## Figure 1a

## Variable Heavy Chain DNA

**3076_VH1A** (SEQ ID NO: 1):
CAGGTGCAATTGGTTCAGTCTGGCGCGGAAGTGAAAAAACCGGGCAGCAGCGTGAAAGTGAGCTGC
AAAGCCTCCGGAGGCACTTTTTCTTCTAATGCTATTTCTTGGGTGCGCCAAGCCCCTGGGCAGGGTC
TCGAGTGGATGGGCAATATCTGGCCGATTTTTGGCACTGCGAATTACGCGCAGAAGTTTCAGGGCC
GGGTGACCATTACCGCGGATGAAAGCACCAGCACCGCGTATATGGAACTGAGCAGCCTGCGTAGCG
AAGATACGGCCGTGTATTATTGCGCGCGTAATGGTTATCTTGATACTAATACTTATATTGATTATTGG
GGCCAAGGCACCCTGGTGACGGTTAGCTCA

**3078_VH3** (SEQ ID NO: 2):
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTGATTATGCTATGTCTTGGGTGCGCCAAGCCCCTGGGAAGG
GTCTCGAGTGGGTGAGCGCTATCCGTTATGATGGTAGCAATACCTATTATGCGGATAGCGTGAAAGG
CCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGG
AAGATACGGCCGTGTATTATTGCGCGCGTTATTATTCTGGTATTTATCAGCATATTGATTATTGGGGC
CAAGGCACCCTGGTGACGGTTAGCTCA

**3081_ VH3** (SEQ ID NO: 3):
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATGCTCTTCATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCTCTATCTCTGGTCTTGGTAGCACTACCTATTATGCGGATAGCGTGAAAGGC
CGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGA
AGATACGGCCGTGTATTATTGCGCGCGTTATCATTATGAGTATCATTATTTTTCTTCTGGTTTTGATAA
TTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**3085_ VH1A** (SEQ ID NO: 4):
CAGGTGCAATTGGTTCAGAGCGGCGCGGAAGTGAAAAAACCGGGCGCGAGCGTGAAAGTGAGCTG
CAAAGCCTCCGGATATACCTTTACTGGTTATTATATTAATTGGGTCCGCCAAGCCCCTGGGCAGGGT
CTCGAGTGGATGGGCTGGATCTTTCCGAATGGTGGCTCTACGGGTTACGCGCAGAAGTTTCAGGGC
CGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCAGCCTGCGTAGC
GAAGATACGGCCGTGTATTATTGCGCGCGTGGTAATATTTTTATTTTTGATTATTGGGGCCAAGGCAC
CCTGGTGACGGTTAGCTCA

**3086_VH3** (SEQ ID NO: 5):
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTACTTCTTATTATATGCATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCTATATCGATTCTTCTGGTAGCTCTACCTATTATGCGGATAGCGTGAAAGGC
CGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGA
AGATACGGCCGTGTATTATTGCGCGCGTCAGCTTATGCCTTTTGGTGGTTATTTTGATGTTTGGGGC
CAAGGCACCCTGGTGACGGTTAGCTCA

**3087_ VH3** (SEQ ID NO: 6):
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG

TCTCGAGTGGGTGAGCGGTATCTCTGGTGATCCTAGCAATACCTATTATGCGGATAGCGTGAAAGGC
CGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGA
AGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGCTTATTGGGGCC
AAGGCACCCTGGTGACGGTTAGCTCA

**3088_ VH3** (SEQ ID NO: 7):
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATGCTATGAATTGGGTGCGCCAAGCCCCTGGGAAGG
GTCTCGAGTGGGTGAGCGGTATCTCTTCTTGGGGTAGCTCTACCTATTATGCGGATAGCGTGAAAGG
CCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGG
AAGATACGGCCGTGTATTATTGCGCGCGTGAGGATGGTTCTTATATGACTGATTATTTTGCTTATTGG
GGCCAAGGCACCCTGGTGACGGTTAGCTCA

**3089_ VH2** (SEQ ID NO: 8):
CAGGTGCAATTGAAAGAAAGCGGCCCGGCCCTGGTGAAACCGACCCAAACCCTGACCCTGACCTGT
ACCTTTTCCGGATTTAGCCTGTCTTCTGATGGTATGGGTGTGGGTTGGATTCGCCAGCCGCCTGGGA
AAGCCCTCGAGTGGCTGGCTCTTATCGATTGGGATGATGATAAGCGTTATAGCACCAGCCTGAAAAC
GCGTCTGACCATTAGCAAAGATACTTCGAAAAATCAGGTGGTGCTGACTATGACCAACATGGACCCG
GTGGATACGGCCACCTATTATTGCGCGCGTTTTAATTGGTTTTATCGTCTTGCTTTTGTTAATCCTGAT
GTTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**3101_ VH2** (SEQ ID NO: 9):
CAGGTGCAATTGAAAGAAAGCGGCCCGGCCCTGGTGAAACCGACCCAAACCCTGACCCTGACCTGT
ACCTTTTCCGGATTTAGCCTGTCTACTTCTCGTGTTGGTGTGTCTTGGATTCGCCAGCCGCCTGGGA
AAGCCCTCGAGTGGCTGGCTCATATCGATTGGAATGATGATAAGTATTATAGCACCAGCCTGAAAAC
GCGTCTGACCATTAGCAAAGATACTTCGAAAAATCAGGTGGTGCTGACTATGACCAACATGGACCCG
GTGGATACGGCCACCTATTATTGCGCGCGTGAGGATCGTCTTCTTGGTGGTTATGGTTATGATGTTT
GGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**3102_ VH4** (SEQ ID NO: 10):
CAGGTGCAATTGCAAGAAAGTGGTCCGGGCCTGGTGAAACCGGGCGAAACCCTGAGCCTGACCTG
CACCGTTTCCGGAGGCAGCATTTCTGGTAATTATTGGTCTTGGATTCGCCAGGCCCCTGGGAAGGG
TCTCGAGTGGATTGGCGATTATCATGGCTCTACCTATTATAATCCGAGCCTGAAAGGCCGGGTGACC
ATTAGCGTTGATACTTCGAAAAACCAGTTTAGCCTGAAACTGAGCAGCGTGACGGCGGAAGATACGG
CCGTGTATTATTGCGCGCGTGAGCAGTATCATTGGGGTCTTGCTTGGACTGGTTTTGATAATTGGGG
CCAAGGCACCCTGGTGACGGTTAGCTCA

**3127_ VH5** (SEQ ID NO: 11):
CAGGTGCAATTGGTTCAGAGCGGCGCGGAAGTGAAAAAACCGGGCGAAAGCCTGAAAATTAGCTGC
AAAGGTTCCGGATATTCCTTTTCTACTTCTTGGGTTGGTTGGGTGCGCCAGATGCCTGGGAAGGGTC
TCGAGTGGATGGGCATTATCGATCCGGATATTAGCTATACCTCTTATTCTCCGAGCTTTCAGGGCCA
GGTGACCATTAGCGCGGATAAAAGCATTAGCACCGCGTATCTTCAATGGAGCAGCCTGAAAGCGAG
CGATACGGCCATGTATTATTGCGCGCGTTATCTTATGGGTCTTGGTTATGATGTTTGGGGCCAAGGC
ACCCTGGTGACGGTTAGCTCA

**3128_ VH2** (SEQ ID NO: 12):
CAGGTGCAATTGAAAGAAAGCGGCCCGGCCCTGGTGAAACCGACCCAAACCCTGACCCTGACCTGT
ACCTTTTCCGGATTTAGCCTGTCTTCTTCTGGTATGTCTGTGTCTTGGATTCGCCAGCCGCCTGGGA
AAGCCCTCGAGTGGCTGGCTCGTATCTATTCTGATGATTCTAAGTCTTATAGCACCAGCCTGAAAAC
GCGTCTGACCATTAGCAAAGATACTTCGAAAAATCAGGTGGTGCTGACTATGACCAACATGGACCCG
GTGGATACGGCCACCTATTATTGCGCGCGTGCTGCTCATTGGAATGGTCCTCTTTTTGATGTTTGGG
GCCAAGGCACCCTGGTGACGGTTAGCTCA

**3129_ VH3** (SEQ ID NO: 13):
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTAATTATTCTATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCTATATCTATGGTGGTGGTAGCTATACCTATTATGCGGATAGCGTGAAAGGC
CGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGA
AGATACGGCCGTGTATTATTGCGCGCGTCAGGCTGGTATGTATTTTGATGTTTGGGGCCAAGGCACC
CTGGTGACGGTTAGCTCA

**3130_ VH4** (SEQ ID NO: 14):
CAGGTGCAATTGCAAGAAAGTGGTCCGGGCCTGGTGAAACCGGGCGAAACCCTGAGCCTGACCTG
CACCGTTTCCGGAGGCAGCATTGGTTATTATTGGAATTGGATTCGCCAGGCCCCTGGGAAGGGTCT
CGAGTGGATTGGCCATATCTCTCGTTTTGGCTCTACCAATTATAATCCGAGCCTGAAAGGCCGGGTG
ACCATTAGCGTTGATACTTCGAAAAACCAGTTTAGCCTGAAACTGAGCAGCGTGACGGCGGAAGATA
CGGCCGTGTATTATTGCGCGCGGGAGTATACTGGTAATGATTGGTATCGTCAGCAGGGTCAGCATG
CTGATTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**3131_ VH2** (SEQ ID NO: 15):
CAGGTGCAATTGAAAGAAAGCGGCCCGGCCCTGGTGAAACCGACCCAAACCCTGACCCTGACCTGT
ACCTTTTCCGGATTTAGCCTGTCTAATTCTGGTGTTGGTGTGGGTTGGATTCGCCAGCCGCCTGGGA
AAGCCCTCGAGTGGCTGGCTGATATCTATTCTGATACTACTAAGCGTTATAGCACCAGCCTGAAAAC
GCGTCTGACCATTAGCAAAGATACTTCGAAAAATCAGGTGGTGCTGACTATGACCAACATGGACCCG
GTGGATACGGCCACCTATTATTGCGCGCGTTATGGTGAGGCTTATTTTGATTATTGGGGCCAAGGCA
CCCTGGTGACGGTTAGCTCA

**6183_VH3** (SEQ ID NO: 77)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCGGTATTAATATGGAGTCTACTCGTATTTATTATGCTGATTCTGTTAAGGGTC
GTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGAA
GATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGCTTATTGGGGCCA
AGGCACCCTGGTGACGGTTAGCTCA

**6184_VH3** (SEQ ID NO: 78)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCGCTATTTCTCATGATGGTAATGTTAAGTATTATGCTGATTCTGTTAAGGGTC
GTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGAA
GATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGCTTATTGGGGCCA
AGGCACCCTGGTGACGGTTAGCTCA

**6185_VH3** (SEQ ID NO: 79)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCGCTATTTCTATGAATGGTGATTATATTTCTTATGCTGATTCTGTTAAGGGTC
GTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGAA
GATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGCTTATTGGGGCCA
AGGCACCCTGGTGACGGTTAGCTCA

**6186_VH3** (SEQ ID NO: 80)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCGCTATTAATCTTTCTGGTTCTGCTAAGTATTATGCTGATTCTGTTAAGGGTC
GTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGAA
GATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGCTTATTGGGGCCA
AGGCACCCTGGTGACGGTTAGCTCA

**6187_VH3** (SEQ ID NO: 81)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCGCTATTTCTTCTAATGGTGATATTACTTATTATGCTGATTCTGTTAAGGGTC
GTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGAA
GATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGCTTATTGGGGCCA
AGGCACCCTGGTGACGGTTAGCTCA

**6188_VH3** (SEQ ID NO: 82)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCGCTATTTCTACTAATGGTTGGCAGACTTATTATGCTGATTCTGTTAAGGGTC
GTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGAA
GATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGCTTATTGGGGCCA
AGGCACCCTGGTGACGGTTAGCTCA

**6189_VH3** (SEQ ID NO: 83)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCGCTATTAATATGATTGGTAATGTTACTAATTATGCTGATTCTGTTAAGGGTC
GTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGAA
GATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGCTTATTGGGGCCA
AGGCACCCTGGTGACGGTTAGCTCA

**6190_VH3** (SEQ ID NO: 84)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCTATATTAATCCTAATGGTATGATGACTAATTATGCTGATTCTGTTAAGGGTC
GTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGAA
GATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGCTTATTGGGGCCA
AGGCACCCTGGTGACGGTTAGCTCA

**6192_VH3** (SEQ ID NO: 85)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCGTTATTTCTCCTGGTGGTGAGGCTAAGTCTTATGCTGATTCTGTTAAGGGT
CGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGA
AGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGCTTATTGGGGCC
AAGGCACCCTGGTGACGGTTAGCTCA

**6195_VH3** (SEQ ID NO: 86)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCGCTATTTCTGGTAATGGTGGTCATACTTATTATGCTGATTCTGTTAAGGGTC
GTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGAA
GATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGCTTATTGGGGCCA
AGGCACCCTGGTGACGGTTAGCTCA

**6197_VH3** (SEQ ID NO: 87)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCGCTATTTCTATGGATGGTGTTTATAAGTATTATGCTGATTCTGTTAAGGGTC
GTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGAA
GATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGCTTATTGGGGCCA
AGGCACCCTGGTGACGGTTAGCTCA

**6200_VH3** (SEQ ID NO: 88)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCGCTATTTCTAATAATGGTAATGTTACTTATTATGCTGATTCTGTTAAGGGTC
GTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGAA
GATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGCTTATTGGGGCCA
AGGCACCCTGGTGACGGTTAGCTCA

**6201_VH3** (SEQ ID NO: 89)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCGCTATTTCTATGCATGGTGATACTACTTATTATGCTGATTCTGTTAAGGGTC
GTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGAA
GATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGCTTATTGGGGCCA
AGGCACCCTGGTGACGGTTAGCTCA

**6204_VH3** (SEQ ID NO: 90)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATGCTATGAATTGGGTGCGCCAAGCCCCTGGGAAGG
GTCTCGAGTGGGTGAGCCATATTCGTAAGAAGAATACTTCTTATACTACTGAGTATGCTGCTTCTGTT
AAGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCG

TGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGAGGATGGTTCTTATATGACTGATTATTTTGCTT
ATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**6214_VH3** (SEQ ID NO: 91)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATGCTATGAATTGGGTGCGCCAAGCCCCTGGGAAGG
GTCTCGAGTGGGTGAGCAATATTCAGCGTGTTGGTTCTACTTATTATGCTGATTCTGTTAAGGGTCGT
TTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGAAGA
TACGGCCGTGTATTATTGCGCGCGTGAGGATGGTTCTTATATGACTGATTATTTTGCTTATTGGGGCC
AAGGCACCCTGGTGACGGTTAGCTCA

**3077_VH1B** (SEQ ID NO: 111)
CAGGTGCAATTGGTTCAGAGCGGCGCGGAAGTGAAAAAACCGGGCGCGAGCGTGAAAGTGAGCTG
CAAAGCCTCCGGATATACCTTTACTTCTTATTCTATTAATTGGGTCCGCCAAGCCCCTGGGCAGGGT
CTCGAGTGGATGGGCTATATCGATCCGAATCGTGGCAATACGAATTACGCGCAGAAGTTTCAGGGC
CGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCAGCCTGCGTAGC
GAAGATACGGCCGTGTATTATTGCGCGCGTGAGTATATTTATTTTATTCATGGTATGCTTGATTTTTG
GGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**3079_VH3** (SEQ ID NO: 112)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTAATTATGGTATGCATTGGGTGCGCCAAGCCCCTGGGAAGG
GTCTCGAGTGGGTGAGCAATATCCGTTCTGATGGTAGCTGGACCTATTATGCGGATAGCGTGAAAG
GCCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCG
GAAGATACGGCCGTGTATTATTGCGCGCGTCGTTATTGGTCTAAGTCTCATGCTTCTGTTACTGATTA
TTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**3080_ VH3** (SEQ ID NO: 113)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATGGTATGCATTGGGTGCGCCAAGCCCCTGGGAAGG
GTCTCGAGTGGGTGAGCAATATCTATTCTGATGGTAGCAATACCTTTTATGCGGATAGCGTGAAAGG
CCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGG
AAGATACGGCCGTGTATTATTGCGCGCGTAATATGTATCGTTGGCCTTTTCATTATTTTTTTGATTATT
GGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

## Figure 1b

## Variable Heavy Chain Peptide

(CDR Regions in **Bold** or <u>underlined</u>)

**3076_VH1A** (SEQ ID NO: 16):
QVQLVQSGAEVKKPGSSVKVSCKAS**GGTFSSNAIS**WVRQAPGQGLEWMG**NIWPIFGTANYAQKFQG**R
VTITADESTSTAYMELSSLRSEDTAVYYCAR**NGYLDTNTYIDY**WGQGTLVTVSS

**3078_VH3** (SEQ ID NO: 17):
QVQLVESGGGLVQPGGSLRLSCAASGFTFSDYAMSWVRQAPGKGLEWVS**AIRYDGSNTYYADSVKG**R
FTISRDNSKNTLYLQMNSLRAEDTAVYYCAR**YYSGIYQHIDY**WGQGTLVTVSS

**3081_ VH3** (SEQ ID NO: 18):
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYALHWVRQAPGKGLEWVSSISGLGSTTYYADSVKGRF
TISRDNSKNTLYLQMNSLRAEDTAVYYCAR**YHYEYHYFSSGFDN**WGQGTLVTVSS

**3085_ VH1A** (SEQ ID NO: 19):
QVQLVQSGAEVKKPGASVKVSCKAS**GYTFTGYYIN**WVRQAPGQGLEWMG**WIFPNGGSTGYAQKFQG**R
VTMTRDTSISTAYMELSSLRSEDTAVYYCAR**GNIFIFDY**WGQGTLVTVSS

**3086_VH3** (SEQ ID NO: 20):
QVQLVESGGGLVQPGGSLRLSCAASGFTFTSYYMHWVRQAPGKGLEWVSYIDSSGSSTYYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCAR**QLMPFGGYFDV**WGQGTLVTVSS

**3087_ VH3** (SEQ ID NO: 21):
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSGISGDPSNTYYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCAR**DLPLVYTGFAY**WGQGTLVTVSS

**3088_ VH3** (SEQ ID NO: 22):
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSGISSWGSSTYYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCAR**EDGSYMTDYFAY**WGQGTLVTVSS

**3089_ VH2** (SEQ ID NO: 23):
QVQLKESGPALVKPTQTLTLTCTFSGFSLSSDGMGVGWIRQPPGKALEWLALIDWDDDKRYSTSLKTRL
TISKDTSKNQVVLTMTNMDPVDTATYYCARFNWFYRLAFVNPDVWGQGTLVTVSS

**3101_ VH2** (SEQ ID NO: 24):
QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSRVGVSWIRQPPGKALEWLAHIDWNDDKYYSTSLKTRLT
ISKDTSKNQVVLTMTNMDPVDTATYYCAREDRLLGGYGYDVWGQGTLVTVSS

**3102_ VH4** (SEQ ID NO: 25):
QVQLQESGPGLVKPGETLSLTCTVS**GGSISGNYWS**WIRQAPGKGLEWIG**DYHGSTYYNPSLKG**RVTISV
DTSKNQFSLKLSSVTAEDTAVYYCARE**QYHWGLAWTGFDN**WGQGTLVTVSS

**3127_ VH5** (SEQ ID NO: 26):
QVQLVQSGAEVKKPGESLKISCKGS**GYSFSTSWVG**WVRQMPGKGLEWMGI**IDPDISYTSYSPSFQG**QV
TISADKSISTAYLQWSSLKASDTAMYYCAR**YLMGLGYDV**WGQGTLVTVSS

**3128_ VH2** (SEQ ID NO: 27):
QVQLKESGPALVKPTQTLTLTCTFS**GFSLSSSGMSVS**WIRQPPGKALEWLA**RIYSDDSKSYSTSLKT**RLTI
SKDTSKNQVVLTMTNMDPVDTATYYCAR**AAHWNGPLFDV**WGQGTLVTVSS

**3129_ VH3** (SEQ ID NO: 28):
QVQLVESGGGLVQPGGSLRLSCAAS**GFTFSNYSMN**WVRQAPGKGLEWVS**YIYGGGSYTYYADSVKG**R
FTISRDNSKNTLYLQMNSLRAEDTAVYYCAR**QAGMYFDV**WGQGTLVTVSS

**3130_ VH4** (SEQ ID NO: 29):
QVQLQESGPGLVKPGETLSLTCTVS**GGSIGYYWN**WIRQAPGKGLEWIG**HISRFGSTNYNPSLKG**RVTISV
DTSKNQFSLKLSSVTAEDTAVYYCARE**YTGNDWYRQQGQHADY**WGQGTLVTVSS

**3131_ VH2** (SEQ ID NO: 30):
QVQLKESGPALVKPTQTLTLTCTFS**GFSLSNSGVGVG**WIRQPPGKALEWLA**DIYSDTTKRYSTSLKT**RLTI
SKDTSKNQVVLTMTNMDPVDTATYYCAR**YGEAYFDY**WGQGTLVTVSS

**6183_VH3** (SEQ ID NO: 92)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSGINMESTRIYYADSVKGRF
TISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

**6184_VH3** (SEQ ID NO: 93)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISHDGNVKYYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

**6185_VH3** (SEQ ID NO: 94)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISMNGDYISYADSVKGRF
TISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

**6186_VH3** (SEQ ID NO: 95)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAINLSGSAKYYADSVKGRF
TISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

**6187_VH3** (SEQ ID NO: 96)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISSNGDITYYADSVKGRF
TISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

**6188_VH3** (SEQ ID NO: 97)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISTNGWQTYYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

**6189_VH3** (SEQ ID NO: 98)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAINMIGNVTNYADSVKGRF
TISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

**6190_VH3** (SEQ ID NO: 99)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSYINPNGMMTNYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

**6192_VH3** (SEQ ID NO: 100)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSVISPGGEAKSYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

**6195_VH3** (SEQ ID NO: 101)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISGNGGHTYYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

**6197_VH3** (SEQ ID NO: 102)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISMDGVYKYYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

**6200_VH3** (SEQ ID NO: 103)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISNNGNVTYYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

**6201_VH3** (SEQ ID NO: 104)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISMHGDTTYYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

**6204_VH3** (SEQ ID NO: 105)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSHIRKKNTSYTTEYAASVKG
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREDGSYMTDYFAYWGQGTLVTVSS

**6214_VH3** (SEQ ID NO: 106)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSNIQRVGSTYYADSVKGRF
TISRDNSKNTLYLQMNSLRAEDTAVYYCAREDGSYMTDYFAYWGQGTLVTVSS

**3077_VH1B** (SEQ ID NO: 114)
QVQLVQSGAEVKKPGASVKVSCKAS**GYTFTSYSIN**WVRQAPGQGLEWMGY**IDPNRGNTNYAQKFQG**R
VTMTRDTSISTAYMELSSLRSEDTAVYYCA**REYIYFIHGMLDF**WGQGTLVTVSS

**3079_VH3** (SEQ ID NO: 115)
QVQLVESGGGLVQPGGSLRLSCAAS**GFTFSNYGMH**WVRQAPGKGLEWVS**NIRSDGSWTYYADSVKG**
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR**RYWSKSHASVTDY**WGQGTLVTVSS

**3080_VH3** (SEQ ID NO: 116)
QVQLVESGGGLVQPGGSLRLSCAAS**GFTFSSYGMH**WVRQAPGKGLEWVS**NIYSDGSNTFYADSVKG**R
FTISRDNSKNTLYLQMNSLRAEDTAVYYCAR**NMYRWPFHYFFDY**WGQGTLVTVSS

## Figure 2a

## Variable Light Chain DNA

**3076_Vl lambda 2** (SEQ ID NO: 31):
GATATCGCACTGACCCAGCCAGCTTCAGTGAGCGGCTCACCAGGTCAGAGCATTACCATCTCGTGT
ACGGGTACTAGCAGCGATATTGGTGCTTATGTGTCTTGGTACCAGCAGCATCCCGGGAAGGCGCCG
AAACTTATGATTTATGAGGTTTCTTCTCGTCCCTCAGGCGTGAGCAACCGTTTTAGCGGATCCAAAAG
CGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGACGAAGCGGATTATTATTGCTC
TTCTTATGATCTTACTCCTCCTGGTAAGGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGCCAG

**3078_Vl lambda 3** (SEQ ID NO: 32):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGTGT
AGCGGCGATAATATTGGTCATTATTATGTTTCTTGGTACCAGCAGAAACCCGGGCAGGCGCCAGTTC
TTGTGATTTATGGTGATAATAATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCAACAGCGG
CAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATTATTGCGCTTC
TGATGTTGGTTCTCTTGATGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGCCAG

**3081_ Vk kappa 3** (SEQ ID NO: 33):
GATATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACCCTGAG
CTGCAGAGCGAGCCAGACTGGTTCTACTTCTTATCTGGCTTGGTACCAGCAGAAACCAGGTCAAGCA
CCGCGTCTATTAATTTATGATGCTTCTAAGCGTGCAACTGGGGTCCCGGCGCGTTTTAGCGGCTCTG
GATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAACCTGAAGACTTTGCGACTTATTATTG
CCATCAGTATTATAACGTTCCTCATACCTTTGGCCAGGGTACGAAAGTTGAAATTAAACGTACG

**3085_ Vl lambda 1** (SEQ ID NO: 34):
GATATCGTGCTGACCCAGCCGCCTTCAGTGAGTGGCGCACCAGGTCAGCGTGTGACCATCTCGTGT
AGCGGCAGCAGCAGCAACATTGGTAATAATTATGTGTCTTGGTACCAGCAGTTGCCCGGGACGGCG
CCGAAACTTCTGATTTATGGTGATGATCAGCGTCCCTCAGGCGTGCCGGATCGTTTTAGCGGATCCA
AAAGCGGCACCAGCGCGAGCCTTGCGATTACGGGCCTGCAAAGCGAAGACGAAGCGGATTATTATT
GCCAGTCTTATGGTACTTTTTCTTCTTTTGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGCCAG

**3086_Vk kappa 1** (SEQ ID NO: 35):
GATATCCAGATGACCCAGAGCCCGTCTAGCCTGAGCGCGAGCGTGGGTGATCGTGTGACCATTACC
TGCAGAGCGAGCCAGAATATTTCTCAGTGGCTGAATTGGTACCAGCAGAAACCAGGTAAAGCACCG
AAACTATTAATTTATGGTGCTTCTAATTTGCAAAGCGGGGTCCCGTCCCGTTTTAGCGGCTCTGGATC
CGGCACTGATTTTACCCTGACCATTAGCAGCCTGCAACCTGAAGACTTTGCGACTTATTATTGCCAG
CAGTATTATGATCTTCCTAATACCTTTGGCCAGGGTACGAAAGTTGAAATTAAACGTACG

**3087_ Vl lambda 3** (SEQ ID NO: 36):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGTGT
AGCGGCGATAATCTTCGTCATTATTATGTTTATTGGTACCAGCAGAAACCCGGGCAGGCGCCAGTTC
TTGTGATTTATGGTGATTCTAAGCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCAACAGCGG
CAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATTATTGCCAGAC
TTATACTGGTGGTGCTTCTCTTGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGCCAG

**3088_ Vl lambda 3** (SEQ ID NO: 37):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGTGT
AGCGGCGATAATATTGGTCATTATTATGTTTCTTGGTACCAGCAGAAACCCGGGCAGGCGCCAGTTC
TTGTGATTTATTCTGATTCTAATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCAACAGCGG
CAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATTATTGCCAGTC
TTATAATGGTACTTATGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGCCAG

**3089_ Vk kappa 3** (SEQ ID NO: 38):
GATATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACCCTGAG
CTGCAGAGCGAGCCAGTCTGTTTCTTCTTCTTATCTGGCTTGGTACCAGCAGAAACCAGGTCAAGCA
CCGCGTCTATTAATTTATGGTGCTTCTTCTCGTGCAACTGGGGTCCCGGCGCGTTTTAGCGGCTCTG
GATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAACCTGAAGACTTTGCGGTTTATTATTG
CCAGCAGGGTTATAATTCTCCTTTTACCTTTGGCCAGGGTACGAAAGTTGAAATTAAACGTACG

**3101_ Vl lambda 3** (SEQ ID NO: 39):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGTGT
AGCGGCGATTCTCTTGGTTCTTATTATGTTCATTGGTACCAGCAGAAACCCGGGCAGGCGCCAGTTC
TTGTGATTGGTGATGATACTAAGCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCAACAGCG
GCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATTATTGCGGTT
CTCGTACTGGTTATAATAATTCTTTTGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGCCAG

**3102_ V'l lambda 3** (SEQ ID NO: 40):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGTGT
AGCGGCGATAATCTTGGTCATTATTATGTTTCTTGGTACCAGCAGAAACCCGGGCAGGCGCCAGTTC
TTGTGATTTATGATGATTCTGATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCAACAGCGG
CAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATTATTGCGGTGC
TTATGCTATGCATATGACTGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGCCAG

**3127_ Vl lambda 2** (SEQ ID NO: 41):
GATATCGCACTGACCCAGCCAGCTTCAGTGAGCGGCTCACCAGGTCAGAGCATTACCATCTCGTGT
ACGGGTACTAGCAGCGATGTTGGTGCTATTAATTATGTGTCTTGGTACCAGCAGCATCCCGGGAAGG
CGCCGAAACTTATGATTTATGATGTTAATAAGCGTCCCTCAGGCGTGCCGGATCGTTTTAGCGGATC
CAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGACGAAGCGGATTATTA
TTGCGGTTCTTATACTATGCAGGTTGGTTCTTATGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTG
GCCAG

**3128_ Vl lambda 3** (SEQ ID NO: 42):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGTGT
AGCGGCGATAATATTGGTCATTATTATGCTCATTGGTACCAGCAGAAACCCGGGCAGGCGCCAGTTG
TTGTGATTTATGATGATAATGATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCAACAGCGG
CAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATTATTGCCAGGC
TTATACTGGTGATGGTGGTCGTGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGCCAG

**3129_ Vl lambda 3** (SEQ ID NO: 43):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGTGT
AGCGGCGATAATCTTGGTTCTAAGGTTGTTTCTTGGTACCAGCAGAAACCCGGGCAGGCGCCAGTT

CTTGTGATTTATTATGATAATAAGCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCAACAGCG
GCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATTATTGCCAGT
CTTATACTTTTGAGTCTGGTTCTGTTGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGCCAG

**3130_ Vl lambda 3** (SEQ ID NO: 44):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGTGT
AGCGGCGATAATCTTGGTCATTATTATGTTGATTGGTACCAGCAGAAACCCGGGCAGGCGCCAGTTC
TTGTGATTTATGCTGATAATAATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCAACAGCGG
CAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATTATTGCTCTTCT
TATTCTCAGCAGTCTATGGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGCCAG

**3131_ Vl lambda 3** (SEQ ID NO: 45):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGTGT
AGCGGCGATAATCTTGGTAATTTTTATGTTCATTGGTACCAGCAGAAACCCGGGCAGGCGCCAGTTC
TTGTGATTTATGAGGATTCTAATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCAACAGCGG
CAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATTATTGCTCTTCT
TGGGATATGTATCGTACTATTTTTGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGCCAG

**6278_Vl lambda 3** (SEQ ID NO: 107)
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGTGT
AGCGGCGATAATATTGGTCATTATTATGTTTCTTGGTACCAGCAGAAACCCGGGCAGGCGCCAGTTC
TTGTGATTTATTCTGATTCTAATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCAACAGCGG
CAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATTATTGCCAGTC
TGCTGATAATTTTCCTTTTGTGTTTGGCGGCGGCACGAAGTTAACCGTCCTAGGTCAG

**6279_ Vl lambda 3** (SEQ ID NO: 108)
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGTGT
AGCGGCGATAATATTGGTCATTATTATGTTTCTTGGTACCAGCAGAAACCCGGGCAGGCGCCAGTTC
TTGTGATTTATTCTGATTCTAATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCAACAGCGG
CAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATTATTGCCAGTC
TTATACTATGTCTGATGTTCTTGTTGTGTTTGGCGGCGGCACGAAGTTAACCGTCCTAGGTCAG

**3077_Vk kappa 2** (SEQ ID NO: 117)
GATATCGTGATGACCCAGAGCCCACTGAGCCTGCCAGTGACTCCGGGCGAGCCTGCGAGCATTAGC
TGCAGAAGCAGCCAAAGCCTGCTTTTTATTGATGGCAATAATTATCTGAATTGGTACCTTCAAAAACC
AGGTCAAAGCCCGCAGCTATTAATTTATCTTGGTTCTAATCGTGCCAGTGGGGTCCCGGATCGTTT
TAGCGGCTCTGGATCCGGCACCGATTTTACCCTGAAAATTAGCCGTGTGGAAGCTGAAGACGTGGG
CGTGTATTATTGCCAGCAGTATTCTTCTAAGTCTGCTACCTTTGGCCAGGGTACGAAAGTTGAAATTA
AACGTACG

**3079_Vk kappa 1** (SEQ ID NO: 118)
GATATCCAGATGACCCAGAGCCCGTCTAGCCTGAGCGCGAGCGTGGGTGATCGTGTGACCATTACC
TGCAGAGCGAGCCAGGATATTTCTGCTTTTCTGAATTGGTACCAGCAGAAACCAGGTAAAGCACCGA
AACTATTAATTTATAAGGTTTCTAATTTGCAAAGCGGGGTCCCGTCCCGTTTTAGCGGCTCTGGATCC
GGCACTGATTTTACCCTGACCATTAGCAGCCTGCAACCTGAAGACTTTGCGACTTATTATTGCCAGCA
GGCTTATTCTGGTTCTATTACCTTTGGCCAGGGTACGAAAGTTGAAATTAAACGTACG

**3080_Vl lambda 3** (SEQ ID NO: 119)
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGTGT
AGCGGCGATAATATTGGTAATAAGTATGTTTCTTGGTACCAGCAGAAACCCGGGCAGGCGCCAGTTG
TTGTGATTTATGGTGATAATAATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCAACAGCGG
CAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATTATTGCTCTTCT
TATGATTCTTCTTATTTTGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGCCAG

## Figure 2b

## Variable Light Chain Peptide

(CDR Regions in **Bold** or <u>underlined</u>)

**3076_Vl lambda 2** (SEQ ID NO: 46):
DIALTQPASVSGSPGQSITISCTGTSSDIGAYVSWYQQHPGKAPKLMIYEVSSRPSGVSNRFSGSKSGNT
ASLTISGLQAEDEADYYCSSYDLTPPGKVFGGGTKLTVLGQ

**3078_Vl lambda 3** (SEQ ID NO: 47):
DIELTQPPSVSVAPGQTARISCSGDNIGHYYVSWYQQKPGQAPVLVIYGDNNRPSGIPERFSGSNSGNTA
TLTISGTQAEDEADYYCASDVGSLDVFGGGTKLTVLGQ

**3081_ Vk kappa 3** (SEQ ID NO: 48):
DIVLTQSPATLSLSPGERATLSCRASQTGSTSYLAWYQQKPGQAPRLLIYDASKRATGVPARFSGSGSGT
DFTLTISSLEPEDFATYYCHQYYNVPHTFGQGTKVEIKRT

**3085_ Vl lambda 1** (SEQ ID NO: 49):
DIVLTQPPSVSGAPGQRVTISC**SGSSSNIGNNYVS**WYQQLPGTAPKLLIY**GDDQRPS**GVPDRFSGSKSG
TSASLAITGLQSEDEADYYC**QSYGTFSSF**VFGGGTKLTVLGQ

**3086_Vk kappa 1** (SEQ ID NO: 50):
DIQMTQSPSSLSASVGDRVTITCRASQNISQWLNWYQQKPGKAPKLLIYGASNLQSGVPSRFSGSGSGT
DFTLTISSLQPEDFATYYCQQYYDLPNTFGQGTKVEIKRT

**3087_ Vl lambda 3** (SEQ ID NO: 51):
DIELTQPPSVSVAPGQTARISCSGDNLRHYYVYWYQQKPGQAPVLVIYGDSKRPSGIPERFSGSNSGNT
ATLTISGTQAEDEADYYCQTYTGGASLVFGGGTKLTVLGQ

**3088_ Vl lambda 3** (SEQ ID NO: 52):
DIELTQPPSVSVAPGQTARISCSGDNIGHYYVSWYQQKPGQAPVLVIYSDSNRPSGIPERFSGSNSGNTA
TLTISGTQAEDEADYYCQSYNGTYVFGGGTKLTVLGQ

**3089_ Vk kappa 3** (SEQ ID NO: 53):
DIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGVPARFSGSGSGT
DFTLTISSLEPEDFAVYYCQQGYNSPFTFGQGTKVEIKRT

**3101_ Vl lambda 3** (SEQ ID NO: 54):
DIELTQPPSVSVAPGQTARISCSGDSLGSYYVHWYQQKPGQAPVLVIGDDTKRPSGIPERFSGSNSGNT
ATLTISGTQAEDEADYYCGSRTGYNNSFVFGGGTKLTVLGQ

**3102_ Vl lambda 3** (SEQ ID NO: 55):
DIELTQPPSVSVAPGQTARISCSGDNLGHYYVSWYQQKPGQAPVLVIYDDSDRPSGIPERFSGSNSGNT
ATLTISGTQAEDEADYYCGAYAMHMTVFGGGTKLTVLGQ

**3127_ Vl lambda 2** (SEQ ID NO: 56):
DIALTQPASVSGSPGQSITISCTGTSSDVGAINYVSWYQQHPGKAPKLMIYDVNKRPSGVPDRFSGSKSG
NTASLTISGLQAEDEADYYCGSYTMQVGSYVFGGGTKLTVLGQ

**3128_ Vl lambda 3** (SEQ ID NO: 57):
DIELTQPPSVSVAPGQTARISCSGDNIGHYYAHWYQQKPGQAPVVVIYDDNDRPSGIPERFSGSNSGNT
ATLTISGTQAEDEADYYCQAYTGDGGRVFGGGTKLTVLGQ

**3129_ Vl lambda 3** (SEQ ID NO: 58):
DIELTQPPSVSVAPGQTARISCSGDNLGSKVVSWYQQKPGQAPVLVIYYDNKRPSGIPERFSGSNSGNTA
TLTISGTQAEDEADYYCQSYTFESGSVVFGGGTKLTVLGQ

**3130_ Vl lambda 3** (SEQ ID NO: 59):
DIELTQPPSVSVAPGQTARISCSGDNLGHYYVDWYQQKPGQAPVLVIYADNNRPSGIPERFSGSNSGNT
ATLTISGTQAEDEADYYCSSYSQQSMVFGGGTKLTVLGQ

**3131_ Vl lambda 3** (SEQ ID NO: 60):
DIELTQPPSVSVAPGQTARISCSGDNLGNFYVHWYQQKPGQAPVLVIYEDSNRPSGIPERFSGSNSGNT
ATLTISGTQAEDEADYYCSSWDMYRTIFVFGGGTKLTVLGQ

**6278_ Vl lambda 3** (SEQ ID NO: 109)
DIELTQPPSVSVAPGQTARISCSGDNIGHYYVSWYQQKPGQAPVLVIYSDSNRPSGIPERFSGSNSGNTA
TLTISGTQAEDEADYYCQSADNFPFVFGGGTKLTVLGQ

**6279_ Vl lambda 3** (SEQ ID NO: 110)
DIELTQPPSVSVAPGQTARISCSGDNIGHYYVSWYQQKPGQAPVLVIYSDSNRPSGIPERFSGSNSGNTA
TLTISGTQAEDEADYYCQSYTMSDVLVVFGGGTKLTVLGQ

**3077_Vk kappa 2** (SEQ ID NO: 120)
DIVMTQSPLSLPVTPGEPASISC**RSSQSLLFIDGNNYLN**WYLQKPGQSPQLLI**YLGSNRAS**GVPDRFSGS
GSGTDFTLKISRVEAEDVGVYYC**QQYSSKSA**TFGQGTKVEIKRT

**3079_Vk kappa 1** (SEQ ID NO: 121)
DIQMTQSPSSLSASVGDRVTITC**RASQDISAFLN**WYQQKPGKAPKLLI**YKVSNLQS**GVPSRFSGSGSGT
DFTLTISSLQPEDFATYYC**QQAYSGSI**TFGQGTKVEIKRT

**3080_Vl lambda3** (SEQ ID NO: 122)
DIELTQPPSVSVAPGQTARISC**SGDNIGNKYVS**WYQQKPGQAPVVVIY**GDNNRPS**GIPERFSGSNSGNT
ATLTISGTQAEDEADYYC**SSYDSSYF**VFGGGTKLTVLGQ

## Figure 3

### Variable Heavy Chain Consensus Sequences

(CDR Regions in **Bold**)

**VH1A Consensus (SEQ ID NO: 61):**
QVQLVQSGAEVKKPGSSVKVSCKAS**GGTFSSYAIS**WVRQAPGQGLEWMG**GIIPIFGTANYAQKFQG**RVTI
TADESTSTAYMELSSLRSEDTAVYYCAR**WGGDGFYAMDY**WGQGTLVTVSS.

**VH2 Consensus (SEQ ID NO: 62)**
QVQLKESGPALVKPTQTLTLTCTFS**GFSLSTSGVGVG**WIRQPPGKALEWLA**LIDWDDDKYYSTSLKT**RLT
ISKDTSKNQVVLTMTNMDPVDTATYYCAR**WGGDGFYAMDY**WGQGTLVTVSS

**VH3 Consensus** (SEQ ID NO: 63):

(1) QVQLVESGGG LVQPGGSLRL SCAAS**GFTFS SYAMS**WVRQA PGKGLEWVS**A**
(51) **ISGSGGSTYY ADSVKG**RFTI SRDNSKNTLY LQMNSLRAED TAVYYCAR**WG**
(101) **GDGFYAMDYW** GQGTLVTVS S

**VH4 Consensus** (SEQ ID NO: 64):
QVQLQESGPGLVKPSETLSLTCTVS**GGSISSYYWS**WIRQPPGKGLEWIG**YIYYSGSTNYNPSLKS**RVTIS
VDTSKNQFSLKLSSVTAADTAVYYCAR**WGGDGFYAMDY**WGQGTLVTVSS

**VH5 Consensus** (SEQ ID NO: 65):
QVQLVQSGAEVKKPGESLKISCKGS**GYSFTSYWIG**WVRQMPGKGLEWMG**IIYPGDSDTRYSPSFQG**QVTI
SADKSISTAYLQWSSLKASDTAMYYCAR**WGGDGFYAMDY**WGQGTLVTVSS

## Figure 4

### Variable Light Chain Consensus Sequences

(CDR Regions in **Bold**)

**Vl_λ1 Consensus (SEQ ID NO: 66):**
DIVLTQPPSVSGAPGQRVTISC**SGSSSNIGSNYVS**WYQQLPGTAPKLLIY**DNNQRPS**GVPDRFSGSKSGT
SASLAITGLQSEDEADYYC**QQHYTTPP**VFGGGTKLTVLGQ

**Vl_λ2 Consensus (SEQ ID NO: 67):**
DIALTQPASVSGSPGQSITISC**TGTSSDVGGYNYVS**WYQQHPGKAPKLMIY**DVSNRPS**GVSNRFSGSKSG
NTASLTISGLQAEDEADYYC**QQHYTTPP**VFGGGTKLTVLGQ

**Vl_λ3 Consensus** (SEQ ID NO: 68):

(1) DIELTQPPSV SVAPGQTARI SC**SGDALGDK YAS**WYQQKPG QAPVLVIY**DD**
(51) **SDRPS**GIPER FSGSNSGNTA TLTISGTQAE DEADYYC**QQH YTTPP**VFGGG
(101) TKLTVLG

**Vl_k1 Consensus** (SEQ ID NO: 69):

(1) DIQMTQSPSS LSASVGDRVT ITC**RASQGIS SYLA**WYQQKP GKAPKLLIY**A**
(51) **ASSLQS**GVPS RFSGSGSGTD FTLTISSLQP EDFATYYC**QQ HYTTPP**TFGQ
(101) GTKVEIKR

**Vl_k3 Consensus** (SEQ ID NO: 70):
DIVLTQSPATLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRLLIY**GASSRAT**GVPARFSGSGSGT
DFTLTISSLEPEDFAVYYC**QQHYTTPP**TFGQGTKVEIKRT

## Figure 5

## Peptide Sequence of CD38

(SEQ ID NO: 71):

```
1     mancefspvs gdkpccrlsr raqlclgvsi lvlilvvvla vvvprwrqqw sgpgttkrfp

61    etvlarcvky teihpemrhv dcqsvwdafk gafiskhpcn iteedyqplm klgtqtvpcn

121   killwsrikd lahqftqvqr dmftledtll gyladdltwc gefntskiny qscpdwrkdc

181   snnpvsvfwk tvsrrfaeaa cdvvhvmlng srskifdkns tfgsvevhnl qpekvqtlea

241   wvihggreds rdlcqdptik elesiiskrn iqfsckniyr pdkflqcvkn pedssctsei
```

# Figure 6

## Nucleotide Sequence of Chimeric OKT10

Heavy Chain (SEQ ID NO: 72):

caggtggaat tggtggaatc tggaggatcc ctgaaactct cctgtgcagc ctcaggattc gattttagta
gatcctggat gaattgggtc cggcaggctc caggaaaagg gctagaatgg attggagaaa ttaatccaga
tagcagtacg ataaactata cgacatctct aaaggataaa ttcatcatct ccagagacaa cgccaaaaat
acgctgtacc tgcaaatgac caaagtgaga tctgaggaca cagcccttta ttactgtgca agatatggta
actggtttcc ttattggggc caagggactc tggtcactgt cagctcagcc tccaccaagg gtccatcggt
cttccccctg gcaccctcct ccaagagcac ctctgggggc acagcggccc tgggctgcct ggtcaaggac
tacttccccg aaccggtgac ggtgtcgtgg aactcaggcg ccctgaccag cggcgtgcac accttcccgg
ctgtcctaca gtcctcagga ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac
ccagacctac atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg tcagtcttcc
tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag gtcacatgcg tggtggtgga
cgtgagccac gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag
acaaagccgc gggaggagca gtacaacagc acgtaccggg tggtcagcgt cctcaccgtc ctgcaccagg
actggctgaa tggcaaggag tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac
catctccaaa gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc gtggagtggg
agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt
cctctacagc aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg
catgaggctc tgcacaacca ctacacgcag aagagcctct ccctgtctcc gggtaaa

Light Chain (SEQ ID NO: 73):

gatatcctga tgacccagtc tcaaaaaatc atgcccacat cagtgggaga cagggtcagc gtcacctgca
aggccagtca aaatgtggat actaatgtag cctggtatca acagaaacca ggacagtctc ctaaagcact
gatttactcg gcatcctacc gatacagtgg agtccctgat cgcttcacag gcagtggatc tgggacagat

ttcactctca ccatcaccaa tgtgcagtct gaggacttgg cagagtattt ctgtcagcaa tatgacagct

atcctctcac gttcggtgct gggaccaagc tggacctgaa acgtacggtg gctgcaccat ctgtcttcat

cttcccgcca tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag gagagtgtca

cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg ctgagcaaag cagactacga

gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc ctgagctcgc ccgtcacaaa gagcttcaac

aggggagagt gt

**Figure 7: DNA sequence of pMOPRH®_h_IgG1_1**

```
                  StyI
                  ~~~~~~~
601     TCGCTATTAC CATGGTGATG CGGTTTTGGC AGTACATCAA TGGGCGTGGA
        AGCGATAATG GTACCACTAC GCCAAAACCG TCATGTAGTT ACCCGCACCT

                                                      AatII
                                                      ~~~~~~
651     TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA
        ATCGCCAAAC TGAGTGCCCC TAAAGGTTCA GAGGTGGGGT AACTGCAGTT

701     TGGGAGTTTG TTTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA
        ACCCTCAAAC AAAACCGTGG TTTTAGTTGC CCTGAAAGGT TTTACAGCAT

751     ACAACTCCGC CCCATTGACG CAAATGGGCG GTAGGCGTGT ACGGTGGGAG
        TGTTGAGGCG GGGTAACTGC GTTTACCCGC CATCCGCACA TGCCACCCTC

801     GTCTATATAA GCAGAGCTCT CTGGCTAACT AGAGAACCCA CTGCTTACTG
        CAGATATATT CGTCTCGAGA GACCGATTGA TCTCTTGGGT GACGAATGAC

                  pMORPH®_Ig_FOR 100.0%                 NheI
                  ~~~~~~~~~~~~~~~~~~~~~~~               ~~~~~~
851     GCTTATCGAA ATTAATACGA CTCACTATAG GGAGACCCAA GCTGGCTAGC
        CGAATAGCTT TAATTATGCT GAGTGATATC CCTCTGGGTT CGACCGATCG

              M  K   H  L  W   F  F  L   L  L  V  A   A  P  R ·
901     GCCACCATGA AACACCTGTG GTTCTTCCTC CTGCTGGTGG CAGCTCCCAG
        CGGTGGTACT TTGTGGACAC CAAGAAGGAG GACGACCACC GTCGAGGGTC

                          EcoRI                 BlpI          StyI
                          ~~~~~~~               ~~~~~~~~      ~
                                                      A  S  T ·
        · W  V  L   S  Q  V  E   F  C  R   R  L  A   Q
951     ATGGGTCCTG TCCCAGGTGG AATTCTGCAG GCGGTTAGCT CAGCCTCCAC
        TACCCAGGAC AGGGTCCACC TTAAGACGTC CGCCAATCGA GTCGGAGGTG

        StyI          BbsI
        ~~~~~         ~~~~~~
        · K  G  P   S  V  F  P   L  A  P   S  S  K   S  T  S  G ·
1001    CAAGGGTCCA TCGGTCTTCC CCCTGGCACC CTCCTCCAAG AGCACCTCTG
        GTTCCCAGGT AGCCAGAAGG GGGACCGTGG GAGGAGGTTC TCGTGGAGAC

        · G  T  A   A  L  G   C  L  V  K   D  Y  F   P  E  P
1051    GGGGCACAGC GGCCCTGGGC TGCCTGGTCA AGGACTACTT CCCCGAACCG
        CCCCGTGTCG CCGGGACCCG ACGGACCAGT TCCTGATGAA GGGGCTTGGC
```

```
          V  T  V  S   W  N  S   G  A  L   T  S  G  V   H  T  F ·
1101      GTGACGGTGT CGTGGAACTC AGGCGCCCTG ACCAGCGGCG TGCACACCTT
          CACTGCCACA GCACCTTGAG TCCGCGGGAC TGGTCGCCGC ACGTGTGGAA

          · P  A  V   L  Q  S  S   G  L  Y   S  L  S   S  V  V  T ·
1151      CCCGGCTGTC CTACAGTCCT CAGGACTCTA CTCCCTCAGC AGCGTGGTGA
          GGGCCGACAG GATGTCAGGA GTCCTGAGAT GAGGGAGTCG TCGCACCACT

          · V  P  S   S  S  L   G  T  Q  T   Y  I  C   N  V  N
1201      CCGTGCCCTC CAGCAGCTTG GGCACCCAGA CCTACATCTG CAACGTGAAT
          GGCACGGGAG GTCGTCGAAC CCGTGGGTCT GGATGTAGAC GTTGCACTTA

                              StyI
                            ~~~~~~~
          H  K  P  S   N  T  K   V  D  K   K  V  E  P   K  S  C ·
1251      CACAAGCCCA GCAACACCAA GGTGGACAAG AAAGTTGAGC CCAAATCTTG
          GTGTTCGGGT CGTTGTGGTT CCACCTGTTC TTTCAACTCG GGTTTAGAAC

          · D  K  T   H  T  C  P   P  C  P   A  P  E   L  L  G  G ·
1301      TGACAAAACT CACACATGCC CACCGTGCCC AGCACCTGAA CTCCTGGGGG
          ACTGTTTTGA GTGTGTACGG GTGGCACGGG TCGTGGACTT GAGGACCCCC

                    BbsI                          StyI
                  ~~~~~~~~                      ~~~~~~~
          · P  S  V   F  L  F   P  P  K  P   K  D  T   L  M  I
1351      GACCGTCAGT CTTCCTCTTC CCCCCAAAAC CCAAGGACAC CCTCATGATC
          CTGGCAGTCA GAAGGAGAAG GGGGGTTTTG GGTTCCTGTG GGAGTACTAG

                                                          BbsI
                                                         ~~~~~
          S  R  T  P   E  V  T   C  V  V   V  D  V  S   H  E  D ·
1401      TCCCGGACCC CTGAGGTCAC ATGCGTGGTG GTGGACGTGA GCCACGAAGA
          AGGGCCTGGG GACTCCAGTG TACGCACCAC CACCTGCACT CGGTGCTTCT

          BbsI
          ~
          · P  E  V   K  F  N  W   Y  V  D   G  V  E   V  H  N  A ·
1451      CCCTGAGGTC AAGTTCAACT GGTACGTGGA CGGCGTGGAG GTGCATAATG
          GGGACTCCAG TTCAAGTTGA CCATGCACCT GCCGCACCTC CACGTATTAC

          · K  T  K   P  R  E   E  Q  Y  N   S  T  Y   R  V  V
1501      CCAAGACAAA GCCGCGGGAG GAGCAGTACA ACAGCACGTA CCGGGTGGTC
          GGTTCTGTTT CGGCGCCCTC CTCGTCATGT TGTCGTGCAT GGCCCACCAG

          S  V  L  T   V  L  H   Q  D  W   L  N  G  K   E  Y  K ·
1551      AGCGTCCTCA CCGTCCTGCA CCAGGACTGG CTGAATGGCA AGGAGTACAA
          TCGCAGGAGT GGCAGGACGT GGTCCTGACC GACTTACCGT TCCTCATGTT

          · C  K  V   S  N  K  A   L  P  A   P  I  E   K  T  I  S ·
1601      GTGCAAGGTC TCCAACAAAG CCCTCCCAGC CCCCATCGAG AAAACCATCT
          CACGTTCCAG AGGTTGTTTC GGGAGGGTCG GGGGTAGCTC TTTTGGTAGA

                                                  BsrGI
                                                 ~~~~~~
          · K  A  K   G  Q  P   R  E  P  Q   V  Y  T   L  P  P
1651      CCAAAGCCAA AGGGCAGCCC CGAGAACCAC AGGTGTACAC CCTGCCCCCA
```

```
        GGTTTCGGTT TCCCGTCGGG GCTCTTGGTG TCCACATGTG GGACGGGGGT
         S  R  D  E   L  T  K   N  Q  V   S  L  T  C   L  V  K ·
1701    TCCCGGGATG AGCTGACCAA GAACCAGGTC AGCCTGACCT GCCTGGTCAA
        AGGGCCCTAC TCGACTGGTT CTTGGTCCAG TCGGACTGGA CGGACCAGTT

        · G  F  Y   P  S  D  I   A  V  E   W  E  S   N  G  Q  P ·
1751    AGGCTTCTAT CCCAGCGACA TCGCCGTGGA GTGGGAGAGC AATGGGCAGC
        TCCGAAGATA GGGTCGCTGT AGCGGCACCT CACCCTCTCG TTACCCGTCG

        · E  N  N   Y  K  T   T  P  P  V   L  D  S   D  G  S
1801    CGGAGAACAA CTACAAGACC ACGCCTCCCG TGCTGGACTC CGACGGCTCC
        GCCTCTTGTT GATGTTCTGG TGCGGAGGGC ACGACCTGAG GCTGCCGAGG

         F  F  L  Y   S  K  L   T  V  D   K  S  R  W   Q  Q  G ·
1851    TTCTTCCTCT ACAGCAAGCT CACCGTGGAC AAGAGCAGGT GGCAGCAGGG
        AAGAAGGAGA TGTCGTTCGA GTGGCACCTG TTCTCGTCCA CCGTCGTCCC

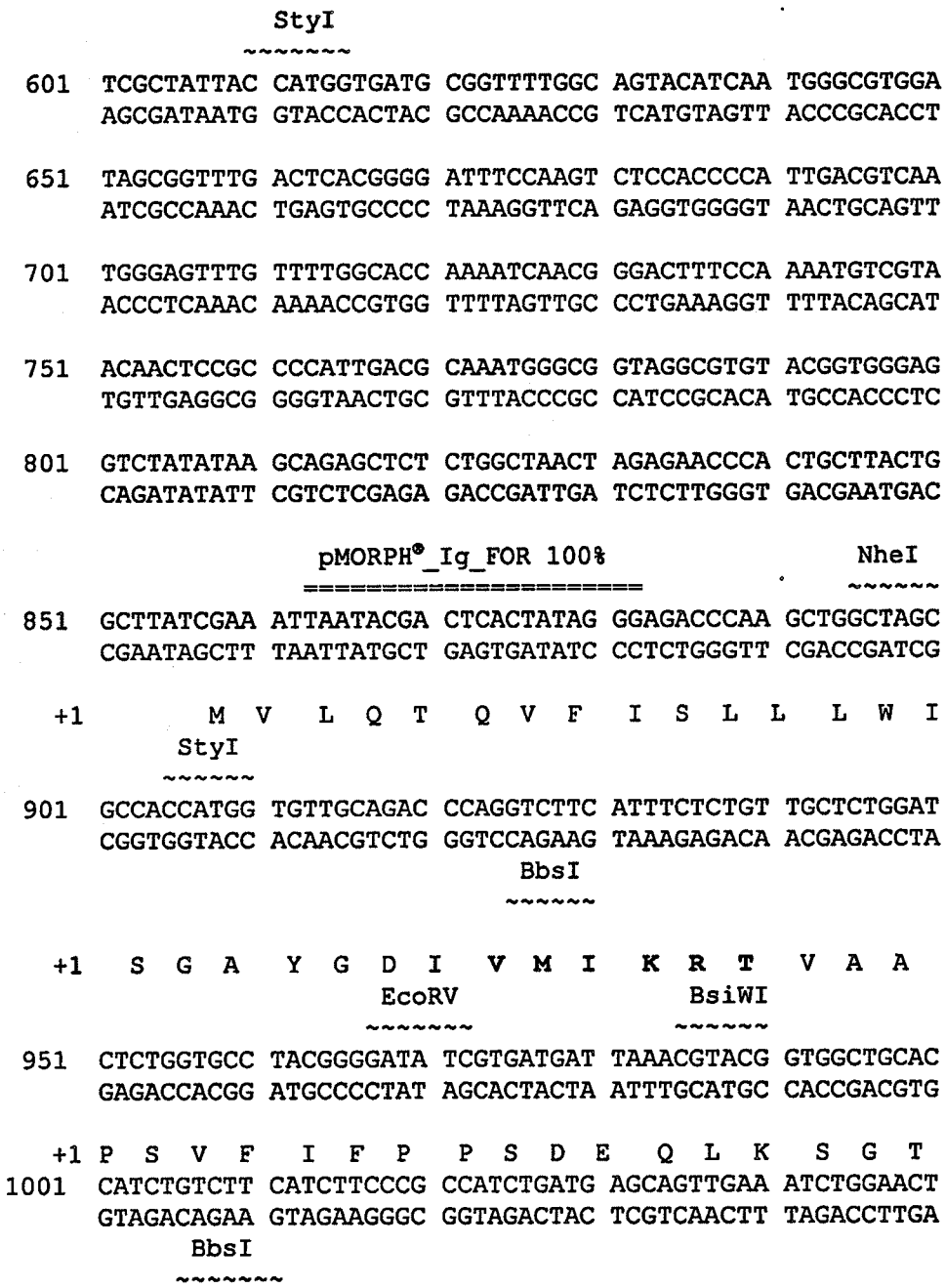
             BbsI                  NsiI
             ~~~~~~~               ~~~~~~
        · N  V  F   S  C  S  V   M  H  E   A  L  H   N  H  Y  T ·
1901    GAACGTCTTC TCATGCTCCG TGATGCATGA GGCTCTGCAC AACCACTACA
        CTTGCAGAAG AGTACGAGGC ACTACGTACT CCGAGACGTG TTGGTGATGT

             SapI                                          PmeI
             ~~~~~~~~                                      ~~~~~~~~
        · Q  K  S   L  S  L   S  P  G  K   *
1951    CGCAGAAGAG CCTCTCCCTG TCTCCGGGTA AATGAGGGCC CGTTTAAACC
        GCGTCTTCTC GGAGAGGGAC AGAGGCCCAT TTACTCCCGG GCAAATTTGG

2001    CGCTGATCAG CCTCGACTGT GCCTTCTAGT TGCCAGCCAT CTGTTGTTTG
        GCGACTAGTC GGAGCTGACA CGGAAGATCA ACGGTCGGTA GACAACAAAC

                   ~~~~~~~~~~~~~~~~~~~
                   pMORPH® Ig REV 100.0%
2051    CCCCTCCCCC GTGCCTTCCT TGACCCTGGA AGGTGCCACT CCCACTGTCC
        GGGGAGGGGG CACGGAAGGA ACTGGGACCT TCCACGGTGA GGGTGACAGG
```

**Figure 8: DNA Sequence of Ig kappa light chain expression vector pMORPH®_h_Igκ_1**



```
   +1  A  S  V  V   C  L  L   N  N  F   Y  P  R  E   A  K  V
1051  GCCTCTGTTG TGTGCCTGCT GAATAACTTC TATCCCAGAG AGGCCAAAGT
      CGGAGACAAC ACACGGACGA CTTATTGAAG ATAGGGTCTC TCCGGTTTCA

   +1   Q  W  K   V  D  N  A   L  Q  S   G  N  S   Q  E  S
1101  ACAGTGGAAG GTGGATAACG CCCTCCAATC GGGTAACTCC CAGGAGAGTG
      TGTCACCTTC CACCTATTGC GGGAGGTTAG CCCATTGAGG GTCCTCTCAC

   +1 V  T  E  Q   D  S  K   D  S  T  Y   S  L  S   S  T  L
1151  TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCCTG
      AGTGTCTCGT CCTGTCGTTC CTGTCGTGGA TGTCGGAGTC GTCGTGGGAC

   +1  T  L  S  K   A  D  Y   E  K  H   K  V  Y  A   C  E  V
         BlpI
       ~~~~~~~
1201  ACGCTGAGCA AAGCAGACTA CGAGAAACAC AAAGTCTACG CCTGCGAAGT
      TGCGACTCGT TTCGTCTGAT GCTCTTTGTG TTTCAGATGC GGACGCTTCA

   +1   T  H  Q   G  L  S  S   P  V  T   K  S  F   N  R  G
1251  CACCCATCAG GGCCTGAGCT CGCCCGTCAC AAAGAGCTTC AACAGGGGAG
      GTGGGTAGTC CCGGACTCGA GCGGGCAGTG TTTCTCGAAG TTGTCCCCTC

   +1 E  C  *
                        PmeI                  pMORPH®_Ig_REV 100%
                     ~~~~~~~~~~               ==================
1301  AGTGTTAGGG GCCCGTTTAA ACCCGCTGAT CAGCCTCGAC TGTGCCTTCT
      TCACAATCCC CGGGCAAATT TGGGCGACTA GTCGGAGCTG ACACGGAAGA


      =
1351  AGTTGCCAGC CATCTGTTGT TTGCCCCTCC CCCGTGCCTT CCTTGACCCT
      TCAACGGTCG GTAGACAACA AACGGGGAGG GGGCACGGAA GGAACTGGGA
```

**Figure 9: DNA Sequence of HuCAL® Ig lambda light chain vector pMORPH®_h_Igλ_1**

```
                 StyI
                ~~~~~~~
601  TCGCTATTAC CATGGTGATG CGGTTTTGGC AGTACATCAA TGGGCGTGGA
     AGCGATAATG GTACCACTAC GCCAAAACCG TCATGTAGTT ACCCGCACCT

651  TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA
     ATCGCCAAAC TGAGTGCCCC TAAAGGTTCA GAGGTGGGGT AACTGCAGTT

701  TGGGAGTTTG TTTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA
     ACCCTCAAAC AAAACCGTGG TTTTAGTTGC CCTGAAAGGT TTTACAGCAT

751  ACAACTCCGC CCCATTGACG CAAATGGGCG GTAGGCGTGT ACGGTGGGAG
     TGTTGAGGCG GGGTAACTGC GTTTACCCGC CATCCGCACA TGCCACCCTC

801  GTCTATATAA GCAGAGCTCT CTGGCTAACT AGAGAACCCA CTGCTTACTG
     CAGATATATT CGTCTCGAGA GACCGATTGA TCTCTTGGGT GACGAATGAC

                    pM_Ig_FOR  100.0%                  NheI
                   ======================              ~~~~~~
851  GCTTATCGAA ATTAATACGA CTCACTATAG GGAGACCCAA GCTGGCTAGC
     CGAATAGCTT TAATTATGCT GAGTGATATC CCTCTGGGTT CGACCGATCG

 +1        M  A  W  A  L  L  L  T  L  L  T  Q  G  T
          StyI
         ~~~~~~
901  GCCACCATGG CCTGGGCTCT GCTGCTCCTC ACCCTCCTCA CTCAGGGCAC
     CGGTGGTACC GGACCCGAGA CGACGAGGAG TGGGAGGAGT GAGTCCCGTG

 +2                                          T  V  L  G  Q
 +1   G  S  W  A  D  I  V  M  H  E  V
       BamHI        EcoRV              HpaI       StyI
      ~~~~~~       ~~~~~~             ~~~~~~     ~~~~~~
951  AGGATCCTGG GCTGATATCG TGATGCACGA AGTTAACCGT CCTAGGTCAG
     TCCTAGGACC CGACTATAGC ACTACGTGCT TCAATTGGCA GGATCCAGTC

 +2  P  K  A  A  P  S  V  T  L  F  P  P  S  S  E  E  L
       StyI
      ~~~~~~
1001 CCCAAGGCTG CCCCCTCGGT CACTCTGTTC CCGCCCTCCT CTGAGGAGCT
     GGGTTCCGAC GGGGGAGCCA GTGAGACAAG GGCGGGAGGA GACTCCTCGA

 +2   Q  A  N  K  A  T  L  V  C  L  I  S  D  F  Y  P
1051 TCAAGCCAAC AAGGCCACAC TGGTGTGTCT CATAAGTGAC TTCTACCCGG
     AGTTCGGTTG TTCCGGTGTG ACCACACAGA GTATTCACTG AAGATGGGCC
```

```
   +2 G  A  V  T   V  A  W   K  G  D  S   S  P  V   K  A  G
1101  GAGCCGTGAC AGTGGCCTGG AAGGGAGATA GCAGCCCCGT CAAGGCGGGA
      CTCGGCACTG TCACCGGACC TTCCCTCTAT CGTCGGGGCA GTTCCGCCCT

   +2  V  E  T  T   T  P  S   K  Q  S   N  N  K  Y   A  A  S
1151  GTGGAGACCA CCACACCCTC CAAACAAAGC AACAACAAGT ACGCGGCCAG
      CACCTCTGGT GGTGTGGGAG GTTTGTTTCG TTGTTGTTCA TGCGCCGGTC

   +2   S  Y  L   S  L  T  P   E  Q  W   K  S  H   R  S  Y
1201  CAGCTATCTG AGCCTGACGC CTGAGCAGTG GAAGTCCCAC AGAAGCTACA
      GTCGATAGAC TCGGACTGCG GACTCGTCAC CTTCAGGGTG TCTTCGATGT

   +2 S  C  Q  V   T  H  E   G  S  T  V   E  K  T   V  A  P
                                          BbsI
                                          ~~~~~~
1251  GCTGCCAGGT CACGCATGAA GGGAGCACCG TGGAGAAGAC AGTGGCCCCT
      CGACGGTCCA GTGCGTACTT CCCTCGTGGC ACCTCTTCTG TCACCGGGGA

   +2  T  E  C  S   *
                          PmeI
                          ~~~~~~~~
1301  ACAGAATGTT CATAGGGGCC CGTTTAAACC CGCTGATCAG CCTCGACTGT
      TGTCTTACAA GTATCCCCGG GCAAATTTGG GCGACTAGTC GGAGCTGACA
                                                pM_Ig_REV 100%
                                                ==========

1351  GCCTTCTAGT TGCCAGCCAT CTGTTGTTTG CCCCTCCCCC GTGCCTTCCT
      CGGAAGATCA ACGGTCGGTA GACAACAAAC GGGGAGGGGG CACGGAAGGA
      pM_Ig_REV  100.0%
      ==========
```

**Figure 10**

| Designation: | Format | Affinity Maturation | Heavy chain from: | Light chain from: |
|---|---|---|---|---|
| MOR06183 | Fab/IgG1 | new H-CDR2 | MOR06183 | MOR03087 (parental) |
| MOR06184 | Fab/IgG1 | new H-CDR2 | MOR06184 | MOR03087 (parental) |
| MOR06185 | Fab/IgG1 | new H-CDR2 | MOR06185 | MOR03087 (parental) |
| MOR06186 | Fab/IgG1 | new H-CDR2 | MOR06186 | MOR03087 (parental) |
| MOR06187 | Fab/IgG1 | new H-CDR2 | MOR06187 | MOR03087 (parental) |
| MOR06188 | Fab/IgG1 | new H-CDR2 | MOR06188 | MOR03087 (parental) |
| MOR06189 | Fab/IgG1 | new H-CDR2 | MOR06189 | MOR03087 (parental) |
| MOR06190 | Fab/IgG1 | new H-CDR2 | MOR06190 | MOR03087 (parental) |
| MOR06192 | Fab/IgG1 | new H-CDR2 | MOR06192 | MOR03087 (parental) |
| MOR06195 | Fab/IgG1 | new H-CDR2 | MOR06195 | MOR03087 (parental) |
| MOR06197 | Fab/IgG1 | new H-CDR2 | MOR06197 | MOR03087 (parental) |
| MOR06200 | Fab/IgG1 | new H-CDR2 | MOR06200 | MOR03087 (parental) |
| MOR06201 | Fab/IgG1 | new H-CDR2 | MOR06201 | MOR03087 (parental) |
| MOR06204 | Fab/IgG1 | new H-CDR2 | MOR06204 | MOR03088 (parental) |
| MOR06214 | Fab/IgG1 | new H-CDR2 | MOR06214 | MOR03088 (parental) |
| MOR06278 | Fab | new L-CDR3 | MOR03088 (parental) | MOR06278 |
| MOR06279 | Fab | new L-CDR3 | MOR03088 (parental) | MOR06279 |
| MOR06347 | IgG1 | new L-CDR3 | MOR03088 (parental) | MOR06278 |
| MOR06348 | IgG1 | new L-CDR3 & H-CDR2 | MOR06214 | MOR06278 |

**FIGURE 11: CD38-expression analysis of Lymphocytes and Erythrocytes**

**A: MOR 3087**

**B: MOR 3088**

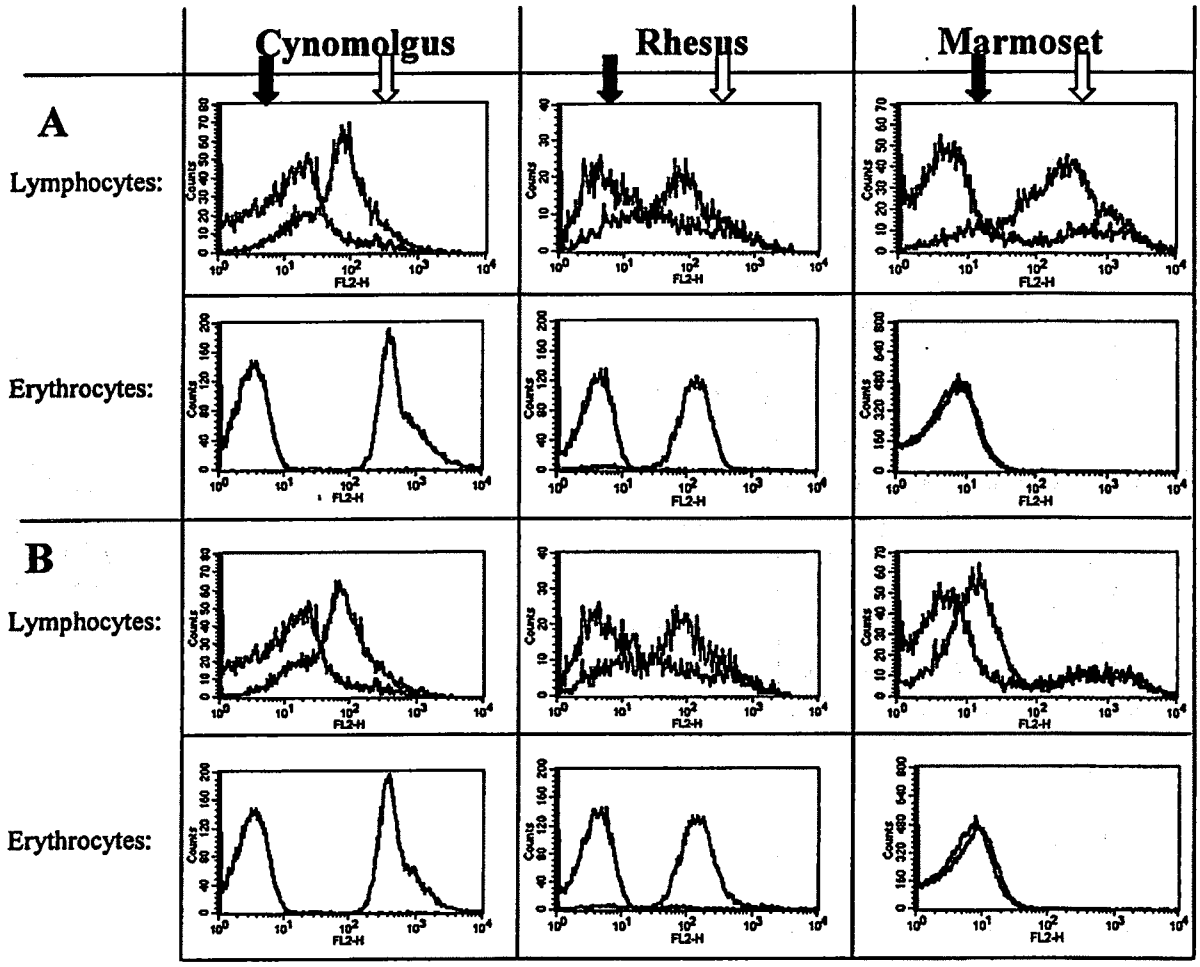


**Figure 12: CD38 expression analysis of Lymphocytes and Erythrocytes**

**MOR 03087:**

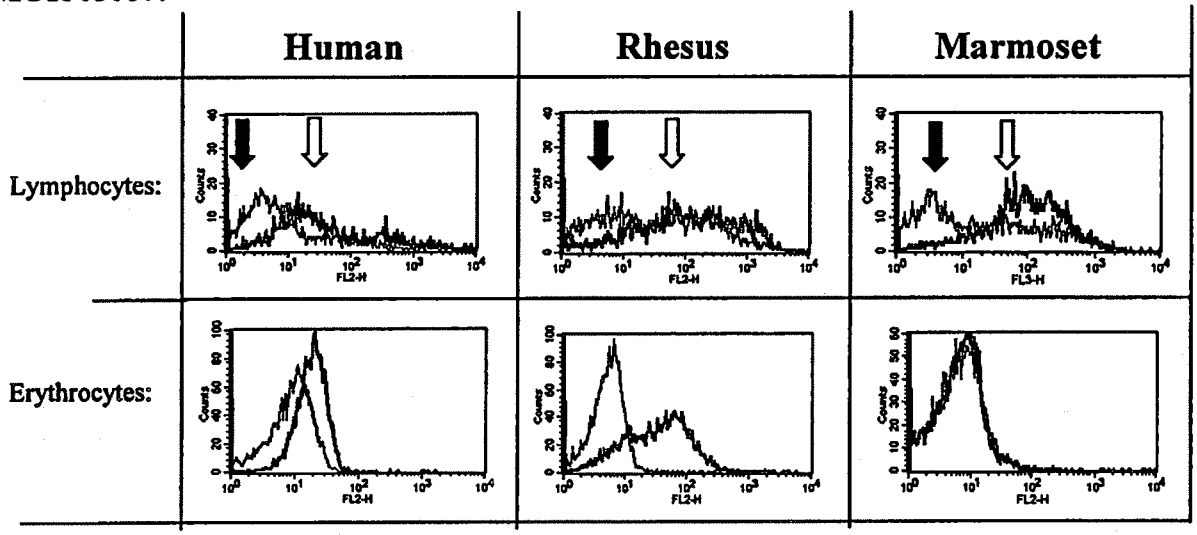


**Figure 13: Overview Cross-Reactivity Anti-CD38 Antibodies**

| | Human | | Rhesus | | Cynomolgus | | Marmoset | |
|---|---|---|---|---|---|---|---|---|
| Species/Tissue: / Anti-CD38 MAbs: | PBMCs | Erythr. | PBMCs | Erythr. | PBMCs | Erythr. | PBMCs | Erythr. |
| 3076 | + | n.d. | - | - | - | - | - | - |
| 3077 | + | - | - | - | - | - | - | - |
| 3078 | + | n.d. | - | - | - | - | - | - |
| 3079 | + | + | - | - | - | - | - | - |
| 3080 | + | +/- | + | - | + | - | - | - |
| 3081 | + | n.d. | - | - | - | - | - | - |
| 3085 | + | n.d. | - | - | - | - | - | - |
| 3086 | + | n.d. | - | - | - | - | - | - |
| 3087 | + | +/- | + | + | + | + | + | - |
| 3088 | + | - | + | + | + | + | + | - |
| 3089 | + | n.d. | - | - | - | - | - | - |
| 3101 | + | n.d. | - | - | - | - | - | - |
| 3102 | + | n.d. | - | - | - | - | - | - |
| 3127 | + | n.d. | - | - | - | - | - | - |
| 3128 | + | n.d. | - | - | - | - | - | - |
| 3129 | + | n.d. | - | - | - | - | - | - |
| 3130 | + | n.d. | - | - | - | - | - | - |
| 3131 | + | n.d. | - | - | - | - | - | - |

+ : positive staining
+/-: weak positive staining
- : negative staining
n.d.: not determined

**Figure 14a:**

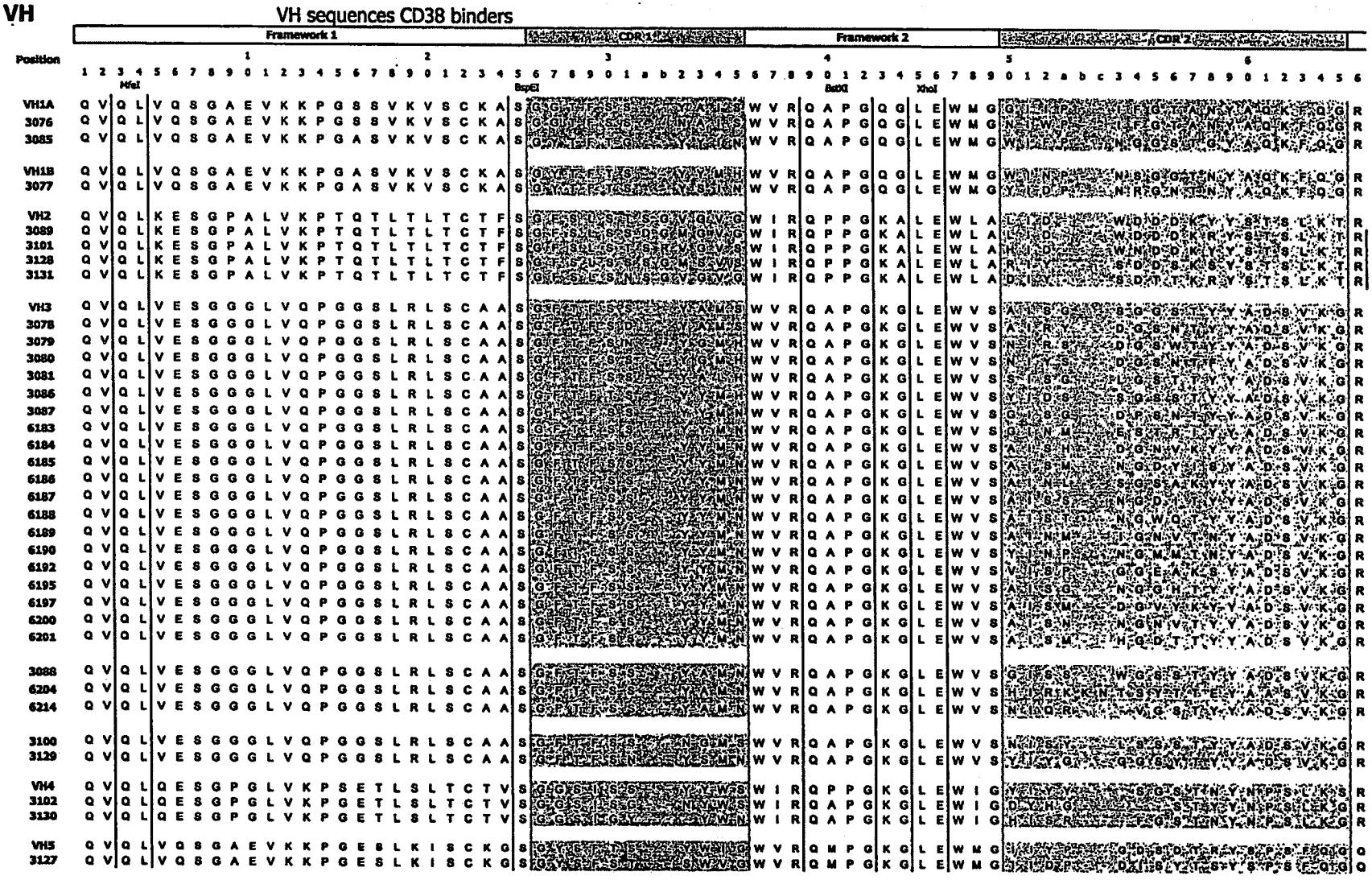

VH
VH sequences CD38 binders
Framework 1
CDR 1
Framework 2
CDR 2
Position
MfeI
BspEI
BstXI
XhoI
VH1A
3076
3085
VH1B
3077
VH2
3089
3101
3128
3131
VH3
3078
3079
3080
3081
3086
3087
6183
6184
6185
6186
6187
6188
6189
6190
6192
6195
6197
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3130
VH5
3127

Figure 14a to be continued :

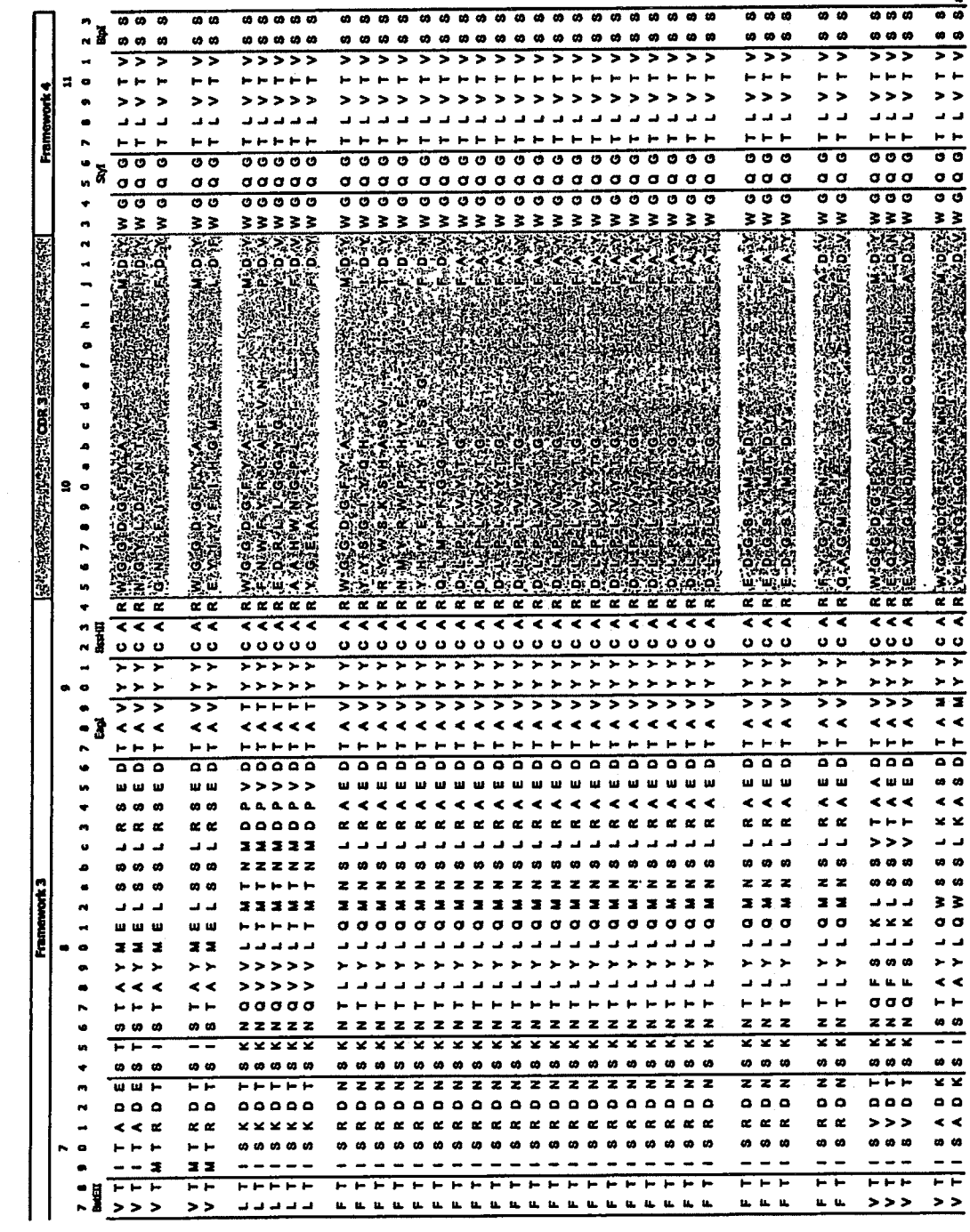
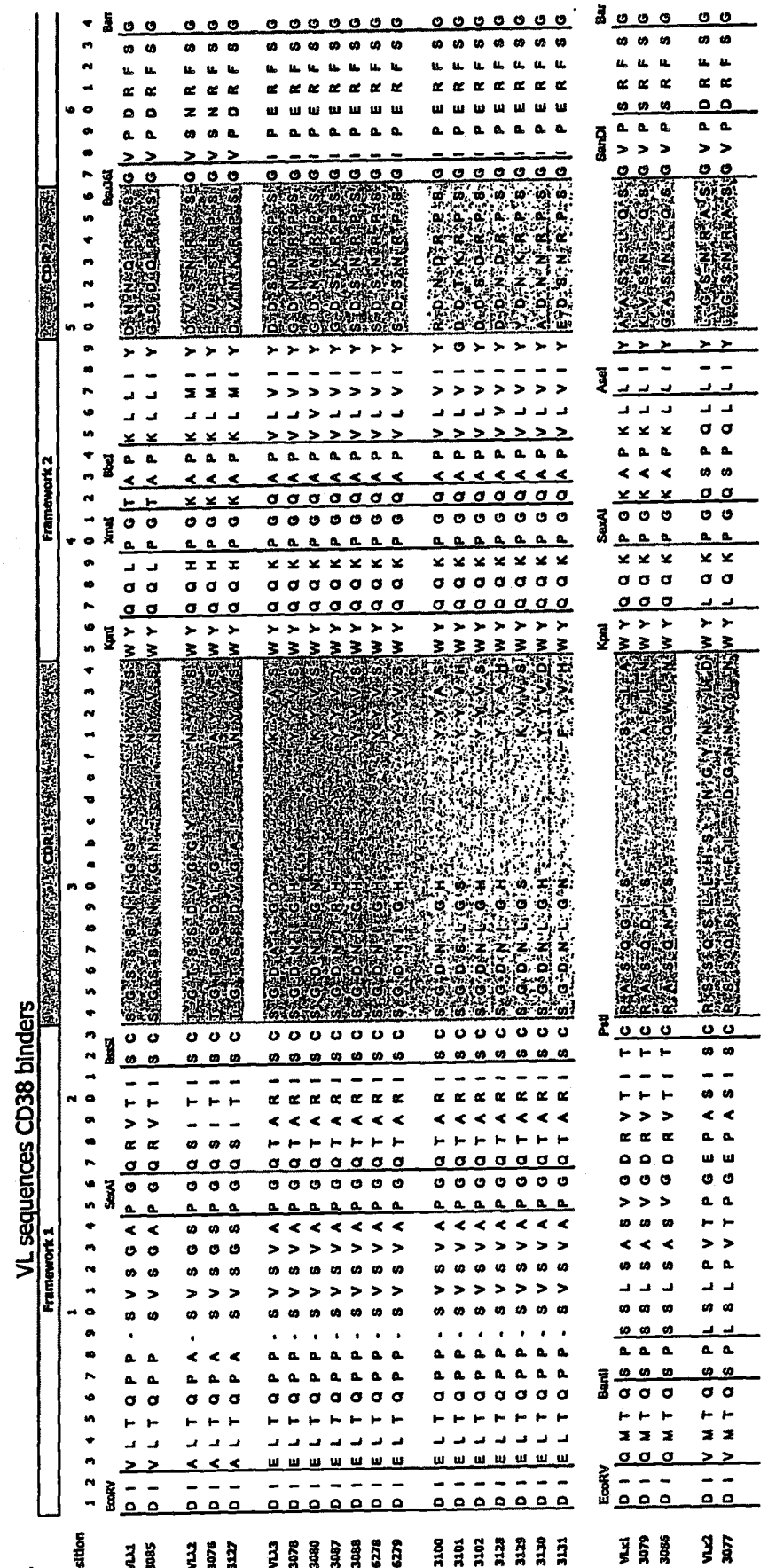


Figure 14b:


VL
VL sequences CD38 binders
Framework 1
CDR1
Framework 2
CDR2
Framework 3
Position
EcoRV
BamII
SexAI
BssSI
KpnI
XmaI
BbeI
AseI
PstI
BauXI
SanDI
BarI
VLk1
3085
VLk2
3076
VLk3
3078
3080
3087
3088
6278
6279
3100
3101
3102
3128
3129
3130
3131
VLx1
3079
3086
VLx2
3077

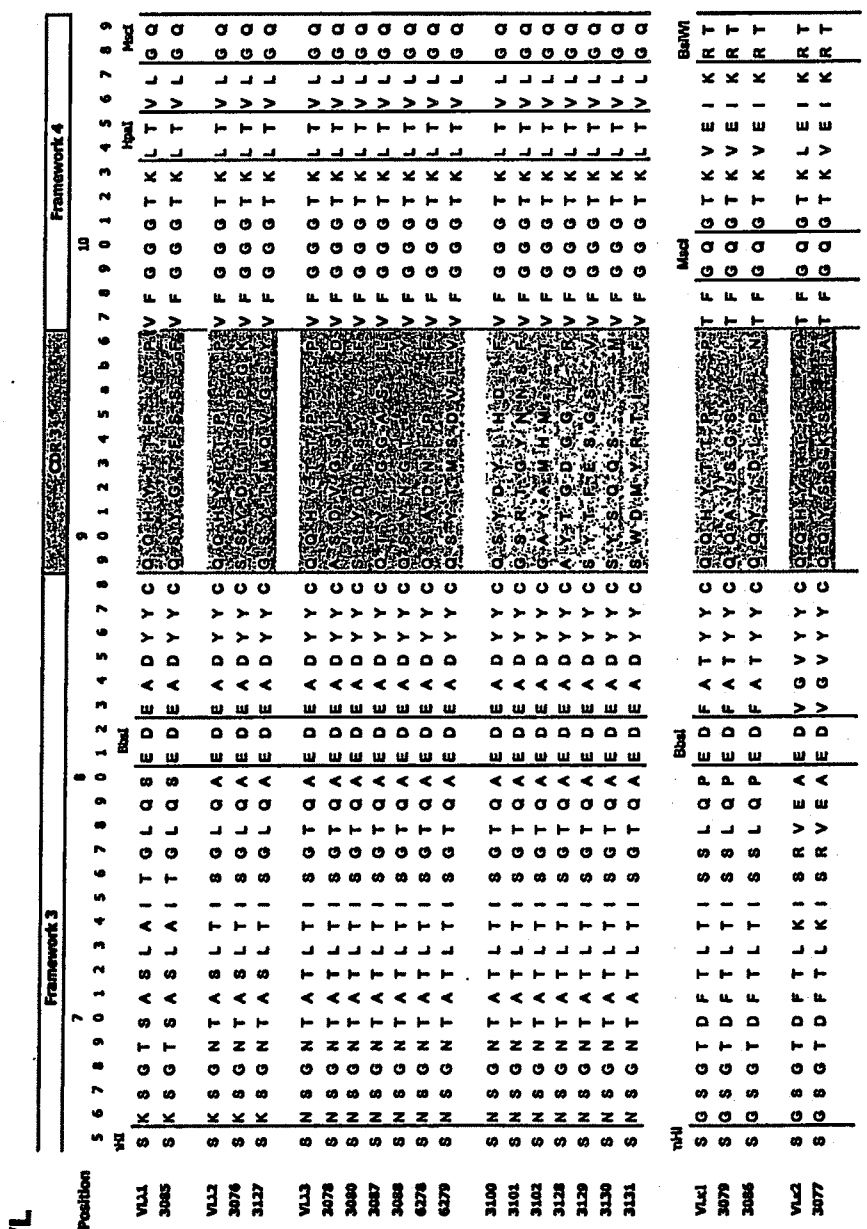



Figure 14b to be continued: