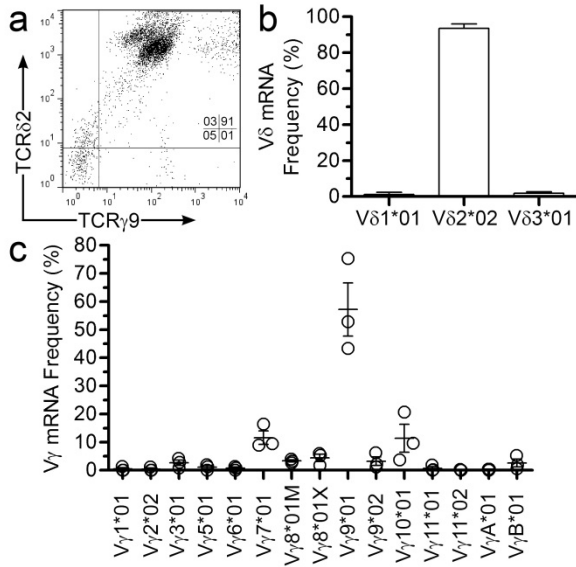
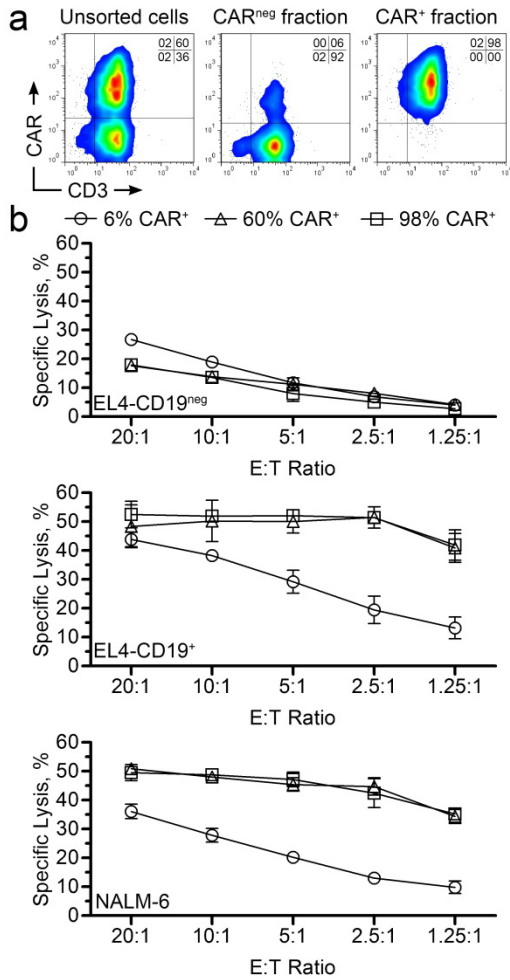


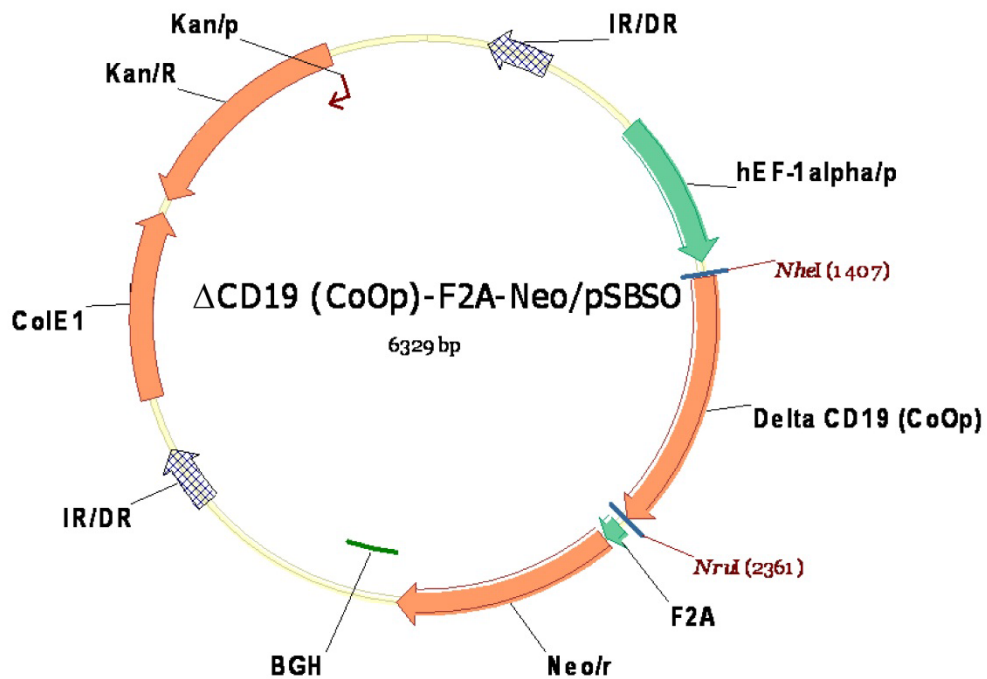
SUPPLEMENT



Supplemental Figure S1: Distribution of V δ and V γ in $\gamma\delta$ T cells expanded on aminobisphosphonate. (a) Representative flow cytometry plot from T cells following 36 days of numeric expansion with Zol. **(b)** V δ and **(c)** V γ allele mRNA expression in Zol-expanded T cells. Data are mean \pm SD (n = 3). Quadrant frequencies of flow plot are displayed.



Supplemental Figure S2: Specific lysis of CD19⁺ tumor cell lines by CAR⁺, CAR⁺⁺, and CAR⁺⁺⁺ $\gamma\delta$ T cells. (a) Phenotype of T cells at day 19 of co-culture either unsorted (left) or from CAR sorting at day 15 where CAR^{neg} and CAR⁺ fractions are displayed in the middle and right, respectively. (b) Four-hour CRA (Day 19 of co-culture on aAPC) of $\gamma\delta$ T cells genetically modified to enforce expression of CD19-specific CAR with 6% (CAR⁺, circles), 60% (CAR⁺⁺, triangles), and 98% (CAR⁺⁺⁺, squares) expression of CAR targeting EL4-CD19^{neg} (top), EL4-CD19⁺ (middle), and CD19⁺ NALM-6 tumor cells. Data are mean \pm SD (n = 3). Quadrant frequencies of flow plots are displayed.



Supplemental Figure S3: *Sleeping Beauty* DNA transposon (designated ΔCD19-F2A-Neo) to co-express truncated human CD19 and neomycin phosphotransferase for *in vitro* selection. Abbreviations: IR/DR: inverted repeat/direct repeat, hEF-1alpha/p: human elongation factor-1α hybrid promoter, Delta CD19 (CoOp): codon-optimized CD19 exodomain and transmembrane domain, F2A: furin-T2A cleavage domains, Neo/r: neomycin phosphotransferase, BGH: bovine growth hormone polyA tail, ColE1: *E. coli* origin of replication, Kan/R: kanamycin resistance, Kan/p: kanamycin resistance promoter. Digestion with *Nru* I and *Nhe* I enzymes yields 954 and 5,375 basepair fragments.

Supplemental Table 1. Antibodies used in study

Antibody specificity	Clone	Vendor
Fc*	H10104	Invitrogen
anti-CD19scFv mAb*	136.20.1	Cooper Lab
CD3	SK7	BD Biosciences
CD4	RPA-T4	BD Biosciences
CD8	RPA-T8	BD Biosciences
CD19	HIB19	BD Biosciences
CD27	M-T271	BD Biosciences
CD28	L293	BD Biosciences
CD45RA	HI100	BD Biosciences
CD45RO	UCHL1	BD Biosciences
CD56	B159	BD Biosciences
CD57	NK-1	BD Biosciences
CD62L	Dreg 56	BD Biosciences
CD64	10.1	BD Biosciences
CD86	2331 FUN-1	BD Biosciences
CD137	4B4-1	BD Biosciences
CD137L	C65-485	BD Biosciences
CCR7	TG8	eBiosciences
CXCR4	12G5	BD Biosciences
CLA	HECA-452	BD Biosciences
TCR $\alpha\beta$	WT31	BD Biosciences
TCR $\gamma\delta$	B1	BD Biosciences
TCR δ 1	TS-1	Thermo/Pierce
TCR δ 2	B6	BD Biosciences
TCR γ 9	B3	BD Biosciences
invariant NKT	6B11	BD Biosciences
IFN γ	4S.B3	BD Biosciences
TNF α	MAb11	BD Biosciences

*To describe CAR expression

Supplemental Table 2: Direct TCR Expression Assay (DTEA)

Customer Identifier	Accession	Targeted Region	Target Sequence
TRAV1-1	TCRVA_001.1	192-292	TACAATGCTCTGGATGGTTTGGAGGAGACAGGTCGTTTT TCTTCATTTCCTTAGTCGCTCTGATAGTTATGGTTACCTCC TTCTACAGGAGCTCCAGATGA
TRAV1-2	TCRVA_002.1	187-287	TGTCTTACAATGTTCTGGATGGTTTGGAGGAGAAAGGT CGTTTTTCTTCATTTCCTTAGTCGGTCTAAAGGGTACAGT TACCTCCTTTTGAAGGAGCTCCA
TRAV2	TCRVA_003.1	177-277	TACCTTCACTTCCCGGGATGTGCACCAAGACTCCTTGTT AAAGGCTCAAAGCCTTCTCAGCAGGGACGATAACAAT GACCTATGAACGGTTCTCTTCAT
TRAV3	TCRVA_004.1	6-106	TCTGCACCCATCTCGATGCTTGGATGCTCTTCACATTG AGTGGGCTGAGAGCTCAGTCAGTGGCTCAGCCGGAAGA TCAGGTCAACGTTGCTGAAGGGA
TRAV4	TCRVA_005.1	159-259	CAACAGTTTTCCAGCCAAGGACCACGATTTATTATTCAA GGATAACAAGACAAAAGTTACAAACGAAGTGGCCTCCCT GTTTATCCCTGCCGACAGAAAGT
TRAV5	TCRVA_006.1	118-218	TTATAAACTGCACTTACACAGACAGCTCCTCCACCTACT TATACTGGTATAAGCAAGAACCTGGAGCAGGTCTCCAG TTGCTGACGTATATTTTTTCAA
TRAV6	TCRVA_007.1	183-283	AGAGGCCCTGTTTTCTTGCTACTCATACGTGAAAATGAG AAAGAAAAAAGGAAAGAAAGACTGAAGGTCACCTTG ATACCACCCTTAAACAGAGTTTGT
TRAV7	TCRVA_008.1	126-226	AGCTGCACGTA CTGT CAGTCGTTTTAAACAATTTGCAG TGGTACAGGCAAATA CAGGGATGGGTCCCAAACACCT ATTATCCATGTATTCAGCTGGAT
TRAV8-1	TCRVA_009.1	108-208	TCACTGGAGTTGGGATGCAACTATTCCTATGGTGGAECT GTTAATCTCTTCTGGTATGTCCAGTACCCTGGTCAACAC CTTCAGCTTCTCCTCAAGTACT
TRAV8-2	TCRVA_010.1	206-306	CACATCAGCGGCCACCCTGGTTAAAGGCATCAACGGTT TTGAGGCTGAATTTAAGAAGAGTGAAACCTCCTTCCAC CTGACGAAACCCTCAGCCCATATG
TRAV8-3	TCRVA_011.1	49-149	CTGCCAGAGCCCAGTCAGTGACCCAGCCTGACATCCAC ATCACTGTCTCTGAAGGAGCCTCACTGGAGTTGAGATG TAACTATTCCTATGGGGCAACACC
TRAV8-6	TCRVA_013.1	206-306	TTTATCAGGATCCACCCTGGTTAAAGGCATCAACGGTTT TGAGGCTGAATTTAACAAGAGTCAAACCTCCTTCCACTT GAGGAAACCCTCAGTCCATATA
TRAV9-1	TCRVA_014.1	49-149	GAATCAATGGAGATTCAGTGGTCCAGACAGAAGGCCAA GTGCTCCCCTCTGAAGGGGATTCCCTGATTGTGAACTGC TCCTATGAAACCACACAGTACCC
TRAV9-2	TCRVA_015.1	31-131	TACTCTTACTGCTTGGAAAGAACCCTGGAAATTCAGTG ACCCAGATGGAAGGGCCAGTGACTCTCTCAGAAGAGGC CTTCTGACTATAAACTGCACGTA
TRAV10	TCRVA_016.1	164-264	GTGGTATAAGCAAGATACTGGGAGAGGTCTGTTTTCCC TGACAATCATGACTTTTCAGTGAGAACACAAAGTCGAAC GGAAGATATACAGCAACTCTGGAT
TRAV11	TCRVA_017.1	135-235	TATCAGGAGAGAACACTCTTCAATTTCCACTGGTTCCGG CAGGATCCGGGGAGAAGACTTGTGTCTTTGACCTTAATT CAATCAAGCCAGAAGGAGCAGG
TRAV12-1	TCRVA_018.1	140-240	CAACAGTGCTTCTCAGTCTTTCTTCTGGTACAGACAGGA TTGCAGGAAAGAACCTAAGTTGCTGATGTCCGTATACT CCAGTGGTAAATGAAGATGGAAGG

TRAV12-2	TCRVA_019.1	116-216	CATTGCCTCTCTCAACTGCACTTACAGTGACCGAGGTTCCAGTCCTTCTTCTGGTACAGACAATATTCTGGGAAAAGCCCTGAGTTGATAATGTTTCATA
TRAV12-3	TCRVA_020.1	99-199	AGTGTTCAGAGGGAGCCATTGTTTCTCTCAACTGCACTTACAGCAACAGTGCTTTTCAATACTTCATGTGGTACAGACAGTATTCCAGAAAAGGCCCTG
TRAV13-1	TCRVA_021.1	189-289	CAGCTTATTATAGACATTTCGTTCAAATGTGGGCGAAAA GAAAGACCAACGAATTGCTGTTACATTGAACAAGACAGCCAAACATTTCTCCCTGCACATCA
TRAV13-2	TCRVA_022.1	99-199	CAGGAGGGTGACAACCTCTATTATCAACTGTGCTTATTCAAACAGCGCTCAGACTACTTCATTTGGTACAAGCAAGATCTGGAAAAGGTCCTCAATTCA
TRAV14/DV 4	TCRVA_023.1	232-332	ATGCAACAGAAGGTCGCTACTCATTGAATTTCCAGAAGGCAAGAAAAATCCGCCAACCTTGTCATCTCCGCTTCACA ACTGGGGGACTCAGCAATGTATTT
TRAV16	TCRVA_024.1	222-322	ATCAAAGGCTTCACTGCTGACCTTAACAAAGGCGAGACATCTTTCCACCTGAAGAAACCATTGCTCAAGAGGAAGACTCAGCCATGTATTACTGTGCTC
TRAV17	TCRVA_025.1	201-301	TTAATACGTTCAAATGAAAGAGAGAAACACAGTGGAAGATTAAGAGTCACGCTTGACACTTCCAAGAAAAGCAGTTCCTTGATCACGGCTTCCCGC
TRAV18	TCRVA_026.1	198-298	CTGAAAAGTTTCAGAAAACCAGGAGACGGACAGCAGAGGTTTTTCAGGCCAGTCCTATCAAGAGTGACAGTTCCTTCCACCTGGAGAAGCCCTCGGTGCAGC
TRAV19	TCRVA_027.1	227-327	GCAAAATGAAATAAGTGGTCGGTATTCTTGGAACCTCCAGAAATCCACCAGTTCCTTCAACTTCACCATCACAGCCTCACAAGTCGTGGACTCAGCAGTA
TRAV20	TCRVA_028.1	136-236	ACACAGTCAGCGGTTTAAAGAGGGCTGTTCTGGTATAGGCAAGATCCTGGGAAAGGCCCTGAATTCCTCTTCACCCTGTATTTCAGCTGGGGAAGAAAAGGA
TRAV21	TCRVA_029.1	176-276	TGGGAAAGGTCCTCACATCTCTGTTGCTTATTTCAGTCAAGTCAGAGAGAGCAAACAAGTGAAGACTTAATGCCTCGCTGGATAAATCATCAGGACGTAGT
TRAV22	TCRVA_030.1	183-283	CAGCTCATCAACCTGTTTTACATTCCCTCAGGGACAAAA CAGAATGGAAGATTAAGCGCCACGACTGTGCTACGGAACGCTACAGCTTATTGTACATTT
TRAV23/DV 6	TCRVA_031.1	159-259	GAGAACACTGCGTTTGACTACTTTCCATGGTACCAACAATTCCCTGGGAAAGGCCCTGCATTATTGATAGCCATACGTCCAGATGTGAGTGAAAAGAAAG
TRAV24	TCRVA_032.1	88-188	CTCAGTCACTGCATGTTTCAGGAGGGAGACAGCACCAATTTCACCTGCAGCTTCCCTTCCAGCAATTTTTATGCCTTACTGGTACAGATGGGAAACTGC
TRAV25	TCRVA_033.1	43-143	CACAGGTGAATGGACAACAGGTAATGCAAATTCCTCAGTACCAGCATGTACAAGAAGGAGAGGACTTCACCACGTA CTGCAATTCCTCAACTACTTTAAG
TRAV26-1	TCRVA_034.1	106-206	ACCTGCCTTGTAATCACTCTACCATCAGTGGAAATGAGTATGTGTATTGGTATCGACAGATTCACTCCAGGGGCCACAGTATATCATTTCATGGTCTAAA
TRAV26-2	TCRVA_035.1	11-111	GACAAGCATTACTGTACTCCTATCTTTGGGTATTATGGGTGATGCTAAGACCACACAGCCAAATTCATGGAGAGTACGAAGAAGAGCCTGTTCACTTG
TRAV27	TCRVA_036.1	69-169	CAGAGCCCTCAGTTTCTAAGCATCCAAGAGGGAGAAAA TCTCACTGTGTACTGCAACTCCTCAAGTGTTTTTTCCAGCTTACAATGGTACAGACAGGAGC
TRAV29/DV	TCRVA_037.1	193-293	ACCCTGCTGAAGGTCCTACATTCTGATATCTATAAGTT

5			CCATTAAGGATAAAAATGAAGATGGAAGATTCACTGTC TTCTTAAACAAAAGTGCCAAGCA
TRAV30	TCRVA_038.1	141-241	GCTTTATATTCTGTACACTGGTACAGGCAGAAGCATGGT GAAGCACCCGTCTTCCTGATGATATTACTGAAGGGTGG AGAACAGAAGGGTCATGAAAAAA
TRAV34	TCRVA_039.1	169-269	AAAAGTATGGTGAAGGTCTTATCTTCTTGATGATGCTAC AGAAAGGTGGGGAAGAGAAAAGTCATGAAAAGATAAC TGCCAAGTTGGATGAGAAAAAGCA
TRAV35	TCRVA_040.1	216-316	TTGACCTCAAATGGAAGACTGACTGCTCAGTTTGGTATA ACCAGAAAGGACAGCTTCCTGAATATCTCAGCATCCAT ACCTAGTGATGTAGGCATCTACT
TRAV36/DV 7	TCRVA_041.1	156-256	AGCCTACTATGGTACAAGCAGGAAAAGAAAGCTCCAC ATTTCTATTTATGCTAACTTCAAGTGGAAATTGAAAAGAA GTCAGGAAGACTAAGTAGCATAT
TRAV38-1	TCRVA_042.1	250-350	TCTCTGTGAACTTCCAGAAAGCAGCCAAATCCTTCAGTC TCAAGATCTCAGACTCACAGCTGGGGGACACTGCGATG TATTTCTGTGCTTTCATGAAGCA
TRAV38- 2/DV8	TCRVA_043.1	249-349	TTCTCTGTGAACTTCCAGAAAGCAGCCAAATCCTTCAGT CTCAAGATCTCAGACTCACAGCTGGGGGATGCCGCGAT GTATTTCTGTGCTTATAGGAGCG
TRAV39	TCRVA_044.1	49-149	GTGGAGAGCTGAAAGTGGAAACAAAACCCTCTGTTCTG AGCATGCAGGAGGGAAAAAACTATACCATCTACTGCAA TATTCAACCACCTTCAGACAGACT
TRAV40	TCRVA_045.1	6-106	TCCTCTCTGGACTTTCTAATTCTGATCTTAATGTTGGAG GAACCAGCAGCAATTCAGTCAAGCAGACGGGCCAAATA ACCTCTCGGAGGGAGCATCTG
TRAV41	TCRVA_046.1	38-138	GCTTCAGCTAAGCTGTGTAAGTGCCGCCAAAAATGAAG TGGAGCAGAGTCCTCAGAACCTGACTGCCCAGGAAGGA GAATTTATCACAATCAACTGCAGT
TRBV2	TCRVB_001.1	220-320	CAGAGAAGTCTGAAATATTCGATGATCAATTCTCAGTT GAAAGGCCTGATGGATCAAATTTCACTCTGAAGATCCG GTCCACAAAGCTGGAGGACTCAGC
TRBV3-1	TCRVB_002.1	86-186	AATACCTGGTCACACAGATGGGAAACGACAAGTCCATT AAATGTGAACAAAATCTGGGCCATGATACTATGTATTG GTATAAACAGGACTCTAAGAAATT
TRBV4-1	TCRVB_003.1	143-243	CAGGGCTATGTATTGGTACAAGCAGAAAGCTAAGAAGC CACCGGAGCTCATGTTTGTCTACAGCTATGAGAACTCT CTATAAATGAAAGTGTGCCAAGT
TRBV4-2	TCRVB_004.1	138-238	GGGCATAACGCTATGTATTGGTACAAGCAAAGTGCTAA GAAGCCACTGGAGCTCATGTTTGTCTACAACCTTAAAG AACAGACTGAAAACAACAGTGTGC
TRBV4-3	TCRVB_005.1	138-238	GGTCATAACGCTATGTATTGGTACAAGCAAAGTGCTAA GAAGCCACTGGAGCTCATGTTTGTCTACAGTCTTGAAG AACGGGTTGAAAACAACAGTGTGC
TRBV5-1	TCRVB_006.1	194-294	TTTGAATACTTCAGTGAGACACAGAGAAACAAAGGAAA CTTCCCTGGTTCGATTCTCAGGGCGCCAGTTCTCTAACTC TCGCTCTGAGATGAATGTGAGCA
TRBV5-4	TCRVB_007.1	151-251	CAACACTGTGTCCTGGTACCAACAGGCCCTGGGTCAGG GGCCCCAGTTTATCTTTCAGTATTATAGGGAGGAAGAG AATGGCAGAGGAAACTTCCCTCT
TRBV5-5	TCRVB_008.1	148-248	AGAGTGTGTCCTGGTACCAACAGGTCCTGGGTCAGGGG CCCCAGTTTATCTTTCAGTATTATGAGAAAGAAGAGAG AGGAAGAGGAAACTTCCCTGATCG
TRBV5-6	TCRVB_009.1	145-245	ACACTGTGTCCTGGTACCAACAGGCCCTGGGTCAGGGG CCCCAGTTTATCTTTCAGTATTATGAGGAGGAAGAGAG

			ACAGAGAGGCAACTTCCTGATCG
TRBV5-8	TCRVB_010.1	131-231	TATCTCTGGGCACACCAGTGTGTACTGGTACCAACAGG CCCTGGGTCTGGGCCTCCAGTTCCTCCTTTGGTATGACG AGGGTGAAGAGAGAAACAGAGGA
TRBV6-1	TCRVB_011.1	124-224	GTGCCCAGGATATGAACCATAACTCCATGTACTGGTAT CGACAAGACCCAGGCATGGGACTGAGGCTGATTTATTA CTCAGTCTTGAGGGTACCACTGA
TRBV6-2	TCRVB_012.1	150-250	ATGTACTGGTATCGACAAGACCCAGGCATGGGGCTGAG GCTGATTCATTACTCAGTTGGTGAGGGTACAACCTGCCA AAGGAGAGGTCCCTGATGGCTACA
TRBV6-4	TCRVB_013.1	181-281	GGCTAAGGCTCATCCATTATTCAAATACTGCAGGTACC ACTGGCAAAGGAGAAGTCCCTGATGGTTATAGTGTCTC CAGAGCAAACACAGATGATTTCCC
TRBV6-5	TCRVB_014.1	142-242	ATGAATACATGTCCTGGTATCGACAAGACCCAGGCATG GGGCTGAGGCTGATTCATTACTCAGTTGGTGCTGGTATC ACTGACCAAGGAGAAGTCCCAA
TRBV6-6	TCRVB_015.1	159-259	TATCGACAAGACCCAGGCATGGGGCTGAAGCTGATTTA TTATTCACTTGGTGCTGGTATCACTGATAAAGGAGAAG TCCCGAATGGCTACAACGTATCTG
TRBV6-8	TCRVB_016.1	133-233	ATATGAACCATGGATACATGTCCTGGTATCGACAAGAC CCAGGCATGGGGCTGAGACTGATTTACTACTCAGCTGC TGCTGGTACTACTGACAAAGAAGT
TRBV6-9	TCRVB_017.1	164-264	GGCATGGGGCTGAGGCGCATTCACTACTCAGTTGCTGCT GGTATCACTGACAAAGGAGAAGTCCCCGATGGCTACAA TGATCCAGATCAAACACAGAGG
TRBV7-2	TCRVB_018.1	117-217	CTCAGGTGTGATCCAATTTTCAGGTCATACTGCCCTTAC TGGTACCGACAGAGCCTGGGGCAGGGCCTGGAGTTTTT AATTTACTTCCAAGGCAACAGTG
TRBV7-3	TCRVB_019.1	163-263	GACAAAGCCTGGGGCAGGGCCAGAGTTTCTAATTTAC TTCCAAGGCACGGGTGCGGCAGATGACTCAGGGCTGCC CAACGATCGGTTCTTTGCAGTCAG
TRBV7-4	TCRVB_020.1	125-225	TGATTCAATTTTCGGGTCATGTAACCCTTTATTGGTACCG ACAGACCCTGGGGCAGGGCTCAGAGGTTCTGACTTACT CCCAGAGTGATGCTCAACGAGAC
TRBV7-6	TCRVB_021.1	76-176	CTCCCAGGTACAAAGTCACAAAGAGGGGACAGGATGTA GCTCTCAGGTGTGATCCAATTTTCGGGTCATGTATCCCTT TATTGGTACCGACAGGCCCTGGG
TRBV7-7	TCRVB_022.1	74-174	GTCTCCAGGTACAAAGTCACAAAGAGGGGACAGGATG TAACTCTCAGGTGTGATCCAATTTTCAGTCATGCAACCC TTTATTGGTATCAACAGGCCCTG
TRBV7-8	TCRVB_023.1	194-294	GACTTATTTCCAGAATGAAGCTCAACTAGACAAATCGG GGCTGCCAGTGATCGCTTCTTTGCAGAAAGGCCTGAG GGATCCGTCTCCACTCTGAAGATC
TRBV7-9	TCRVB_024.1	13-113	TCCTCTGCTGGATGGCCCTGTGTCTCCTGGGGGACAGATC ACGCAGATACTGGAGTCTCCAGAACCCAGACACAAG ATCACAAGAGGGGACAGAATGT
TRBV9	TCRVB_025.1	175-275	ACCAGGGCCTCCAGTTCCTCATTCACTATTATAATGGAG AAGAGAGAGCAAAAGGAAACATTCTTGAACGATTCTCC GCACAACAGTTCCTGACTTGCA
TRBV10-1	TCRVB_026.1	176-276	ACATGGGCTGAGGCTGATCCATTACTCATATGGTGTTC AGACACTAACAAAGGAGAAGTCGCTGCCTCCTCCCAGA CATCTGTATATTTCTGCGCCAGC
TRBV10-2	TCRVB_027.1	62-162	TGGAATCACCCAGAGCCCAAGATACAAGATCACAGAGA CAGGAAGGCAGGTGACCTTGATGTGTCAACAGACTTGG AGCCACAGCTATATGTTCTGGTAT

TRBV10-3	TCRVB_028.1	192-292	ATCCATTACTCATATGGTGTTAAAGATACTGACAAAGG AGAAGTCTCAGATGGCTATAGTGTCTCTAGATCAAAGA CAGAGGATTCCTCCTCACTCTGG
TRBV11-1	TCRVB_029.1	131-231	TATTTCTGGCCATGCTACCCTTTACTGGTACCGGCAGAT CCTGGGACAGGGCCCGGAGCTTCTGGTTCAATTCAGG ATGAGAGTGTAGTAGATGATTCA
TRBV11-2	TCRVB_030.1	131-231	TATATCTGGCCATGCTACCCTTTACTGGTACCAGCAGAT CCTGGGACAGGGCCCAAAGCTTCTGATTTCAGTTTCAGA ATAACGGTGTAGTGGATGATTCA
TRBV11-3	TCRVB_031.1	73-173	AGTCTCCCAGATATAAGATTATAGAGAAAAACAGCCT GTGGCTTTTTGGTGCAATCCTATTTCTGGCCACAATACC CTTTACTGGTACCTGCAGAACTT
TRBV12-3	TCRVB_032.1	150-250	CTTTTCTGGTACAGACAGACCATGATGCGGGGACTGGA GTTGCTCATTTACTTTAACAACAACGTTCCGATAGATGA TTCAGGGATGCCCCGAGGATCGAT
TRBV12-5	TCRVB_034.1	120-220	AGATGTCAGCCAATTTTAGGCCACAATACTGTTTTCTGG TACAGACAGACCATGATGCAAGGACTGGAGTTGCTGGC TACTTCCGCAACCGGGCTCCTC
TRBV13	TCRVB_035.1	87-187	GCTGCTGGAGTCATCCAGTCCCAAGACATCTGATCAA AGAAAAGAGGGAAACAGCCACTCTGAAATGCTATCCTA TCCCTAGACACGACACTGTCTACT
TRBV14	TCRVB_036.1	233-333	TATGCCAACAATCGATTCTTAGCTGAAAGGACTGGAG GGAGTATTCTACTCTGAAGGTGCAGCCTGCAGAACTG GAGGATTCTGGAGTTTATTCTGT
TRBV15	TCRVB_037.1	187-287	CCCAAAGCTGCTGTTCCACTACTATGACAAAGATTTTAA CAATGAAGCAGACACCCCTGATAACTTCCAATCCAGGA GGCCGAACACTTCTTTCTGCTTT
TRBV16	TCRVB_038.1	194-294	GATTTCCCTTCCAGAATGAAAATGTCTTTGATGAAACAG GTATGCCAAGGAAAGATTTTCAGCTAAGTGCCTCCCA AATTCACCCTGTAGCCTTGAGATC
TRBV18	TCRVB_039.1	156-256	TGGTATCGGCAGCTCCCAGAGGAAGGTCTGAAATTCAT GGTTTATCTCCAGAAAGAAAATATCATAGATGAGTCAG GAATGCCAAAGGAACGATTTTCTG
TRBV19	TCRVB_040.1	195-295	TACTACTCACAGATAGTAAATGACTTTTCAGAAAGGAGA TATAGCTGAAGGGTACAGCGTCTCTCGGGAGAAGAAGG AATCCTTTCCTCTCACTGTGACAT
TRBV20-1	TCRVB_041.1	95-195	TGTGAAGATCGAGTGCCGTTCCCTGGACTTTCAGGCCAC AACTATGTTTTGGTATCGTCAGTTCCCAGAACAGAGTCT CATGCTGATGGCAACTTCCAAT
TRBV24-1	TCRVB_042.1	124-224	GTTCTCAGACTAAGGGTCATGATAGAATGTACTGGTAT CGACAAGACCCAGGACTGGGCCTACGGTTGATCTATTA CTCCTTTGATGTCAAAGATATAAA
TRBV25-1	TCRVB_043.1	181-281	AACTACACCTCATCCACTATTCCTATGGAGTTAATTCCA CAGAGAAGGGAGATCTTTCCTCTGAGTCAACAGTCTCC AGAATAAGGACGGAGCATTTTCC
TRBV27	TCRVB_044.1	162-262	CGACAAGACCCAGGGCTGGGCTTAAGGCAGATCTACTA TTCAATGAATGTTGAGGTGACTGATAAGGGAGATGTTT CTGAAGGGTACAAAGTCTCTCGAA
TRBV28	TCRVB_045.1	47-147	AGGCCTCGTAGATGTGAAAGTAACCCAGAGCTCGAGAT ATCTAGTCAAAGGACGGGAGAGAAAGTTTTTCTGGAA TGTGTCCAGGATATGGACCATGAA
TRBV29-1	TCRVB_046.1	190-290	CAAATCAGGGCTCTGAGGCCACATATGAGAGTGGATTT GTCATTGACAAGTTTTCCATCAGCCGCCCAAACCTAAC ATTCTCAACTCTGACTGTGAGCAA
TRBV30	TCRVB_047.1	5-105	CTGCTCTCCTTGCCCTTCTCCTGGGCACTTCTTTGGG

			GTCAGATCTCAGACTATTCATCAATGGCCAGCGACCCT GGTGCAGCCTGTGGGCAGCCCCG
TRDV1*01	M22198.1	109-209	GTGGCCTTCAGCTACTCTGGTATGGATGGTTCCAAGTGT GAGTAAAAATGTTAAGGATGGAAGGATTCCAAACAGGC ATATGGTATTTCTCATGGACTTG
TRDV2*02	Y13426.1	148-248	GAGAAAAGGACATCTATGGCCCTGGTTTCAAAGACAAT TTCCAAGGTGACATTGATATTGCAAAGAACCTGGCTGT ACTTAAGATACTTGCACCATCAGA
TRDV2*01	X15275.1	295-395	AAATTTAACGTCTAGGGAAGGAAGCAGAAACCCTGTCA CCAATTAATAAGCTGCCTTAATCTCCTCTCAGTTGGCC TAACTTACCTGAACCGTACTATT
TRDV2*01	X15207.1	435-535	CTTAAGATACTTGCACCATCAGAGAGAGATGAAGGGTC TTACTACTGTGCCTGTGACACCCACCCTGCTGCAGCTCT ACTTCTGAGCAGCTCAAAAACCA
TRDV3*01	M23326.1	491-591	GGACGGTTTTCTGTGAAACACATTCTGACCCAGAAAGC CTTTCACTTGGTGATCTCTCCAGTAAGGACTGAAGACAG TGCCACTTACTACTGTGCCTTTA
TRGV1*01	M12949.1	294-394	GGAAGGCCCCACAGTGTCTTCTGTACTATGAACCCTACT ACTCCAGGGTTGTGCTGGAATCAGGAATCACTCCAGGA AAGTATGACACTGGAAGCACAAG
TRGV10*01	X07206.1	304-404	CACCTGATCTATATTGTCTCAACAAAATCCGCAGCTCGA CGCAGCATGGGTAAAGACAAGCAACAAAGTGGAGGCAA GAAAGAATTCTCAAACCTCACTT
TRGV11*01	Y11227.1	401-501	AAATAAAGTTCTTAGAGAAAGAAGATGAGGTGGTGTAC CACTGTGCCTGCTGGATTAGGCACCACAGTGTTCGAGTT GTCAAGATAAGGTACACAGAAAC
TRGV11*02	TCRgd_002.1	0-100	ACTTGGGCAGTTGGAACAACCTGAAATATCTATTCCA GACCAGCAAATAAGAGTGCCACATATCTTGAAGGCA TCCATCCAAGGCTTTAGCAGTAAA
TRGV2*02	M27337.1	307-407	GACTCTGGGGTCTATTACTGTGCCACCTGGGACGCTCGA AGTTATTATAAGAAACTCTTTGGCAGTGGAAACAACACT TGTTGTCACAGATAAACAACCTTG
TRGV3*01	X15271.1	40-140	GAGGAAGGCTTGGGAGTCCCCTAAGACACATCTTCAGT CACTTCTCTCTGCCTGTGTCTCAGGAAACCAGCTCCTCC TACTGTCTTCTGTGCTAGGGATC
TRGV5*01	M13431.1	277-377	CCTACAGCAGGAGGGGAAGACCCACAGCATCTTCTGC ACTATGAAGTCTCCAACCTCAAGGGATGTGTTGGAATCA GGTCTCAGTCTTGGAAGTATTAT
TRGV6*01	M13432.1	142-242	TTATGTTGTTCCCATTGCAGCCAGTCAGATATCTACTAA CTTGGAAGCGAAAATAAAGTCAGGCACCAGGCAGATG GGTTCATCTGCTGTAATCACCTGT
TRGV7*01	M13433.1	211-311	TCCATACTATGACCCCTACTACTCCAGGGTTGTGTTGGA ATCAAGAATCAGTAGAGGAAAGTATTTTACTTATGCAA GCATGAGGAGGAGCTGGAATG
TRGV8*01	M13434.1	354-454	TGGAATCAGGAATCAGTCGAGAAAAGTATCATACTTAT GCAAGCACAGGGAAGAGCCTTAAATTTATACTGGAAAA TCTAATTGAACGTGACTCTGGGGT
TRGV8*01	X15273.1	97-197	CTTACTGTCTTCTGTGTTAGGGATCACTTCCTTGTGAGT GGGACCTGAGTTTTGAGAGGGTCTTCTGCTCCTCTTCGT CTGGTCCCCTTACTTCCAAGAC
TRGV9*02	X15274.1	15-115	GAACACAGCAGCTTTTAAGGGATGCACTGGGGAGAGCA GTTTGTA AAAATACCTGGGACGGATTAATGTCTTGGC TTAGAGAAAGAACAACAGACAAT
TRGV9*01	X07205.1	368-468	TCCGTCAGGCAAATTTGAGGTGGATAGGATACCTGAAA CGTCTACATCCACTCTCACCATTCAATGTAGAGAAAC

			AGGACATAGCTACCTACTACTGT
TRGVA*01	X07208.1	291-391	TGTGCAGTGGGATTCCATCCTGAAAGCAGATAAAATCA TAGCCAAGGATGGCAGCAGCTCTATCTTGGCAGTACTG AAGTTGGAGACAGGCATCGAGGGC
TRGVB*01	X07209.1	347-447	TGCTTAGGTGAGAAAAACAAGAACTTGAGGCAAGAA CAAATTTCAAATGTCTACTTCAGTCTTACCATAAACT TCATAGGAAAGGAAGATGAGGCCA
TRGV8*01	X15273.1	97-197	CTTACTGTCTTCTGTGTTAGGGATCACTTCCTTGTTGAGT GGGACCTGAGTTTGTAGAGGGTCTTCTGCTCCTCTTCGT CTGGTCCCTTACTTCCAAGAC