Table S1: Additional notes about rhesus macaque TRBV genes

Rhesus macaque gene	Human gene homologue	Additional notes
TRBV5-1	TRBV5-1	**Ambiguity in the identification of the 5' end of the exon.** The 5' end of the exon, as determined by comparison with the human TRBV5 exon, has 9 n.t. before the existence of a start codon.
TRBV5-2	TRBV5-1	
TRBV6-2	TRBV6-1	**Partial gene and exon sequences at the 5' end.** The gene is missing 121 n.t. and the exon is missing 49 n.t..
TRBV6-5	TRBV6-9	**Partial gene and exon sequences at the 3' end.** The gene is missing 48 n.t. and the exon is missing 9 n.t..
TRBV6-8	TRBV6-5	**Partial gene and exon sequences at the 3' end.** The gene is missing 85 n.t. end and the exon is missing 46 n.t..
TRBV7-1	TRBV7-1	**Partial gene and exon sequences at the 5' end.** The gene is missing 199 n.t. and the exon is missing 57 n.t..
TRBV7-2	TRBV7-3	**Partial gene and exon sequences at the 5' end.** The gene is missing 235 n.t. and the exon is missing 125 n.t..

Supporting Information Data Files:

Rhesus_macaque_TRBV.fsa: TRBV genes extracted from the rhesus macaque genome. The gene features reported include L-PART1, V-INTRON, V-EXON, V-HEPTAMER, V-SPACER, and V-NONAMER. The FASTA header fields include the species name, rhesus macaque chromosome 3 accession number (NC_007860.1), start and end positions of gene feature in the rhesus macaque chromosome 3, strand (-1 indicates that the reported sequences are the reverse complement), gene name, and gene feature.

Rhesus_macaque_TRBD.fsa: TRBD genes extracted from the rhesus macaque genome. The gene features reported include 5'D-NONAMER, 5'D-SPACER, 5'D-HEPTAMER, D-REGION, 3'D-HEPTAMER, 3'D-SPACER, and 3'D-NONAMER. The FASTA header fields include the species name, rhesus macaque chromosome 3 accession number (NC_007860.1), start and end positions of gene feature in the rhesus macaque chromosome 3, strand (-1 indicates that the reported sequences are the reverse complement), gene name, and gene feature.

Rhesus_macaque_TRBJ.fsa: TRBJ genes extracted from the rhesus macaque genome. The gene features reported include J-NONAMER, J-SPACER, and J-HEPTAMER. The FASTA header fields include the species name, rhesus macaque chromosome 3 accession number (NC_007860.1), start and end positions of gene feature in the rhesus macaque chromosome 3, strand (-1 indicates that the reported sequences are the reverse complement), gene name, and gene feature.