Vet. Res. (2010) 41:54 Ruminant MR1 and MAIT cells Supplementary Figure 1.

Ovine and bovine MAIT cell TCR  $\alpha$  chain nucleotide sequences and location of primers. In red: primers used for cloning and sequencing of bovine and ovine MAIT TCR; in blue: primers used in MAIT V region and  $\alpha$  chain constant region qPCR; in pink: qPCR probes; in grey: CDR regions.

I. van Rhijin

ovine	primer boovUntr3f <mark>AGCGCCTGGTTTGTGGTGTGC</mark> CTGCAGCAGATGTGGAATTTTTTCCTTCTTTGTGTTTCCCC
ovine bovine	TGACAGTGAGAGGCTCTGCAGGAAAAGGCGTTGAGCAGCCCACTGAGTTGACGGTTATGG CAGCCCACTGAGGAAAAGGCGTTAAG CAGCCCACTGAGTTGATGGCTATAG primer ~1″
ovine bovine	CDR1 AAGGAGCCTCTGCCCAGGTCAACTGCACCTACCAGACATCTGGGTTCAATGGACTGTTCT AAGGAGCCTCTGCCCAGGTTAACTGCACCTACCAGACATCTGGATTCAATGGACTGTTCT
ovine bovine	CDR2 GGTACCAGCGACATGATGGTGGAGCACCTGTGTTTCTCTCTTACAATGTTTTGGATGGT GGTACCAGCAACACGATGGTGGAGCACCTGTGTTTCTCTCTTACAATGTTCTGGATGGT T
	primer boAV19
ovine bovine	TGGAGACGAGAGGTCATTTTTCTTCATTCCTTAGACGCTCTGATGCACACAG <mark>TTACCTCC</mark> TGGAGACGAGAGGTCATTTTTCTT <mark>CATTCCTTAGACGCTCTGATGCACA</mark> CAG <mark>TTACCTCC</mark>
ovine bovine	probe boAV19 CDR3 TTCTGAAGGAACTCCACATGAAAGA TTCTGAAGGAACTCCACATGAAAGA CTTTGCCTCTTACCTCTGTGTGTGTGTGATGGATGGCA
	primers boAJ33/ovAJ33
ovine bovine	ACTATCGGTTGATCTGGGGCTCTGGGACCAAGCTAATTATAAAGCCAGAAATCAAGGACC ACTATCAGTGGATCTGGGGCTCTGGGACCAAACTAATTATAAAGCCAGAAGTCAAGGACC
ovine bovine	CCAACCCCACTGTGTACCAGCTGAGAAGCCCCGAATCCAGCAACACTTCTGTCTG
ovine bovine	TCACCGATTTTGACTCAAATCAAATCAACCTGACACAAATTGGGGGGGTACGAGTGGAACA TCACCGATTTTGATTCAAATCAAGTCAACATGGAAAAAATCATGGGGTCCGAGGGGGGGG
ovine bovine	TGGTACACAAAACAGACAGCACCGTGCTCAACATGGAGATCCTGGGGTCCAAGAGCA <mark>ACG</mark> CGGTGCACAAAACAACAGCACCGTGCTCAACATGGAGATCCTGGGATCCAAGAGCAACG
ovine bovine	primer NGconst-f probe NGconst GGATAGTGACTTGGGGAAACACCAGCGATTCTGGATGCACAA <mark>ACACCTTCAACGAGAACA</mark> GGATAGTGACTTGGGGAAACACCAGCGATGCTG <mark>GATGCGAATACACCTTCAACG</mark> AGACCA primer alpha
ovine bovine	primer NGconst-r TTGAGTTTGTCGACAACTTCGGAATCCCCTGTGATG <mark>CCAAGCTGGTAGAGAAAAGCTTTG</mark> T <mark>TCCCTTCGCCTCCAGCTTGGAAATCT</mark> CCTGTAATG <mark>CCAACCTGCTAGAGAAAACCTTTG</mark> probe const alpha primer "K"
ovine	AAACAGATGTGAACCTAAACTCCCAAAACCTGTCAGTGACTGTGTTCCGCATCCTCCTCC
ovine	primer CorovC3r TGA <mark>AGGTGGTCGGGTTTAACCT</mark>

## Supplementary Figure 2

Alignment of MR1 nucleotide sequences of different species.

Alignment of full-length bovine (bo) (accession number FJ028657.1), ovine (ov) (FJ423039), human (hu) (AJ249778.1), and murine (mu) (AF010448.1) MR1 nucleotide sequences. \* Indicates a position with a fully conserved residue.

	Leader
BoMR1	ATGAT GCT CC TAT TGCCT CT CAT CATTG TA TTA AT GAT GA AGC TC AGC GA TGCTC GG ACT CACTC TC TGA GA TAT TT T
OvMR1	ATGAT GCT CCTAT TGCCT CT CAT CAT TG TA TTA AT GAT GA AGC TC AGC GATGCTC GG ACT CACTC TC TGA GA TAT TT T
HuMR1	ATG GG GGAAC TGA TG GC GTT CC TGTTA CCT CT CAT CATTG TG TTA AT GGT GA AGC ACAGC GA TT CCC GG ACG CA CT CT CT GA GA TATTT T
MuMR1	ATGATECTCCTTTTACCTCTCTCTCTCTCTTTTTTT
MUMAL	
	*** * **** ** ***** ** *** ** ** ** *** *** *** *** ****
BoMR1	CGCCTGGGCATTTCAGAGCCTGGCTATGGGATCCCTGAATTTATTT
OvMR1	CGCCTGGGCATCTCAGAGCCTGGCTATGGGATCCCTGAATTTATTT
HuMRl	CGC CT GGG CGTTT CG GA TCC CA TCC AT GGG GT CCC TG AAT TT ATT TC GGT TG GGT AC GTG GA CT CGC AC CCT AT CAC CA CAT AT GAC AG T
MuMR1	CGTCT GGCTGTTTCC GATCCTGGTCCCGTCGTCCCTGAATTTATCTCTGTTGGGTATGTGGACTCACCCCTATCACTACGACAGT
	** **** * ** ** ** ** * ** ** *********
BoMR1	GTGTC CCAGCTGAAGGAGCCGCGGGCCCTGTGGATGGAGGAAAACCT GGCACCTGATCACTGGGAGAGGTACACACACGCTGCTGCGGGGC
OvMR1	GTCTC CCA GCTGAAG GA GCCAC GTG CC CCATG GAT GG CGGAA AAC CT GGAAC CTG AT CACTG GG AGA GG TAC ACA GC TGC TG CGG GG C
HuMR1	GTC AC TCG GC AGAAG GA GCC AC GGG CC CCA TG GAT GG CAG AGAAC CT CGC GC CTG AT CAC TG GG AGA GG TAC AC TCA GC TGC TG AGG GG C
MuMR1	GTC AC TCG AC AGA AG GA GCC GA AAG CT CCA TG GAT GG CAG AG AG CT GGC AC CTG AT CACTG GG AGA GG TAC ACTCA GC TGC TA AGG GG C
	** * * * ********* ** ** ** ****** ** *
BoMR1	TGGCA GCA GGCGTTC AA GGTGGAAC TGAAGCA GCT GCAGCAT CAC TA CAA TC ACT CA GGGTT TC ACA CT TAC CA GAGAA TGA TT GGC TG T
OvMR1	tggcagcagcgttcaaggtggaactgaagcagctgcagcatcactacaatcactcagggtttaacacttaccagagaatgattggttgg
HuMR1	TGG CA GCA GA TGT TC AA GGT GG AAC TG AAG CG CCT AC AGA GG CAC TA CAA TC ACT CA GGG TC TC ACA CT TAC CA GAG AA TGA TT GGC TG T
MuMR1	TGG CA GCA GA CATTCAA GGC GGAGC TG AGG CA CCTAC AGA GG CAC TA CAA CC ACT CA GGG CT TC ACA CC TAC CA GAG AA TGATT GGC TG T
	********* ******* *** *** *** ** ** **
BoMR1	GAGTTACTGGAGGATGGAAGCATCACGGGATTTCCCCAATATGCATATGATGGACAGGATTTCCTTATCTTCAATAAAGATACCCTGTCC
OvMR1	GAGTTACT GGATGAT GGCAGCACCACGGGATTTCT CCAATAT GCGTATGATGACAGGATTTCATTATCTTCAATAAGATACCCTCTCC
HuMR1	GAGTTECTGGARGATGGARGCACCACGGGATTTCTCGCAGTATGGCATGGATGGGCAGGGCAGGGCATTTCCTGATGAGGACGCCCCTCC
MuMRl	GAGTT GCTAGAAGAT GGCAGCA CCA CA GGGTT TCT CC AGTAT GCA TA TGA TGGACAA GAT TT CA TCA TC AT TA A AGACA CC CT CT C
	*** * ** ** ***** **** *** ** ** ** **
BoMR1	TGGAT GGC CATGGAT AA TGT GG CTGAC ATCAT CAG GC GGG TA TGG GA GGC CAATC GG CAT GA GT TAC AA TAT CA GAA GA ATT GG CTG GAA
OvMR1	TGGAT AGC CA TGGAT AA TGT GG CTA AC ATC AT CAG GC GGG CA TGG GA GGC CA ATC GG CAT GA GT TAC AA TAT CA GAA GA ATT GG CTG GA A
HuMR1	TGGCTGGCTGTAGATAATGTGGCTCACACCATCAAGCAGGCATGGGAGGCCAATCAGCATGAGTTGCTGTATCAAAAGAATTGGCTGGAA
MuMR1	TGGTTGGCCATGGATTATGTGGCTCACATCACCAAGCAAG
PIGHICI	
BoMR1	GAA GA ATG CA TTG CT TG GTT AA AGA GA TTC CT GGAGT ATG GG AAA GA TGC CT TAC AA AGA AC AGG ACCAA AGT CA GAG TC AAT CA C
OvMR1	GAA GAATG TA TTG CT TG GTT AA AGA GA TTC CT GGA GT ATG GG AAA GA TAC CT TAC AA AGG AC AG AGC CC CCC AA AGT CC GAG TC AAT TA C
HuMR1	GAA GAATG TA TTG CC TG GCT AA AGA GA TTC CT GGA GT ATG GG AAA GA CACCC TAC AA AGAAC AG AGC CC CCACT GGT CA GAG TA AAT CG C
MuMR1	GAA GAATG CATTG CCTG GCT AA AGA GG TTC TT GGA AT ATG GA AGA GA TAC CC TAG AA AGA AC AG GC AT CCA GT GGT AA GAA CA ACT CG A
	********* ***** *** ******* *** **** ****
BoMR1	AAA GAAAC TT TCCCAGGGAT TA CAACT CTT TA CTGCAGAGCT TAT GGCTT TT ACCCCCCCA GAAA TTT CCATT AACTGGA TGAAAAAC GGG
OvMR1	AARGAAACTTTCCCAGGGATTACAACTCTTTACTGCAGAGCTCATGGCTTTTACCCCCCAGAAATTTCCATAAACTGGATGAAAAACGGG
HuMR1	AAAGAAACTTTTCCAGGGGTTACAGCTCCTCTTCTGCAAAGCTCATGGCTTTTACCCCCCCAGAAATTTACATGACATGGATGAAAAACGGG
MuMR1	AAGGA AAC TTTTC CA GGGATTA CAA CTTTC TTCTG CA GAGCT CATGGCTT CTACC CA CCA GAAA TTTCC ATGACATGGA TGAAAAATGGG
	** ******* ****** ***** ** ** * ***** ****
BoMR1	GAA GAAAT TT TCCAA GA TACCGATT AT GGAGG CAT TC TTCCC AGT GGGGATG GGACC TAT CAGACTT GG GTG TC TGTTG AGC TG GAT CCT
OvMR1	GAA GAAGT TG TCCAA GACAC CAATT AT GGAGG CAT TC TTC CC AGT GGGGATG GGACC TATCA GACTT GG GTG TC TG TG AGC TG GAT TC T
HuMR1	GAA GAAAT TG TCCAA GA AAT TGATTAT GGAGA CAT TC TTC CCAGT GG GGATG GAACC TAT CAGG CGT GG GCATC AAT TG AGCTT GAT CC T
MuMR1	GAAGAAAT TGCCCAAGAAGT GGATTAC GGAGGGT AC TTCCCAGC GGGGATGGAACC TATCAAACGT GG CTGTCAGT TAATC TGGATCC T
PIGNINI	
-	г
BoMRl	CAGAA TGG TGACA TT TA CTC CT GTC AC GTG GA GCA TG GCG GA GTC CA CAT GG TT CT CAG GG TT TCC AG GAA TC GGA AA CTA TA CTT CT C
0vMR1	CAGAA CGG TGACATT TA CTC CT GTC AC GTG GA GCA TG GCG GC GTC CA CAT GG TTC TT CC GG GTT TC CAG GAT TC GGA AA CTA TG CTT CT G
HuMR1	CAGAGCAACCTTTACTCCTGTCATGTGGAGCACTGCGGTGTCCACATGGTTCTTCAGGTCCCCCCAGGAATCAGAAACTATCCCTCTT
MuMR1	CAGAG CAA TGATGTTTA TTC TTGTCATGTGGA GCA CTGTGGTCGC CAAATGGTTC TGGAGGCCCCTCGGGAAATCAGGGGACATCCTTCGA
	Transmembrane Cytoplasmic domain
BoMR1	GTGGTGAAAGCTGTTGGGTTCATTGTCCTCGCCATTGCCCTGGCTGGAGTTGGCATCCTAGCCTGGCGAAAGAGGCCCCGAGGGAAA
	GTGAT GAAAG CTGTTGGGTTCATTGTC CTCGC CATTG CC CTGGC TGGAGTTGGCATCTTAG CCTGG CGAAG GAAG
HuMRl	GTGAT GAAAG CTGTCTC TGGGTCCA TTGTCCTTGT CA TTGTGCTGGC TGGAG TTGGTGTTCTAGTCTGGAGAAGAAGGCCCCCGAGAGCAA
MuMRl	GTGAGCAC GATCT C TGGAA CCA CAATT CT CAT CA TCGCC CTGGC TGGAGTTGGT GTT CT GATCT GG AGAAGGT CAC AA GAA CT A
	* *** * * * * * *** *******************
BoMR1	AACAA AGT CA TCT GCCT TTC TA CAC CA GAACA CTGA
	ARCAAAGTCATCTACCTTTCTACACCAGAACACTGA
HuMR1	AATGGAGCCATCTACCTTCCAACACCCAGATCGATGA
HuMR1	