KIR3DS08 | Mamu-KIR3DS08 | EU702467 Blokhuis et al., Mol Immunology 2009 |
| Mamu-KIR3DS08*010:02 | Mamu-KIR3DSW39*005:02 | Mamu-KIR3DS08 | Mamu-KIR3DS08 | Mamu-KIR3DS08 | EU702467 Blokhuis et al., Mol Immunology 2009 |
| Mamu-KIR3DS08*012 | Mamu-KIR3DSW39*006 | Mamu-KIR3DS08 | Mamu-KIR3DS08 | Mamu-KIR3DS08 | EU702467 Blokhuis et al., Mol Immunology 2009 |
Table 4  (continued)

| Mamu-KIR3DSW08*015 | Mamu-KIR3DSW39*007 | – | – | LR694578 | Chaichompoo et al., Cell. Immunol 2010 |
| Mamu-KIR3DSW08*016 | Mamu-KIR3DSW39*008 | – | – | LR694579 |
| Mamu-KIR3DSW08*017 | Mamu-KIR3DSW39*009 | – | – | LR694580 |
| Mamu-KIR3DSW08*018:01 | Mamu-KIR3DSW39*010:01 | – | – | LR694581 |
| Mamu-KIR3DSW08*018:02 | Mamu-KIR3DSW39*010:02 | – | – | LR694582 |
| Mamu-KIR3DSW08*014 | Mamu-KIR3DSW39*011 | – | – | LR694577 |
| Mamu-KIR3DSW09*004 | Mamu-KIR3DSW40 mamu-KIR3DSW40*001 | Mamu-KIR3DSW09 Unknown donor EU702466, G-U112273 |
| Mamu-KIR3DSW09*005 | Mamu-KIR3DSW41 Mamu-KIR3DSW41*001 | Mamu-KIR3DSW08 Unknown donor FN424249 |
| Mamu-KIR3DSW09*011 | Mamu-KIR3DSW41*002 Mamu-KIR3DSW08 | Unknown donor LR694585 |

Table 5  Renamed genes and alleles in cynomolgus macaques. The previous names are indicated, and the different gene segments are listed for sequences that are the result of fusion events

| Previous designation | New designation | Recombination segments | Accession number | Reference |
|----------------------|-----------------|------------------------|------------------|-----------|
| Gene | Allele | Gene | Allele | Segment 1 | Segment 2 | |
| Mafa-KIR3DL05 | Mafa-KIR3DL05*001 | Mafa-KIR3DL05*001 | Unknown donor | Mafa-KIR3DL05 | LR655425 |
| Mafa-KIR3DL05 | Mafa-KIR3DL05*002 | Mafa-KIR3DL05*002 | Mafa-KIR3DL01 | Mafa-KIR3DL05 | LR655426 |
| Mafa-KIR3DL05 | Mafa-KIR3DL05*003 | Mafa-KIR3DL05*003 | – | – | LR655427 |
| Mafa-KIR3DSW08 | Mafa-KIR3DSW08*001 | Mafa-KIR3DSW08*001 | – | – | LR655521 |
| Mafa-KIR3DSW08 | Mafa-KIR3DSW08*002 | Mafa-KIR3DSW08*002 | – | – | LR655522 |
| Mafa-KIR3DSW08 | Mafa-KIR3DSW08*003 | Mafa-KIR3DSW08*003 | – | – | LR655523 |
| Mafa-KIR3DSW11 | Mafa-KIR3DSW11*001 | Mafa-KIR3DSW11*001 | – | – | LR655531 |
| Mafa-KIR3DSW09 | Mafa-KIR3DSW09*001 | Mafa-KIR3DSW09*001 | – | – | LR655531 |
Table 6 Overview of the number of alleles and genes represented in the non-human primate part of the IPD-NHK (August 2019). The species included are chimpanzee (Patr), Sumatran orangutan (Poab), Bornean orangutan (Popy), and rhesus macaque (Mamu).

| Gene name                  | Species          | Patr  | Poab  | Popy  | Mamu |
|----------------------------|------------------|-------|-------|-------|------|
| KIR1D                      |                  |       |       |       | 2    |
| KIR2DL4/KIR2DL04*          |                  | 3     |       |       | 24   |
| KIR2DL5                    |                  | 5     |       | 1     |      |
| KIR2DL6                    |                  | 3     |       |       |      |
| KIR2DL7                    |                  | 1     |       |       |      |
| KIR2DL8                    |                  | 3     |       |       |      |
| KIR2DL9                    |                  | 3     |       |       |      |
| KIR2DL10                   |                  | 1     |       |       |      |
| KIR2DL11                   |                  | 1     |       |       |      |
| KIR2DL12                   |                  | 1     |       |       |      |
| KIR2DS4                    |                  | 2     |       |       |      |
| KIR2DS10                   |                  | 1     | 1     |       |      |
| KIR2DS13                   |                  | 1     | 1     |       |      |
| KIR2DS14                   |                  | 2     |       |       |      |
| KIR3DL1/KIR3DL01           |                  | 6     | 9     | 3     | 28   |
| KIR3DL02                   |                  | 4     |       |       | 9    |
| KIR3DL3                    |                  | 4     |       | 1     |      |
| KIR3DL4/KIR3DL04           |                  | 3     |       |       | 4    |
| KIR3DL5/KIR3DL05           |                  | 3     |       |       | 12   |
| KIR3DL06                   |                  | 2     |       |       |      |
| KIR3DL07                   |                  | 13    |       |       |      |
| KIR3DL08                   |                  | 12    |       |       |      |
| KIR3DL10                   |                  | 12    |       |       |      |
| KIR3DL11                   |                  | 8     |       |       |      |
| KIR3DL12                   |                  | 7     |       |       |      |
| KIR3DL20                   |                  | 15    |       |       |      |
| KIR3DLW03                  |                  | 5     |       |       |      |
| KIR3DLX1                   |                  | 1     |       | 1     |      |
| KIR3DS1/KIR3DS01           |                  | 1     |       | 4     |      |
| KIR3DS2/KIR3DS02           |                  | 2     |       | 15    |      |
| KIR3DS03                   |                  | 4     |       |       |      |
| KIR3DS04                   |                  | 6     |       | 4     |      |
| KIR3DS05                   |                  | 4     |       |       |      |
| KIR3DS6/KIR3DS06           |                  | 1     |       | 7     |      |
| KIR3DSW07                  |                  | 2     |       |       |      |
| KIR3DSW08                  |                  | 12    |       |       |      |
| KIR3DSW09                  |                  | 6     |       |       |      |
| KIRDP                      |                  | 1     |       |       |      |

*KIR2DL4 present in Patr, Poab, and Popy, and KIR2DL04 present in Mamu* represent orthologous genes. In the other cases where two gene names are indicated in the table, these do not represent orthologs, and the first mentioned gene in a row can be observed in Patr, Poab, or Popy, and the other in the Mamu.

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