FR1-IMGT CDR1-IMGT FR2-IMGT CDR2-IMGT FR3-IMGT CDR3-IMGT FR4-IMGT

(1-26) (27-38) (39-55) (56-65) (66-104) (105-117) (118-128)

A B BC C C' C'C" C" D E F FG G

(1-15) (16-26) (27-38) (39-46) (47-55) (56-65) (66-74) (75-84) (85-96) (97-104) (105-117) (118-128)

TRGV Clone ——————————————> ——————————> ———————> ————————> ————————> —————————> ———————————> ———————> ——————————> TRGJ TRGC

gene name L-REGION 1 10 15 16 23 26 27 38 3941 46 47 55 56 65 66 74 75 80 84 85 89 96 97 104 105 111 112 117 118 128 gene gene

|........|....| |......|..| |..........| |.|....| |.......| |........| |.......| |....|...| |...|......| |......| |.....|1234321|....| |.........|

TRGV6 MLGCLALLWALLVPGA QEIRLVQLPVIVSRV GNSVTMPCRIN TSV.......SY IHWYRQLE GQAPERLLY LATS..QRDV QWDSVLQGN KVTAKKGNDD KSCTLSLMKLEK SDEGLYYCAAWDS

GL2L6 -------------------------------- GNSVTMPCRIT TSV.......SY IHWYRQLE GQAPERLLY LATS..QRDV QWDSVLQGN KVTAKKGNDD KSCTLSLMKLEK SDEGLYYCAAWDSNPPP......SYNKI FGAGTKLFVI.. 6-2 C6

GL2L13 -------------------------------- GNSVTMPCRIT TSV.......SY IHWYRQLE GQAPERLLY LATS..QRDV QWDSVLQGN KVTAKKGNDD KSCTLSLMKLEK SDEGLYYCAAWDSDTPP......SYNKI FGAGTKLFVI.. 6-2 C6

AB185445 MLGCLALLWALLVPGH QEIRLVQLPVIVSRV GNSVTMPCRIT TSV.......SY IHWYRQLE GQAPERLLY LATS..QRDV QWDSVLQGN KVTAKKGNDD KSCTLSLMKLEK SDEGLYYCAAWDSVE........SYNKI FGAGTKLFVI.. 6-2 C6

TRGV12-1 MRFPGVLLVFLAPVTQV SSNVEGDKMSVTRAT GSSLVITCDLT QNT.......NY IHWYRFRE GTVPQRLLY YDVS..SSKV TLESGISPG RYHAYQS.AG KSYQFVISNLEE SDSGTYYCAVWEK

GL2L17 ------LLVFLAPVTQV SSNVEGDKMSVTRAT GSSLVITCDLT QNT.......NY IHWYRFRE GTVPQRLLY YDVS..SSKV TLESGISPG RYHAYQS.AG KSYQFVISNLEE SDSGTYYCAVWE...............I FGKALELIVAPY 3-1 C3

GL2L36 MRFPGVLLVFLAPVTQV SSNVEGDKMSVTRAT GSSLVITCDLT QNT.......NY IHWYRFRE GTVPQRLLY YDVS..SSKV TLESGISPG RYHAYQS.AG KSYQFVISNLEE SDSGTYYCAVWEKL.........NWKKI FGKALELIVAPY 3-1 C3

AB185446 MRFPGVLLVFLAPVTQV SSNVEGDKMSVTRAT GSSLVITCDLT QNT.......NY IHWYRFRE GTVPQRLLY YDVS..SSKV TLESGISPG RYHAYQS.AG KSYQFVISNLEE SDSGTYYCAAP............NWKKI FGKALELIVAPY 3-1 C3

TRGV12-2 MRFPGVLLVFLVPVTQV SSNVEGDKMSVTRAP GTAVSFTCALT QNT.......NY IHVYTKKE GTAPQRLFY YDIY..YSKF TLESGDSPE KYRVYAG.TS KSYTFTMLYLEE RDSGTYYCALWDK

AB185447 MRFPGVLLVFLVPVTQV SSNVEGDKMSVTRAP GTAVSFTCALT QNT.......NY IHVYTKKE GTAPQRLFY YDIY..YSKF TLESGDSPE KYRVYAG.TS KSYTFTMLYLEE RDSGTYYCALWGY...........WKKI FEKALELIVAPY 4-1 C4

TRGV3 MSVLEAFTFLSFWALGLS LSRVEQSQISVSAEV KKSVDINCKIE STNF....PTEA VHWYRQRM NQALEHLIF VSSV..TVPA QSQIGGKSN KVVARKNSQT FTSTLTVNFIEK EDEGIYYCAGWN

GL1L2 -------------------------------------------------NF....PTEA VHWYRQRT NQALEHLIF VSSV..TVPA QSQIGGKSN KVVARKNSQT FTSTLTVNFIEK EDEGIYYCAGWVNY.......SSRWIKI FGEGTKLIVTPP 5-1 C5

TRGV7  MALLEAVVFSFFWAVGLG MLRLEQPEISITAAR QKSALIACKVS SENF....NDAY IHWYRHKS DQGMEHLMY HVT....VFT LSHLGEKKN KLEARKIAST STATLKINFLEQ EDEATYYCASWFY

AB185441 MALLEAVVFSFFWAVGLG MLRLEQPEISITAAR QKSALIACKVS SENF....NDAY IHWYRHKS DQGMEHLMY HVT....VFT LSHLGEKKN KLEARKIAST STATLKINFLEQ EDEATYYCASWFYSFY........YVKV FGDGTKLAVT.. 5-2 C5

AB185442 MALLEAVVFSFFWAVGLG MLRLEQPEISITAAR QKSALIACKVS SENF....NDAY IHWYRHKS DQGMEHLMY HVT....VFT LSHLGEKKN KLEARKIAST STATLKINFLEQ EDEATYYCASWFK............... .GEGTKLIVTPP 5-1 C5

TRGV10 MVIQTRLTNFAIALNLSGRQYTSG DILTTHPVASITKKR GNTAFLECQIK TDTLK...RNVY THWYRQKP DQPLKRILY ISSN...ENI VYEQGISEE KYEARKWLSN SLVNLRIHGVTE EDTGLYYCACWN

AB185443 MVIQTRLTNFAIALNLSGRQYTSG DILTTHPVASITKKR GNTAFLECQIK TDTLK...RNVY THWYRQKP DQPLKRILY ISSN...ENI VYEQGISEE KYEARKWLSN SLVNLRIHGVTE EDTGLYYCACWNI..........DYVKV FGDGTKLAVT.. 5-2 C5

TRGV4 MWIFLVSLAWVYGET KMRISQDQLSST\*RL DRTVQISCKLS GVPL....KNAI VHWYQQKE GEPLK\*ILY GS......TN SYQLDEPNS SLETVTK.DK GIFYLVISNVVK SDEATYYCACWD

AB185444 MWIFLVSLAWVYGET KMRISQDQLSST\*RL DRTVQISCKLS GVPL....KNAI VHWYQQKE GEPLK\*ILY GS......TN SYQLDEPNS SLETVTK.DK GIFYLVISNVVK SDEATYYCAGRRFG.............. .GDGTKLAVT.. 5-2 C5