

SUPPLEMENT TABLE 1

Listing of GenBank accesssion numbers for new Mamu-KIR3DH, 1D and 2DL4 alleles.

| | | GenBank Accession No. | |
|--------------|-----------|-----------------------|----------|
| KIR3DH | allele 1 | GU564157 | |
| | allele 4 | GU564158 | |
| | allele 5 | GU564159 | |
| | allele 6 | GU564160 | |
| | allele 7 | GU564161 | |
| | allele 8 | GU564162 | |
| | allele 9 | GU564163 | |
| | allele 10 | GU564164 | |
| | allele 11 | GU564165 | |
| | allele 12 | GU564166 | |
| | allele 13 | GU564167 | |
| | allele 14 | GU564168 | |
| | KIR1D | allele 9A | GU564169 |
| | | allele 9B | GU564170 |
| allele 10A | | GU564171 | |
| allele 10 B | | GU564172 | |
| allele 11 | | GU564173 | |
| allele 10sv1 | | GU564174 | |
| allele 11sv1 | | GU564175 | |
| KIR2DL4 | allele 3 | GU564176 | |
| | allele 4 | GU564177 | |
| | allele 5 | GU564178 | |
| | allele 6 | GU564179 | |
| | allele 7A | GU564180 | |
| | allele 7B | GU564181 | |

SUPPLEMENT FIGURE 1 A and B

Alignment of the Mamu-KIR2DL4 sequences of alleles 1, 2, 3, 4, 5, 6, 7 A and 7B at the (A) nucleotide and (B) amino acid level

(A) nucleotide level

| | | |
|-------------------|---|-----|
| Signal peptide | -----CTGGCCTGTCTTGGGTCTTCTGGACCAAGGGTGC | |
| Consensus | -----CTGGCCTGTCTTGGGTCTTCTGGACCAAGGGTGC | |
| KIR2DL4 allele-1 | ATGTCGCCACGGTCGTCATC..... | 63 |
| KIR2DL4 allele-2 | ATGTCGCCACGGTCGTCATC..... | 63 |
| KIR2DL4 allele-3 |G..... | 42 |
| KIR2DL4 allele-4 |A..... | 42 |
| KIR2DL4 allele-5 | | 42 |
| KIR2DL4 allele-6 | | 42 |
| KIR2DL4 allele-7A | | 42 |
| KIR2DL4 allele-7B | | 42 |
| Do domain | CACGTGGTGGTCAGGACAAGCCCTTCTGCTCTGCCTGGCCAGCGCTGGTGCCTCAGGGAGGACACGTGACTCTTTG | |
| Consensus | CACGTGGTGGTCAGGACAAGCCCTTCTGCTCTGCCTGGCCAGCGCTGGTGCCTCAGGGAGGACACGTGACTCTTTG | |
| KIR2DL4 allele-1 | | 143 |
| KIR2DL4 allele-2 | | 143 |
| KIR2DL4 allele-3 |G..... | 122 |
| KIR2DL4 allele-4 |C.G.....C..... | 122 |
| KIR2DL4 allele-5 | | 122 |
| KIR2DL4 allele-6 | | 122 |
| KIR2DL4 allele-7A | | 122 |
| KIR2DL4 allele-7B | | 122 |
| Consensus | GTGTCACTATCGTCCGGGTTAACATCTTCACGCTGTACAAGGAAGACGGGGTGCCTGTCCCTGAGCTCTACAAAAGAA | |
| KIR2DL4 allele-1 | | 223 |
| KIR2DL4 allele-2 | | 223 |
| KIR2DL4 allele-3 |G..... | 202 |
| KIR2DL4 allele-4 |G..... | 202 |
| KIR2DL4 allele-5 | | 202 |
| KIR2DL4 allele-6 | | 202 |
| KIR2DL4 allele-7A | | 202 |
| KIR2DL4 allele-7B | | 202 |
| Consensus | TATTCTGGAACAGTTTCCCTCATTAGCCCTGTGACTGCAGCACATGCAGGGACCTACAGATGTCGAGTTTTTCATCCGCAC | |
| KIR2DL4 allele-1 | | 303 |
| KIR2DL4 allele-2 | | 303 |
| KIR2DL4 allele-3 | | 282 |
| KIR2DL4 allele-4 | | 282 |
| KIR2DL4 allele-5 | | 282 |
| KIR2DL4 allele-6 |T..... | 282 |
| KIR2DL4 allele-7A | | 282 |
| KIR2DL4 allele-7B | | 282 |
| Consensus | TCCCCACTGAGTGGTCGGCACCCAGCAACCCCTGGTGATCATGGTCACA | |
| KIR2DL4 allele-1 | | 354 |
| KIR2DL4 allele-2 | | 354 |
| KIR2DL4 allele-3 | | 333 |
| KIR2DL4 allele-4 | | 333 |
| KIR2DL4 allele-5 | | 333 |
| KIR2DL4 allele-6 | | 333 |
| KIR2DL4 allele-7A | | 333 |
| KIR2DL4 allele-7B | | 333 |

| | | |
|----------------------|--|-----|
| D2 domain | | |
| Consensus | GGTCTATATGAGAAACCTTCTCTCAGCCAGCCGGGCCCCACGGTTCACAGGAGAGAACATGACCTTGTCCCTGCAG | |
| KIR2DL4 allele-1 | | 434 |
| KIR2DL4 allele-2 | | 434 |
| KIR2DL4 allele-3 | | 413 |
| KIR2DL4 allele-4 |G..... | 413 |
| KIR2DL4 allele-5 |T..... | 413 |
| KIR2DL4 allele-6 | | 413 |
| KIR2DL4 allele-7A |A..... | 413 |
| KIR2DL4 allele-7B | | 413 |
| Consensus | | |
| Consensus | TTCCCGCGCTCCTTTGACATGTACCATCTATCCAGGGAGGGGAGGCCCATGAACTTAGGCTCCCTGCAGTGCCGAGCG | |
| KIR2DL4 allele-1 | | 514 |
| KIR2DL4 allele-2 | | 514 |
| KIR2DL4 allele-3 | | 493 |
| KIR2DL4 allele-4 |C..... | 493 |
| KIR2DL4 allele-5 | | 493 |
| KIR2DL4 allele-6 | | 493 |
| KIR2DL4 allele-7A | | 493 |
| KIR2DL4 allele-7B |T..... | 493 |
| Consensus | | |
| Consensus | TCAATGGACATTCCAGGCTGACTTCCTCTGGCCCTGCCACCCACGGAGGGAACACAGATGCTTCGGCTCTCTCCGT | |
| KIR2DL4 allele-1 | | 594 |
| KIR2DL4 allele-2 | | 594 |
| KIR2DL4 allele-3 | | 573 |
| KIR2DL4 allele-4 |G..... | 573 |
| KIR2DL4 allele-5 | | 573 |
| KIR2DL4 allele-6 | | 573 |
| KIR2DL4 allele-7A | | 573 |
| KIR2DL4 allele-7B | | 573 |
| Consensus | | |
| Consensus | GACTCTCCCTACGAGTGGTCAGACCCAAAGTGACCCACTGCCGTTTCTCTCACA | |
| KIR2DL4 allele-1 | | 648 |
| KIR2DL4 allele-2 |G..... | 648 |
| KIR2DL4 allele-3 |A..... | 627 |
| KIR2DL4 allele-4 | | 627 |
| KIR2DL4 allele-5 |G..... | 627 |
| KIR2DL4 allele-6 | | 627 |
| KIR2DL4 allele-7A |- | 626 |
| KIR2DL4 allele-7B |- | 626 |
| Stem | | |
| Consensus | GGAAACCCCTCAAGTAGTTGGCCTTCACCCACTGAACCAAGCTTCAAAA-CTGGTATCGTCACACACCTGCCT | |
| KIR2DL4 allele-1 |-..... | 720 |
| KIR2DL4 allele-2 |AC.G..... | 720 |
| KIR2DL4 allele-3 |-..... | 699 |
| KIR2DL4 allele-4 |-..... | 699 |
| KIR2DL4 allele-5 |G.....G.....T.....G..... | 699 |
| KIR2DL4 allele-6 |G.....A..... | 700 |
| KIR2DL4 allele-7A |-.....C..... | 698 |
| KIR2DL4 allele-7B |-..... | 698 |
| Transmembrane domain | | |
| Consensus | GCTGTGATTAGGTACTCGGTGCCACCATCTTCCTCACCATCCTCCTCTTCTTCT | |
| KIR2DL4 allele-1 | | 776 |
| KIR2DL4 allele-2 | AT..... | 776 |
| KIR2DL4 allele-3 | | 755 |
| KIR2DL4 allele-4 | | 755 |
| KIR2DL4 allele-5 | T..... | 755 |
| KIR2DL4 allele-6 | | 756 |
| KIR2DL4 allele-7A | | 754 |
| KIR2DL4 allele-7B | | 754 |
| Cytoplasmic tail | | |
| Consensus | CCATCGTTGCTGGTGTCCGACAAAAA-GAATGCTGCTGTAATGGACC | |
| KIR2DL4 allele-1 |- | 823 |
| KIR2DL4 allele-2 | T..... | 823 |
| KIR2DL4 allele-3 | A..... | 803 |
| KIR2DL4 allele-4 | | 802 |
| KIR2DL4 allele-5 | T..... | 802 |
| KIR2DL4 allele-6 | | 803 |
| KIR2DL4 allele-7A | | 801 |
| KIR2DL4 allele-7B |C..... | 801 |

KIR2DL4 allele-1 and allele-2 refer to GenBank ac. no. EU702486 and AY728182, respectively.

(B) amino acid level

| | | | |
|----------------------|---|-----|-----|
| Signal peptide | | | |
| Consensus | -----LACLGFFLDQVRRA | | |
| KIR2DL4 allele-1 | MSPTVVI..... | 21 | |
| KIR2DL4 allele-2 | MSPTVVI..... | 21 | |
| KIR2DL4 allele-3 | -----C..... | 14 | |
| KIR2DL4 allele-4 | -----Q..... | 14 | |
| KIR2DL4 allele-5 | -----..... | 14 | |
| KIR2DL4 allele-6 | -----..... | 14 | |
| KIR2DL4 allele-7A | -----..... | 14 | |
| KIR2DL4 allele-7B | -----..... | 14 | |
| Do domain | | | |
| Consensus | HVGGQDKPFCSAWPSAVVPQGGHVTLWCHYRPGFNIFTLYKEDGVPELYKRIFWNSFLISPVTAAHAGTYRCRVFHPHSPTWEWSAPSINPLVIMVT | | |
| KIR2DL4 allele-1 | | | 118 |
| KIR2DL4 allele-2 | | | 118 |
| KIR2DL4 allele-3 |G.....V..... | | 111 |
| KIR2DL4 allele-4 | ...AE.....A.....A..... | | 111 |
| KIR2DL4 allele-5 | | | 111 |
| KIR2DL4 allele-6 |F..... | | 111 |
| KIR2DL4 allele-7A | | | 111 |
| KIR2DL4 allele-7B | | | 111 |
| D2 domain | | | |
| Consensus | GLYEKPSLSAQPGPTVPTGENMTLSCSSRRSFDMYHLSREGEAHELRLPAVPSVNGTFQADFPLGPATHGGNYRCFGSLRDSFYEWSDPDPLPVSVT | | |
| KIR2DL4 allele-1 | | | 216 |
| KIR2DL4 allele-2 | | | 216 |
| KIR2DL4 allele-3 |I..... | | 209 |
| KIR2DL4 allele-4 | ...G.....L.....C..... | | 209 |
| KIR2DL4 allele-5 | ...N..... | | 209 |
| KIR2DL4 allele-6 | | | 209 |
| KIR2DL4 allele-7A |H.....CQTQVTHC.FLSQ | | 209 |
| KIR2DL4 allele-7B |Y.....HC.FLSQ | | 209 |
| Stem | | | |
| Consensus | GNPSSSWPSPTEPSFKTGIVTHLP | | |
| KIR2DL4 allele-1 | | 240 | |
| KIR2DL4 allele-2 |TR... | 240 | |
| KIR2DL4 allele-3 | | 233 | |
| KIR2DL4 allele-4 | | 233 | |
| KIR2DL4 allele-5 |A...*...R... | 233 | |
| KIR2DL4 allele-6 | ...G.....NWYRHTPA | 233 | |
| KIR2DL4 allele-7A | ETLQVVGLH.LNQAS.LVSPHTCL | 233 | |
| KIR2DL4 allele-7B | ETLQVVGLH.LNQAS.LVSSHTCL | 233 | |
| Transmembrane domain | | | |
| Consensus | AVIRYSVATIFLTILLFFL | | |
| KIR2DL4 allele-1 | | 259 | |
| KIR2DL4 allele-2 | I..... | 259 | |
| KIR2DL4 allele-3 | | 252 | |
| KIR2DL4 allele-4 | | 252 | |
| KIR2DL4 allele-5 | V..... | 252 | |
| KIR2DL4 allele-6 | CCD*VLGGHHLPHHPPLLS | 252 | |
| KIR2DL4 allele-7A | L*LGTRWPPSSSPSSSS.S | 252 | |
| KIR2DL4 allele-7B | L*LGTRWPPSSSPSSSS.S | 252 | |
| Cytoplasmic tail | | | |
| Consensus | HRCWCSDKKNAAVMD | | |
| KIR2DL4 allele-1 | | 274 | |
| KIR2DL4 allele-2 | L..... | 274 | |
| KIR2DL4 allele-3 |ECCNG | 267 | |
| KIR2DL4 allele-4 | | 267 | |
| KIR2DL4 allele-5 | L..... | 267 | |
| KIR2DL4 allele-6 | PSLLVLRQ.ECCNG | 267 | |
| KIR2DL4 allele-7A | IVAGAPT.RMLL*WT | 267 | |
| KIR2DL4 allele-7B | IVAGAPT.RMLLSWT | 267 | |

* stop codon

KIR2DL4 allele-1 and allele-2 refer to GenBank ac. no. EU702486 and AY728182, respectively.

SUPPLEMENT FIGURE 2

Alignment of Mamu-KIR2DL4 sequences of 6 clones from 6 monkeys with “early” stop codons showing > 98% homology with Mamu-KIR2DL4 allele 5

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consensus      LACLGFLLDQVRVAHVGGQDKPFCSANPSAVVQGGHVTLWCHYRFGFNIFTLYKEDGVVPELYKRIFWNSFLISPVTAAHAGTYRCRVFHPHSPTWSAPSNFLVIMVTGLYEKPSLS 358
2DL4 mm 04 clone 2.seq LACLGFLLDQVRVAHVGGQDKPFCSANPSAVVQGGHVTLWCHYRFGFNIFTLYKEDGVVPELYKRIFWNSFLISPVTAAHAGTYRCRVFHPHSPTWSAPSNFLVIMVTGLYEKPSLS 358
2DL4 mm 20 clone 1.seq LACLGFLLDQVRVAHVGGQDKPFCSANPSAVVQGGHVTLWCHYRFGFNIFTLYKEDGVVPELYKRIFWNSFLISPVTAAHAGTYRCRVFHPHSPTWSAPSNFLVIMVTGLYEKPSLS 358
2DL4 mm 22 clone 5.seq LACLGFLLDQVRVAHVGGQDKPFCSANPSAVVQGGHVTLWCHYRFGFNIFTLYKEDGVVPELYKRIFWNSFLISPVTAAHAGTY*CRV FHPHSPTWSAPSNFLVIMVTGLYEKPSLS 358
2DL4 mm 25 clone 2.seq LACLGFLLDQVRVAHVGGQDKPFCSANPSAVVQGGHVTLWCHYRFGFNIFTLYKEDGVVPELYKRIFWNSFLISPVTAAHAGTYRCRVFHPHSPTWSAPSNFLVIMVTGLYEKPSLS 358
2DL4 mm 26 clone 1.seq LACLGFLLDQVRVAHVGGQDKPFCSANPSAVVQGGHVTLWCHYRFGFNIFTLYKEDGVVPELYKRIFWNSFLISPVTAHVAGTY*CRV FHPHSPTWSAPSNFLVIMVTGLYEKPSLS 358
2DL4 mm 33 clone 4.seq LACLGFLLDQVRVAHVGGQD*PFCSANPSAVVQGGHVTLWCHYRFGFNIFTLYKEDGVVPELYKRIFWNSFLISPVTAAHAGTYRCRVFHPHSPTWSAPSNFLVIMVTGLYEKPSLS 358

consensus      AQPGETVPTGENMTLSCSSRRSFDMYHLSREGEAHELRLPAVPSVNGTFFQADFFLGPATHGNYRCFGLRDSFYEWSDPSDPLFVSVTGNPSSSWPSPTEPSFKTIGIVTHLPAVIRYSV 718
2DL4 mm 04 clone 2.seq AQPGETVPTGENMTLSCSSRRSFDMYHLSREGEAHELRLPAVPSVNGTFFQADFFLGPATHGNYRCFGLRDSF*EWSAPSDPLFVSVTGNPSSSWPSPTEPSFKTIGIRHLPIVIRYSV 718
2DL4 mm 20 clone 1.seq A*PGETVPTGENMTLSCSSRRSFDMYHLSREGEAHELRLPAVPSVNGTFFQADFFLGPATHGNYRCFGLRDSFYEWSDPSDPLFVSVTGNPSSSWPSPTEPSFKTIGVTHLPAVIRYSV 718
2DL4 mm 22 clone 5.seq AQPGETVPTGENMTLSCSSRRSFDMYHLSREGEAHELRLPAVPSVNGTFFQADFFLGPATHGNYRCFGLRDSFYEWSDPSDPLFVSVTGNPSSSWPSPTEPSFKTIGIVTHLPAVIRYSV 718
2DL4 mm 25 clone 2.seq AQPGETVPTGENMTLSCSSRRSFDMYHLSREGEAHELRLPAVPSVNGTFFQADFFLGPATHGNYRCFGLRDSFYEWSDPSDPLFVSVTGNPSSSWPSPTEPSFKTIGIVTHLPAVIRYSV 718
2DL4 mm 26 clone 1.seq AQPGETVPTGENMTLSCSSRRSFDMYHLSREGEAHELRLPAVPSVNGTFFQADFFLGPATHGNYRCFGLRDSFYEWSDPSDPLFVSVTGNPSSSWPSPTEPSFKTIGIVTHLPAVIRYSV 718
2DL4 mm 33 clone 4.seq AQPGETVPTGENMTLSCSSRRSFDMYHLSREGEAHELRLPAVPSVNGTFFQADFFLGPATHGNYRCFGLRDSFYEWSDPSDPLFVSVTGNPSSSWPSPTEPSFKTIGIVRHLPAVIRYSV 718

consensus      ATIFLTILLFFLHRCWCSDKKNAAVMDP 802
2DL4 mm 04 clone 2.seq ATIFLTILLFFLHRCWCSDKKNAAVMDP 802
2DL4 mm 20 clone 1.seq ATIFLTILLFFLHRCWCSDKKNAAVMDP 802
2DL4 mm 22 clone 5.seq ATIFLTILLFFLHRCWCSDKKNAAVMDP 802
2DL4 mm 25 clone 2.seq ATIFLTILLFFLHRCWCSDKKNAAVMDP 802
2DL4 mm 26 clone 1.seq ATIFLTILLFFLHRCWCSDKKNAAVMDP 802
2DL4 mm 33 clone 4.seq ATIFLTILLFFLHRCWCSDKKNAAVMDP 802
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SUPPLEMENT FIGURE 3

Mamu-KIR1D variants of allele 9A and 9B showing deletions of thymine at position 623 (allele 9A) and adenine at position 662 (allele 9B) using the sequence of KIR1D allele 8 (previously designated KIR3DL7) as a consensus sequence

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Cytoplasmic tail
KIR1D allele-8  AGGAGGTGACATACGCACAGTTGGATCACTGCGTTTTCACACAGGGAAAAATCACTTGCCCTTCTCAGAGGTCCAAGAGACCCCAACAGATACCAGCGT 686
KIR1D allele-9A .....-.....C..... 691
KIR1D allele-9B .....-..... 691
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