SEQUENCE LISTING

SEQ ID NO: 1 > 10/63 1D4_001.ab1

CAGGTCACCTTGAAGGAGTCTGGTCCTCCGCTGGTGAAACCCACACAGACCCTCACGCTGACCTGCACCTTC
TCTGGGTTCTCACTCAGCACTAGTGGAGTGAATGTGGGCTGGATCCGTCAGCCCCCAGGAAAGGCCCTGGAG
TGGCTTGCACTCCTTTATTGGGATGATGATAGGCGCTACAGCCCATCTCTGAGGAGCAGGCTCACCATCACC
AAGGACACCTCCAAAAACCAGGTGGTCCTTACAATGACCAACATGGACCCTGTGGACACAGCCACATATTAC
TGTGCACACAGACGTTGGGAGGATAGTACTTTCCAACACTGGGGCCAGGGCACCCTCGTCACCGTCTCCTCA
G

SEQ ID NO: 2 > 10/63 1D-1_055

GATGTTGTGATGACTCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAGAGAGCCACCCTCTCCTGCAGG
GCCAGTCAGAGTGTTAACAGCAACTTAGCCTGGTACCAGCAGAAACCCGGCCAGGCTCCCAGGCTCCTCATC
TATGGTGCATCCACGAGGGCCACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGAGTTCACT
CTCACCATCAGCAGCCTACAGTCTGAGGATTTTGCAGTTTATTACTGTCAGCACTATCATAACTGGGGTACG
TTCGGCCAAGGGACCAAGGTGGAAATCAAAC

SEQ ID NO: 3 > 10/63 1E3_061

GAGGTGCAGCTGGTGCAGTCTGGGTCTGAGTTGAAGAAGCCTGGGGCCTCAGTAAAAGTTTCCTGCAAGGCT
TCTGGATACACCTTCCCTACGTATGCTATCAATTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATG
GGATGGATCAACACCAACACTGGGAACCCAATGTATGCCCAGGGCTTCACAAGACGGTTTGTCTTCTCCTGG
GACACCTCTGTCAGCACGGCATATCTGCAGATCAGCAGCCTAAAGACTGAAGACACTGCCGTCTATTACTGT
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TCCTCGG

SEQ ID NO: 4 > 10/63 1E-1_053

GAAATTGTGCTGACTCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGTCGG
GCGAGTCAGCCTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCAAAGCTCCTGATC
TATGCCGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAAATTTCACT
CTCACCATCAGCAGCCTGCAGCCTGATGATTTTGTAACTTACTATTGTCAACAGGCTAACAGTTTCCCTTAC
ACTTTTGGCCAGGGGACCAAGTTGGAGATCAAAC

SEQ ID NO: 5 > 10/63 2A5_014

CAAGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCT
TCTGGAGGCTCCTTCAACAATTACGCGATCGGCTGGGTGCGACAGGCCCCTGGGCAAGGGCTTGAGTGGATG
GGAGGGATCATCACCGTCTTTGGTAGAGGAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCG
GACGAATCCACGAGCACAGCCTACATGGAGTTGAGCAGCCTGAGACCTGAGGACACGGCCGTTTATTATTGT
GTGAGAGACTATACTTTCGTTCGGGGAGTGGCCTCCTGGGAATACTGGGGCCAGGGAACCCTGGTCACCGTC
TCCTCAG

SEQ ID NO: 6 > 10/63 2A-4_049

GAAATTGTGCTGACTCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGTCGG
GCGAGTCAGCCTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCAAAGCTCCTGATC
TATGCCGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAAATTTCACT
CTCACCATCAGCAGCCTGCAGCTTGATGATTTTGTAACTTACTATTGTCAACAGGCTAACAGTTTCCCTTAC
ACTTTTGGCCAGGGGACCAAGTTGGAGATCAAAC

SEQ ID NO: 7 > 10/63 2C3_006.ab1 (

CAGGTACAGCTGCAGCAGTCAGGGGCTGAGGTGACGAGGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCT
TCTGGAGCCTCCATCGGCAGCTATACTGTGCACTGGGTACGACAGGCCCCTGGACAAGGCCTTGAGTGGATT
GGAGGCATCAACCCTATCTTTGGGACAGTGAACTACGCACAGAGGTTCCAGGGCAGACTCACGATTAGCGCG
GACGATTCCACGAGTTCAGCCTACATGGAGATGAGCAGCCTGAAATCTGAGGACACGGCCGTGTATTACTGT
GCGAGATCGCAGCGCCATATTTTGACTGGTCATTACACAGACTATTGGGGCCCGGGAACCCTGGTCACCGTC
TCCTCAG

SEQ ID NO: 8 > 10/63 2C-2_058

GATGTTGTGATGACTCAGTCTCCATCCTCCCTGTCTGCATCTGTCGGAGACAGAGTCTCCATCACTTGCCAG
GCGAGTCAGGACATTAAGAACTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATC
TACGATGCATCCAATTTGGAAACAGGGGTCCCCTCCAGGTTCAGTGGAAGTGGATCTGGGACAGATTTTTCT

TTCACCATCAGCAGCCTGCAGCCTGAAGACATTGCAACATATTACTGTCAACATTATGAAAATCTGCCCGCG
CTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAGAC

SEQ ID NO: 9 > 10/63 2E2_004
GAGGTGCAGCTGGTGGAGACTGGGGGAGGCGTGGTCCAGCCTGGGAAGTCCCTGACACTCTCCTGTGCAGCC
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GCAGTTATTTCATATGACGCAAAGAAGCAATACTATGCAGACTCCGTGAAGGGCCGATTCACCGTCTCCAGA
GACGATTCCGAGGGCAAGGTGTATCTTCAAATGAACAGTCTGAGAGGTGACGACGCGGCTGTTTATTTCTGT
GCGAAACTCCAGAGACCCGACAGCACTGTCTGGCCGTTTGACCAGTGGGGCCAGGGAATCCTGGTCATCGTC
TCCCCAG
SEQ ID NO: 10 > 10/63 2E-2_050
GAAACGACACTCACGCAGTCTCCTTCCACCCTGTCTGCATCTGTCGGAGACACAGTCACCATCACTTGTCGG
GCCAGTCAGAGTATCAGTATGTGGTTGGCCTGGTATCAACAAAAACCAGGGAAAGCCCCAAGACTCCTCATC
TACACGACGTCTAATTTACGAACTGGGGTCCCATCCAGGTTCAGCGGCAGTGGATCTGGCACAGAATTCACT
CTCACCATCAGCAGCCTGCAGCCTGAGGATTTTGCGACTTACTACTGCCAACAGTATAAAACTTCTTGGACG
TTCGGCCAGGGGACGAAGGTGGACATCAA

SEQ ID NO: 11 > 10/63 2F1_031
GAGGTGCAGCTGGTGGAGTCCGGGGGAGCCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCC
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TCAGCAATTAGTGTTAGTGATGGTAATACATACTACGCCGACTCCGTGAAGGGCCGCTTCACCATCTCCAGA
GACACTTCCAGGAACACTCTTTATCTACAAATGAACAGCCTGAGAGCCGAGGACACGGCCCTCTATTACTGT
GCGAATGTTCTAGGTTACTGTACTCCCACCACCTGCTATGAAGATCATTGGGGCCAGGGAACCCTGGTCACC
GTCTCCTCAG
SEQ ID NO: 12> 10/63 2F1_059
GATGTTGTGATGACTCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTTACCATCACTTGCCGG
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TATGCTGCATCCAGTTTGCAAAGTGGGGTCTCATCAAGGTTCAGCGCCAGTGGATCTGGGACAGAATTCACT
CTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCTTCAGCATAATAGTTTCCCCGGA
TCGTTCGGCCAAGGGACCAAGGTGGAAATCAAAC

SEQ ID NO: 13> 10/63 2G2_027.ab1
CAGGTCCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGGCCGGGGAGTCTCTGAAGATCTCCTGTAAGGGT
TCTGGATACACCTTTACCACCTACTGGATCGCCTGGGTGCGCCAGGTGCCCGGGAAAGGCCTGGAGTGGATG
GGGATCATCTATCCTAGTGACTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCAGATCACCATCTCAGCC
GACAAGTCCATCAACACCGCCTACCTGCAGTGGACCAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGT
GCGAGACCCGATGATAGTAGTGGCCTTGAGGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCT
TCAG
SEQ ID NO: 14> 10/63 2G-1_079.ab1
GAAATTGTGCTGACTCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGTCGG
GCGAGTCAGCCTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCAAAGCTCCTGATC
TATGCCGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAAATTTCACT
CTCACCATCAGCAGCCTGCAGCCTGATGATTTTGTAACTTACTATTGTCAACAGGCTAACAGTTTCCCTTAC
ACTTTTGGCCAGGGGACCAAGTTGGAGATCAAAC

SEQ ID NO: 15> 10/63 3D2 Heavy chain
> 10/63 3D
CGGCACTCATATAGAGTGGCTAGTCCTGAGACTCTCTTGTGCAGCCTCTGGATTCACCTTCAGCAGCTATGG
CATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATAGCATATGATGGAATCAA
TAAGTACTACGCAGACTTCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAATACGGTATATTT
GCAAATGATCAGCCTGGGACCTGAGGACACGGCTGTCTATTACTGTGCGAGAGAGTATTGTAGCAGTACAAC
CTGTATAAATTCATTTTTGACTCCCGACTACTGGGGCCAGGGAACCCTGGTCATTGTCTCCTCAG
SEQ ID NO: 16> 10/63 3D-2 light chain_071.ab1 (SEQ ID NO: 110)
GAAATTGTGCTGACTCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGTCGG
GCGAGTCAGCCTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCAAAGCTCCTGATC
TATGCCGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGATTCAGCGGCAGTGGATCTGGGACAAATTTCACT
CTCACCATCAGCAGCCTGCAGCCTGATGATTTTGTAACTTACTATTGTCAACAGGCTAACAGTTTCCCTTAC
ACTTTTGGCCAGGGGACCAAGTTGGAGATCAAAC

SEQ ID NO: 17> 10/63 3E1_030
CAAGTGCACCTGGTGCAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCC
TCTGGATTCACCTTTAGCACCTATTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTG
GCCAACATAAAAGCAGATGGGCGTCAAGAATATTATCTGCAGTCTGTGACGGGCCGATTCACCGTCTCCAGA
GACAACGCCAAGAACTCACTGTATCTGGAAATGAGCAGCCTGAGAGCCGAGGACACGGCTATGTATTACTGT
GTGAGAGACGTCTCGTCGTATAGCATCATCTGGTCTGATGCTTTTGAGATCTGGGGCCAAGGGACAATGGTC
ACCGTCTCTCCAG
SEQ ID NO: 18> 10/63 3E-2_069
GAAACGACACTCACGCAGTCTCCATCCTCCCTGTCTGCATCTGTCGGAGACACAGTCACCATCACTTGCCGG
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TATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACT
CTCACAATCACCAGCCTGCAGCCTGAAGATCTTGCAACTTATTACTGTGTACACCATAATGATTATCCTCGG
ACGTTCGGCCAAGGGACCAAGGTGGAAATCAAAC

SEQ ID NO: 19> 10/63 3F1_026
CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCC
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GGAGGAAACATCCCTATCTTTGGTAAAGCAAGCTACGCAGAGAAGTTCCAGGACAGAGTCACGATTACCGCG
GACGAATCCACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTCTATTACTGT
GCGCGGTTCTTCGTTAAGTATAGTGGGAGCCACTACTACTTTGACTCCTGGGGCCAGGGAACCCTGGTCACC
GTCTCCTCAG
SEQ ID NO: 20> 10/63 3F-2_065
GATGTTGTGATGACTCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGTCGG
GCGAGTCAGCCTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCAAAGCTCCTGATC
TATGCCGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAAACTTCACT
CTCACCATCAGCAGCCTGCAGCCTGATGATTTTGTAACTTACTATTGTCAACAGGCTAACAGTTTCCCTTAC
ACTTTTGGCCAGGGGACCAAGTTGGAGATCAAAC

SEQ ID NO: 21> 10/63 4F6_020.ab1
GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGCGAAGCCGGGGGGGTCCCTTAGACTCTCCTGTGCGGCC
TCTGGATTCACTTTCAGTAATGCCTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTT
GGCCGTATTAAAAACAAAATTGATGGTGAGACAACAGACTACGCTGCATCCGTGAAAGGCAGATTCATCATC
TCAAGAGATGACTCAAAAAACACGGTGTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGAGTAT
TGGTGCACCATATATTTCTATGATAGAAGTGGATACTTCTTTGACCACTGGGGCCAGGGAACCCTGGTCACC
GTCTCCTCAG
SEQ ID NO: 22> 10/63 4F-1_076
GAAACGACACTCACGCAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGCAAAGAGCCACCCTCTCCTGCAGG
GCCAGTCAGAGTGTTAGCAGCTACTTAGCCTGGTATCAACAGAAACCTGGCCAGGCTCCCAGGCTCCTCATC
TTTGATGCGTCCCACAGGGCCACTGGCATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCATT
CTCACCATCAGCAGCCTAGAGCCTGAAGATTTTGCAGTTTATTACTGTCTGCAGCGTGGCAAGTGGCCTTCC
TTCGGCCAAGGGACACGACTGGAGATTAAAC

SEQ ID NO: 23> 10/63 5A6_045.ab1
CAGGTGCAGCTGCAGGAGTCGGGGGGAGGCCTGGTTCAGCCGGGGGGGTCCCTGAGACTCTCCTGTGCAGCC
TCTGGATTCACTTTTAGTGACTATGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTC
TCAGGTCTTAGTGAGAGTGGTCATAATACATACTACGCAGACTCCGTGCTGGACCGGTCCGCCATTTCCAGA
GACAATTCCAAGAGTACCCTGTATCTGCAAATGAACAGCCTGACAGCCGAGGACACGGCCGTATATTACTGT
GCGAGATGTTGGAGGGGTTACGATCCTTTGACTGGCTATTATACGGGATACTACTTTGACTACTGGGGCCCG
GGAACCCTGGTCACCGTCTCCTCAG
SEQ ID NO: 24> 10/63 5A-1_074
GAAATTGTGCTGACTCAGTCTCCATCCTCCCTGTCTGCATCTATAGGAGACAGAGTCACCATCACTTGCCGG
GCGAGTCAGGACATTAGCAATTATTTAGCCTGGTATCAGCAGAGACCAGGGAAAGTTCCTAAGCTCCTGATC
TATGCTGCATCCACTTTGCAATCGGGGGTCTCATCTCGATTCAGCGGCAGTGGATCTGGGACAGATTTCACT
CTCACCATCAGCAGCCTACAGCCTGAAGATGTTGCAACTTATTACTGTCAAAAATATAACAATGCCCCTGTC
ACTTTCGGCGGAGGGACCAAGGTGGAGATCAAAC

SEQ ID NO: 25> 10/63 5B1_043
CAGGTACAGCTGCAGCAGTCAGGCCCAGGACTGGTGAGGCCTTCGGAGACCCTGTCCCTCACGTGCAGTGTC
TCTGGAGGCTCCATCAGCAGTATTACTCCCTACTGGGGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAG
TGGATTGGGAGCCTCGCTTATAGTGGGGACACCTACTACAACCCGTCCCTCAAGAGTCGAGTCACCATATCC

TTAGACACGTCCGAGACCCAGTTCTCCCTGAAGGTGAACTCTGTGACCGCCGCAGACACGGCTCTTTATTTC
TGTGCGAGACACCATAGCAGTGGGAACGCCCTCGACTACTGGGGCCAGGGAATCTTGGTCACCGTCTCCTCA
G

SEQ ID NO: 26> 10/63 5B1_053
GAAACGACACTCACGCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGG
GCCAGTCAGGGCATTAGCAGTTATTTAGCCTGGTATCAGCAAAAACCAGGAAAAGCCCCTAAGCTCCTGATC
TTTGGTGCATCCACTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACT
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ACTTTCGGCGGAGGGACCAAGGTGGAGATCAAAC

SEQ ID NO: 27> 10/63 5C2_041
GAAGTGCAGCTGGTGCAGTCTGGGGCTGAGATGGAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGAGT
TCTGGAGGCACCTTCAACAACTATGCTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATG
GGAGGGATCAACCCTCTCTTTCGTACAGTAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCG
GACGAATCCACGAGCACCGCCTACATGGAGCTGAGCAGCCTGAGATCTGACGACACGGCCGTCTATTACTGT
GCGGGTGCATATTGTAGTGCTACCAGCTGCTCTTCAGGGCAGTGGCTGGTTTACTGGGGCCAGGGAACCCTG
GTCACCGTCTCTTCAG

SEQ ID NO: 28> 10/63 5C1_049.ab1
GATGTTGTGATGACTCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCAACCATCAACTGCAAG
TCCAGCCAGAGTGTTTTTCACAGCTCCAATAATAAGAACTACTTAGCCTGGTACCAGCAGAAACCAGGACAG
CCTCCTAGGCTGCTCATCTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGG
TCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTATTGTCAACAA
TATTATAGTAGTCCTCCGGTATTCACTTTCGGCCCTGGGACCAAAGTGGATGTCAAAC

SEQ ID NO: 29> 10/63 5D1_037
GAAGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCT
TCTGGAGGCACCTTCAGCAGCGATTCTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATG
GGGAGCATCATCCCTATCTTTAGTCGAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACCATTAACGCG
GACGAATCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTCAGGTCTGACGACACGGCCTTATATTTCTGT
GCGAGGACTCCAGTGACTGGTCCTGATCTTGACTACTGGGGCCAGGGAACCCTGATCACCGTCTCCTCAG

SEQ ID NO: 30> 10/63 5D-2_070.ab1
GAAGTTGTGCTGACTCAGTCTCCATCCTCTCTGTCTGCATCTGTAGGAGACAGAGTCACAATCACTTGCCGG
GCAAGTGAGAGCATTAGCACCAATTTAAATTGGTTTCAGCAGAAACCAGGGAAGGCCCCTACGCTCCTGATC
CATGCTGCCTCCACTTTGCAAACTGGGGTCCCATCAAGGTTCATTGGCAGTGGATCTGGGACAGATTTCACT
CTCACCGTCAGCAGTCTGCTACCTGAAGATTTTGCAACTTACTTCTGTCAGCAGACTTACAATACCCCTAGG
ACGTTCGGCCAAGGGACCAGGGTGGAAATCAAAC

SEQ ID NO: 31> 10/63 5H3_044
CAGGTGCAGCTGCAGGAGTCCGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTC
TCTGGTGGCTCCATTAACAATAGTAATTACTACTGGAGCTGGATCCGCCAGTCCCCAGGGAGGGGGCTGGAG
TGGATTGGCGGTATATATTTTAGTGGGACCACCTACTACAACCCGTCCCTCCAGAGTCGAGTCACCATATCC
ATAGACACGTCCAAGAATCAATTCTCCCTGAAGCTGAGCTCTGTGACCGCCGCAGACACGGCTATATATTAC
TGTGTGAGACAGATGAATTACTATCATTTGGGGAGTTCTGTCGGGTTCGACCCCTGGGGCCAGGGAGCCCTG
GCCACCGTCTCCTCCG

SEQ ID NO: 32> 10/63 5H-1_095
GATGTTGTGATGACTCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG
GCCAGTCAGAGTGTTAGTAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGTCTCCTCATC
TATGAAGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACT
CTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCAATTTATTACTGTCAGCAGTATAATGACTGGCTGTGG
ACGTTCGGCCAAGGGACCAAGGTGGAAATCAGAC

SEQ ID NO: 33> 10/63 6C8_036
CAGGTGCAGCTGCAGGAGTCGGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCT
TCTGGAGACACCCTCAACACTTACACTCTCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGCTG
GGAGGGATCATCCATCCCTTTGGCACAGAAAACTACGCACAGAAGTTTCAGGGCAGACTCACGATCACCGCG
GACGAATCCACGAGCACAGCCTACATGGAGCTGAGGAGCCTGACATCTGAGGACATGGCCGTGTATTTTTGT
GCGAGACATCACCGCCATATTTTGACTGGTGAGCGCACCGACTACTGGGGCCAGGGAACCCTGGTCACCGTC
TCCTCAG

SEQ ID NO: 34> 10/63 6C-1_091
GAAATTGTGCTGACTCAGTCTCCATCCTCCCTGTCTGCATCTGTTGGAGACAGAGTCACCATCACTTGCCAG

GCGAGTCAGGACATTCGCAACTCTTTAAATTGGTATCAGCAGAAACCGGGGAAAGCCCCTATCCTCCTGATC
TACGATGCATCCAATTTGAAAACAGGGGTCCCATCAAGGTTCAGTGGAAGTGGATCTGGGACAGATTTCACT
TTCACCATCAGCAGCCTGCAGCCTGAGGATATTGCAACATATTTCTGTCAACATTATGATAATCTCCCCCTA
TTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAAC

SEQ ID NO: 35> 10/63 6E6_034
CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCGGGGTCCTCGGTGAAGGTCTCCTGCAAGTCT
TCTGGAGGCACCCTCAACAGCTATACTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGCCTTGAGTGGATG
GGAGGGATCAATCCCATCTTTGGTACAACAAACAACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCG
GACAAATCCACGAACACAGTCTACATGGAGCTGAGCAGCCTGAGGTCTGACGACACGGCCGTGTATTACTGT
GCGAGAGGGGGCCACCATATTTTGACTGGGCGTTACATTGACGACTGGGGCCAGGGAACCCTGGTCACCGTC
TCCTCAG

SEQ ID NO: 36> 10/63 6E1_058
GATGTTGTGATGACTCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAG
GCGAGTCAGGACATTAGCAACTATTTAAATTGGTATCAGCAGAAAGCAGGGAAAGGCCCTAAGCTCCTGATC
TACGATGCATCCAATTTGGAGACAGGGGTCCCATCAAGGTTCAGTGGAAGTGGATCTGGGACAGATTTTACT
TTCACCATCAGCAGCCTGCAGCCTGAAGATGTCGCAACATATTACTGTCAACAGTATGATAATCTCCCTCGG
CACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAAC

SEQ ID NO: 37> 10/63 7E1_061
GAGGTGCAGCTGGTGGAGACCGGGGGAGGCGTGGTCCAGCCTGGGAGGTCTCTGAAACTCTCCTGTGCAGCG
TCTGGATTCAACTTCAATGAGTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTG
GCTGTCGTAGCATATGATGGAATTAATAAATATTATGAAGACTCTGTGAAGGGCCGATTCACCATCTCCAGA
GACAATTCCAAGAACACACTATCTCTGCAAATGAACAGCCTGCAGCCTGAGGACACGGCTGTGTATTTCTGT
GCGAAATCGGCAGGATCTACTTTGAAAACAGTTATTAGTCTTCTGCAGCCTTTTGATATCTGGGGCCAAGGG
ACAATGGTCACCGTCTCTTCAG

SEQ ID NO: 38> 10/63 7E-1_087
GATGTTGTGATGACTCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG
GCCAGTCAGAGTGTTAGCAGCAACTTAGGCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATC
TATGATGCATCCACCAGGGCCACTGGCATCCCACCCAGGTTCAGTGGCAGTGGGTCTGGGACAGAGTTCACT
CTCACCATCAGCAGCCTGCAGTCTGAGGATTTTGCAGTTTATTACTGTCAGCAGTATCATGACTGGCCTCCG
TACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAAC

SEQ ID NO: 39> 10/63 7G1_055
GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGCGAAGCCGGGGGGGTCCCTTAGACTCTCCTGTGCGGCC
TCTGGATTCACTTTCAGTAATGCCTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTT
GGCCGTATTAAAAACAAAATTGATGGTGAGACAACAGACTACGCTGCATCCGTGAAAGGCAGATTCATCATC
TCAAGAGATGACTCAAAAAACACGGTGTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGAGTAT
TGGTGCACCATATATTTCTATGATAGAAGTGGATACTTCTTTGACCACTGGGGCCAGGGAACCCTGGTCACC
GTCTCCTCAG

SEQ ID NO: 40> 10/63 7G-1_081
GATGTTGTGATGACTCAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGCAAAGAGCCACCTTCTCCTGCAGG
GCCAGTCAGAGTGTTAGCAGCTACTTAGCCTGGTATCAACAGAAACCTGGCCAGGCTCCCAGGCTCCTCATC
TTTGATGCGTCCCACAGGGCCACTGGCATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCATT
CTCACCATCAGCAGCCTAGAGCCTGAAGATTTTGCAGTTTATTACTGTCTGCAGCGTGGCAAGTGGCCTTCC
TTCGGCCAAGGGACACGACTGGAGATTAAAC

SEQ ID NO: 41> 10/63 7H-1_060
CAGGTGCAGCTGGTGCAGTCTGGGGGAGGCTTGGCGAAGCCGGGGGGGTCCCTTAGACTCTCCTGTGCGGCC
TCTGGATTCACTTTCAGTAATGCCTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAAGGGCTGGAGTGGGTT
GGCCGTATTAAAAACAAAATTGATGGTGAGACAACAGACTACGCTGCATCCGTGAAAGGCAGATTCATCATC
TCAAGAGATGACTCAAAAAACACGGTGTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGAGTAT
TGGTGCACCATATATTTCTATGATAGAAGTGGATACTTCTTTGACCACTGGGGCCAGGGAACCCTGGTCACC
GTCTCCTCAG

SEQ ID NO: 42> 10/63 7H-1_038
GAAATTGTGCTGACTCAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGCAAAGAGCCACCCTCTCCTGCAGG
GCCAGTCAGAGTGTTAGCAGCTACTTAGCCTGGTATCAACAGAAACCTGGCCAGGCTCCCAGGCTCCTCATC
TTTGATGCGTCCCACAAGACCACTGGCATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCATT
CTCACCATCAGCAGCCTAGAGCCTGAAGATTTTGCAGTTTATTACTGTCTGCAGCGTGGCAAGTGGCCTTCC
TTCGGCCAAGGGACACGACTGGAGATTAAAC

SEQ ID NO: 43> 10/63 8F1_051
GAAGTGCAGCTGGTGCAGTCTGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTC
TCTGGTGGCTCCATCAGCTCTAGTTCTTACTACTGGGGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAA
TGGATTGGGGGTATCTATTACACTGGGACCACCTACTACAATCCGTCCCTGAACAGTCCAGTCACCATATCC
ATAGACATGTCCAAGAATCATTTCTCCCTGGAGTTGACCTCTGTGACCGCCGCAGACACGGCTGTTTATTAC
TGTGCGAGACAAGCGGTTTTTGCAGAAGCAACTGGTACAACCATTGGGGCCATTGACTACTGGGGCCAGGGG
ACCCTGGTCGTCGTCTCCTCAG
SEQ ID NO: 44> 10/63 8F-1_036
GATGTTGTGATGACTCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCATTATCACTTGTCGG
GCGAGTCAGAGTTTTAACAACTGGTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATC
TATGGTGCATCCACTTTACAAAGTGGGGTCCCATCAAGATTCAGCGGCAGTGGATCAGGGACAGATTTCACT
CTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAGCAGTTTCCCGTGG
ACGTTCGGCCAGGGGACCAAGGTGGAGATCAAAC

SEQ ID NO: 45> 10/50_1B1
GAGGTGCAGCTGGTGGAGTCCGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCTCTCACGTGCAGTGTC
TCTGGTGACTCCATCACTAATTACTACTGGGCCTGGATCCGGCAGCCCCCAGGGAAGAGGCTGGAATGGATT
GCGAATCTGTATTACACTGGGGGTACCAATTACAACCCCTCCCTCAAGGCTCGACTCACCACGTCAGTAGAC
ACATCCAAGAACACCTTTTCCCTCAAGGTGAGGTCTGCGACCGCTGCGGACACGGCCGTATATTATTGTGCG
AGAGTGACATCATTGAGTGGGAGCGAGGTCTACGGTATGGACGTCTGGGGCCAAGGGATCACGGTCACCGTC
TCCTCA
SEQ ID NO: 46> 10/50_1B1
GATGTTGTGATGACGCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAG
GCGAGTCAGGACATTAGTAACTCTTTAACTTGGTTTCAGCAGAAACCAGGGAAAGCCCCTAGGCTCCTGATG
TACGCTGCGTCCAATTTGCAAACAGGGGTCCCATCAAGGTTCAGTGGAAGTGGATCTGGGACAGATTTTACT
TTCACCATCAGCAGCCTGCAGCCTGAAGACATTGCAACATATTACTGTCAACAGTATGATAGTATCCCGATC
ACCTTCGGCCAGGGGACACGACTGGAGCTTAAAC

SEQ ID NO: 47> 10/50_1D8
GAGGTCCAGCTGGTGCAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCTGCC
TCTGGATTCACCTTCGCTCCCTTTAGCCTGACCTGGGTCCGCCAGGCTCCAGGGAAGGGACTGGAGTGGGTC
TCATCCATTACTCCTAGTAGTAATTACATATTCTATGCAGACTCAGTGAAGGGCCGATTCACCATCTCCAGA
GACGACGGCAGGAAGTCAGTGTATCTGCAGATGAACAGCCTCAGAGTCGAGGACACGGCTGTGTATTACTGT
GCGAGAGATCCTTCCGGGACTTATGACTACAACTACTACGCAATGGACGTCTGGGGCCCCGGGACCACGGTC
ACCGTCTCCTCA
SEQ ID NO: 48> 10/50_1D1
GAAATTGTGTTGACACAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGTGAAAGAGCCACCCTCTCCTGCAGG
GCCAGTCAGACTGTTGGTAGTAGTTATTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCGCCCAGGCTCCTC
ATCTATGGTACATCCACCAGGGCCACTGGCATCGCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTC
ACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTCTATTACTGTCAACAGTATGGTGGCTCACCT
CCGATCACCTTCGGCCAAGGGACACGACTGGAGACTAAAC

SEQ ID NO: 49> 10/50_2F1
CAGCTGGTGGAGACTGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCAGGT
TCTGGTTACCCCTTTAGTAGTCATGGTTTCAGTTGGGTGCGACAGGCCCCTGGACAGGGGCTTGAGTGGATG
GGATGGACCACCGCTTACAATGGTGAAACACAATATGCACAGAAGTTCCTGGGCAGAGTCACCATGACCACA
GACACTTCCACGAACACAGCCTACATGGAGCTGAGGAGCCTGAGATCTGACGACACGGCCATCTACTATTGT
TATAGCAGCGGTCCTCGATGGGGTCATTTTGATATCTGGGGCCAAGGGACAGTGGTCACCGTCTCTTCAG
SEQ ID NO: 50> 10/50_2F3
GACATCCAGATGACCCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG
GCCAGTCAGAGTGTCGACTTAGCCTGGTTCCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGT
ACATCCAGCAGGGCCACTGGCATCCCAGAAAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACC
ATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCACCAATATGATTCCTCACCGTGGACGTTC
GGCCAAGGGACCAGGGTGGAATTCAAAC

SEQ ID NO: 51>10/50_3H1
CAGGTGCAGCTGCAGGAGTCGGGGGGAGGCTTGGTGCAACCGGGGGGGTCCCTGCGACTCTCCTGTGCAGCC
TCTGGATTCAATTTTGGCGACTATGTCATGGCCTGGGTCCGCCAGGCTCCAGGCAAGGGCCTGGAGTGGGTC

TCAGTTATTTATAATGGTGGAAGTAGTACATATTATGCAGACTCCGTGAAGGGCCGGTTCACCGTCTCCAGG
GATAATTCCAGGAACACGGTGTCTCTGCACATGAGCAGCCTGAGCGCCGAAGACACGGCCCGATATTACTGT
GCGAAAGATCGACAGTCGTTGCATGACCCTGGTTCGGGGAGTTACGTCGCTCTTGACCACTGGGGCCAGGGA
ACCCTGGTCACCGTCTCCTCAG

SEQ ID NO: 52> 10/50_3H1
GAAATTGTGATGACACAGTCTCCATCCTCCCTGCCCGCGTCTCTAGGAGACAGAGTCACCATCACTTGCCGG
GCAAGTCAGAGCATTAGCGGTTCTTTAAATTGGTATCAGCAGAGACCAGGGAAAGCCCCTAAACTCCTGATC
TTTGCTGCATCCCGTTTACACAGTGGGGTCCCTTCAAGGTTCAGTGGCAGTGGATCTGGGCCAGACTTCACT
CTCAGCATCAGCAGTCTGCAACCTGAAGATTTTGCAACTTACTACTGCCAACAGGGGAGCACTTTCGGCGGC
GGGACCAAGGTGGAGTTCAAAC

SEQ ID NO: 53> 10/50_4B2
GAAGTGCAGCTGGTGCAGTCAGGCCCTGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACATGCACTGTC
TCTGGTGGCTCCCTCAGCAGTGATGGTCACTCCTGGGGCTGGCTCCGCCAGCCCCCAGGTAAGGGACTGGAG
TGGATTGGTAACATCTATTATACTGGGACCACCTACTACAATCCGTCCCTCGAGAGTCGAATCACCGTATCC
GTTGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAACTCTGTGGCCGCCGCAGACACGGCTGTCTATTAC
TGTGCGGCCTGGAACGCGGGACCATCGTACTATTTTCACTACTGGGGCCTGGGAACCCTGGTCACCGTTTCC
TC

SEQ ID NO: 54> 10/50_4B1
GAAATTGTGCTGACTCAGTCTCCAGCCACCTTGTCTGTGTCTCCAGGGGAGAGAGCCACCCTCTCCTGCAGG
GCCAGTCAGAGTGTTAGCAACAACTTAGCCTGGTACCAGCAGAGACCTGGCCAGGCTCCCAGGCTCCTCATC
TATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGAGTTCACT
CTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTATGAGTCCTGGTGGACG
TTCGGCCAAGGGACCAAGGTGGAAGTCAAAC

SEQ ID NO: 55> 10/50_5A1
CAGGTACAGCTGCAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCGCTGTT
TATGATGGGTCCTTCAGTGGTTTCTCCTGGACCTGGATCCGCCAGTCCCCAGGGAAGGGGCTGGAGTGGATT
GGGGAAATCAATCACAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGACTCACCATTGCACTTGAC
ACATCCACGAACCAGTTCTCACTGAGGCTGACCTCTGTGAGCGCCGCGGACACGGCTATTTATTATTGTGCG
CTATCTCTGCAAACTCTGGTTCGGGGACTTGTTTATATTAACTTTGACTACTGGGGCCAGGGAAGTCTGGTC
ACCGTCTCCTCAG

SEQ ID NO: 56> 10/50_5A1
GACATCCAGATGACCCAGTCTCCAGCCTCCCTGTCTGCATCTGTGGGAGACCGAGTCACCATCACTTGCCGG
GCAAGTCAGGCCATTACCACCTATTTAAATTGGTATCAACAGAAGCCAGGGAAAGCCCCTAACCTCCTGATC
TATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCACTGGCAGTGGATCTGGGACAGACTTCACT
CTCACCATCAGCAGTCTGCAACCTGGAGATTTTGCAACTTACTACTGTCAACAGAGTTACAATTTGCCTCGG
ACGTTCGGCCATGGGACCAAGGTGGAAATCAAAC

SEQ ID NO: 57> 10/50_5C6
GAGGTGCAGCTGGTGGAGTCTGGGGCTGAGGTGAGGAGGCCTGGGGCCTCAATGAAGGTTTCCTGCAAGGCA
TCTGGATACACCTTCAGCAGCTACTATATACACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGGTG
GGAATAATCAACCCTAGGGGTGGAAGCGCAAGCGTCGCACAGAAGTTCCAGGGCAGAGTCACCCTGACCAGG
GACACGTCCACGAGTACAGTCTACATGGAGTTGAGTAGCCTGAGATCTGAGGACACGGCCCTGTATTTCTGT
GCGAGAGCCGGCGTAGCCCTTTTCTATGACAGTAGTGGGTATGACCCAACTCCCTATGATGCTTTTGAAGTC
TGGGGCCAAGGGACAATGGTCACCGTCTCTTCA

SEQ ID NO: 58> 10/50_5C1
GAAATTGTGATGACGCAGTCTCCCGCCACACTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGTAGG
GCCAGTCAGAGTGTTAGAAGTTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATC
TTTGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGAGTTCACT
CTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCACCAGTATAATCACTGGCCTCGG
ACGTTCGGCCAAGGGACCAAGGTGGAAATCAAAC

SEQ ID NO: 59> 10/50_5D6
GAGGTGCAGCTGGTGCAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACACTCCTGTGTAGCC
TCTGGATTCACCTTTACCACCCATGCCATGGGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTC
TCTGCTATTAGTGCCAGTGGGGATGGCACATACTATGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGA
GACAATTCCAAGAACACTCTCTTTCTGCAAATGAACAGCCTGACGGCCGCGGACACGGCCTTTTATTACTGT
GCGACCATTGACTGGAGCGACAAGGGGGTCTTTGACTACTGGGGCCAGGGAATCCCGGTCACCGTCTCCTCA

SEQ ID NO: 60> 10/50_5D2

GAAATTGTGTTGACGCAGTCTCCATCTTCCGTGTCTGCGTCTGTAGGAGACAGAGTCACCATTACTTGTCGG
GCGAGTCAGGCTGTTGGCAGCTTGTTAGCCTGGTATCAGCAGAAGCCAGGGAAACCCCCTAGGCTCCTTGTC
TATACTGCATCCACTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACT
CTCACCATCACCAGCCTACAGCCTGAAGACTTTGCAACTTACTCTTGTCAACAGGCTTTCAGTTTCCCGTGG
ACGTTCGGCCAAGGGACCAAGGTGGAAATCAGAC

SEQ ID NO: 61> 10/50_6B1
GAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGGAGAAGCCTGGGGCCTCAGTGAAGATTTCCTGCAAGGCA
TCTGGATACACTTTCGCCAACAACTATATACACTGGGTGCGACAAGCCCCTGGACAAGGGCTTCAGTGGATG
GGAGTCATCAACCCTAGAGGTGGTAGTGCAGCCTCGGCACAGATGTTCCAGGGCAGAATCACCATGACCAGG
GACACGTCCACGAGCACAGTCTACCTGGACCTGCGAAGCCTGAGATCTGAGGACACGGCCGTCTATTACTGT
GCGAGAGGGGGAAGGGCCTATTACTATGATTCTTATACGACCCCCCGAGACGGAGAGTCGTGGTGGTTCGAC
CCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
SEQ ID NO: 62> 10/50_6B2
GAAACGACACTCACGCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGGGACAGAGTCACCATCACTTGCCAG
GCGAGTCAAGACATTAGGAAATATTTGAATTGGTATCAGCAGAAACCAGGAAAAGCCCCTAAAGTCCTGATC
TACGATGCATCCAATTTGAAGACAGGGGTCCCATCAAGGTTCAGTGGAGGTGGATCTGGGACAGATTTTACT
TTCACCATCAGCAGCCTGCAGCCTGGAGATATTGCAACATATTACTGTCAGCACTCTGATTATCTCCCGATC
ACCTTCGGCCAAGGGACACGACTGGAGATTGAAC

SEQ ID NO: 63> 10/50_6D3
CAGGTACAGCTGCAGCAGTCAGGGGCTGAGGTAAAGAAGCCTGGGGCCTCAGTTCACCTTTCCTGCAAGGCA
TCTGGATACTCCTTCACCAGCAACTATATGCACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAATGGATG
GGGATAATCAACCCTCGTGGTGGAAGCACAAGCATCGCACAGCAGTTCCAGGGCAGAATCACCATGACCAGG
GACACGTCCACGAGCACAGTCTACATGGAACTGAGAAGCCTGACATCTGAGGACACGGCCGTTTATTACTGT
GCGAGAGCCGGCCCAGCCCTTTATTATGATAGTAGTGGTTATGACCCAACTACTTATGATTCTTTTGAAGTC
TGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
SEQ ID NO: 64> 10/50_6D1
GATGTTGTGATGACTCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG
GCCAGTCAGGGTGTGAGAAGCTATTTAGCCTGGTATCAGCAGAAACCTGGCCAGGCGCCCAGGCTCCTCATC
TATGGTGCGTCCACTAGGGCCACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGTTCTGGGACAGAGTTCACT
CTAACCATCAACAGCCTGCGGTCTGAAGATTCTGCAGTTTATTACTGTCAGCAGTATAATCACTGGCCTCGG
ACGTTCGGCCAAGGGACCAAGGTGGAAATCAAAC

SEQ ID NO: 65> 10/50_6E1
GAAGTGCAGCTGGTGCAGTCTGGGGGAGGCTTGGTACAGCCGGGGGGGTCCCTGAGACTCTCCTGTGTAGCC
TCTGAATTCAGCTTTAGCACCTATGCCATGGGCTGGGCCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTC
TCAGTTATTTATACCGGCGGAGGTAGCACCTACTATGCAGACTCCGTGAGGGGCCGGTTCACCATCTCCAGA
GATAATTCCAAGAACACCCTGTATGTGCAAATGAACAGCCTGACAGTCGACGACACGGCCGTATATTACTGT
GCGGGAGGAGGAATAGTGTCAACGATGGGCGCTTTTGGTTTCTGGGGCCAAGGGACTATGGTCGCCGTCTCT
TCAG
SEQ ID NO: 66> 10/50_6E1
GAAACGACACTCACGCAGTCTCCATCCTTCCTGTCTGCCTCTGTGGGAGACAGAGTCACCATCACTTGCCGG
GCCAGTCAGGAGTTCAGCAGTTATGTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAACTCCTGATT
TATGGTGTATCCACTTTGCACAGTGGGGTCCCATTAAGGTTCAGCGGCGGTGGCTCTGGGACAGAATTCATT
CTCACGATCAGCGGCCTGCAGCCTGAAGATGTCGGAACTTACTACTGTCAACAGACTGGGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAAC

SEQ ID NO: 67> 10/50_7A1
CAGGTCCAGCTGGTGCAGTCTGGGGGAGGGTTGGTACAGCCTGGAGGGTCCCTGAGACTCTCCTGTGCAGCC
TCTGGATTCACCTTCAGTAGTTACGAAATGAACTGGGTCCGCCAGGCTCCAGGGAAGGGCCTGGAGTGGATT
TCATACATTAGTCGTAGTGGTACCGCCACATACTACGCAGACTCTGTGAAGGGCCGATTCACCATCTCCAGA
GACAACGCCAAGAACTCACTGTATCTGCAAATGAACAGCCTGAGGGCCGAGGACATGGCTGTTTATTACTGT
GCGGGAGAAGGTTACTTTGGTTCGGCCGCCATCAACTACTTTGCCTTCTGGGGCCAGGGAACCCTGGTCACC
GTCTCCTCAG
SEQ ID NO: 68> 10/50_7A1
GAAACGACACTCACGCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGGGACAGAGTCACCATCACTTGCCGG
GCAAGTCAGACCATTGGCACCTATTTACATTGGTATCAGCAGAAACCAGGGAAAGCCCCGAAGCTCCTGATC
TTTGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACT

CTCACCATCAGCAGTCTGCAACCTGAAGATTTCGCAACTTACTACTGTCTACAGACTTACAGTAGTTTGTAC
ACTTTTGGCCAGGGGACCAAGCTGGAGATCAAAC

SEQ ID NO: 69> 10/50_7C3
GAGGTGCAGCTGGTGGAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCA
TCTGGATACACCTTCAGCAACTACTATATACACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATG
GGAGTAATAAACCCTCGTGGTGGAAGCGCAAGTAGTGCAGAGAAGTTCCAGGGCAGAATCACCATGACCAGG
GACACGTCCACGAGCACAGTTTACATGGAGCTGAGCAGCCTGAGATCGGAGGACACGGCCGTATTTTACTGT
GCGAGAGGGGGATGGGCCTATTATTATGATAGTTACACGACCCCCCGAGACGGACAGTCGTGGTGGTTCGAC
CCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
SEQ ID NO: 70> 10/50_7C1
GATGTTGTGATGACTCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAG
GCGAGTCAGGACATTAGAAACTTTTTAAATTGGTATCAGCACAAACCAGGGAAAGCCCCAAAGGTCCTGATA
TACGATGCCTCCAAATTGAAAACAGGGGTCCCATCAAGGTTCAGTGGAAGTGGATCTGGGACAGACTTTACT
TTCACCATCCGCAGCCTGCAGCCTGAAGATATTGCGACGTATTACTGTCAACAGTCTGACAATCTCCCGATC
ACCTTCGGCCAAGGGACACGACTGGAGATTAAAC

SEQ ID NO: 71> 10/50_7E1
CAGGTACAGCTGCAGCAGTCCGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTC
TCTGGTGGCTCCATCAATAGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATT
GGGTATATTCATTACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGAGTCACCATATCAGTAGAC
ACGTCCAAGAACCACTTCTCCCTGAAGCTGAACTCTGTGACCGCCGCAGACACGGCCGTCTATTACTGTGCG
AGACATGATTGTAGTGATACCACCTGCCGTGAATACTTCCAGCACTGGGGCCAGGGCACCCTGGTCACCGTC
TCCTCA
SEQ ID NO: 72> 10/50_7E1
GAAACGACACTCACGCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGG
GCAAGTCAGAGCATTAGCACCTTTTTAAATTGGTATCAGAAGAAACCTGGGAAAGCCCCTGAGCTCCTGATC
TCTGCAGCATCCACTTTGCAAAGTGGCGTCCCATCAAGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACT
CTCACCATCAACAGTCTGCAACCCGGAGACTTTGCGACTTACTACTGTCAAGAGAGTTACAGTATGATGTAC
ACTTTTGGCCAGGGGACCAAGGTGGAGATCAAAC

SEQ ID NO: 73> 10/50_7H1
GAGGTGCAGCTGGTGGAGACTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCGTGAGACTCTCCTGTGCAGCC
TCTGGATTCACCTTTAGTAGATATTGGATGAGTTGGGTCCGCCAGGCTCCAGGAAAGGGGCTGGAGTGGGTG
GCCAACATAAATCAAGGTGGAAGTGAGAGGCACTACGTGGACTCTGTGAAGGGCCGATTCACCATCTCCAGA
GACAACGCCAGGAATTCGTTCTACTTAGAAATTAGGAACCTGAGAGTCGAGGACACGGCCGTCTACTATTGT
GCGAGAGAGGGGATGGTCGAGGTGACCGCACTCTCCTTCTTGGACTACTGGGGCGAGGGAAACCTGGTCGCC
GTCTCCTCAG
SEQ ID NO: 74> 10/50_7H1
GAAACTGCGTTCACGCAGTCTCCATCCTCCCTGTCTGCATCCGTTGGAGACACAGTCACCATCACTTGCCGG
GCAAGTCAGACCATTGGCACCTTTTTAAATTGGTATCAGCTGAAGCCAGGGAAAGCCCCTAAACTCCTGATC
TTCGCTACATCTAACTTGCAAGGTGGCGTCCCATCAAGGTTCAGTGGCAGTGGATCTGGGGGAGATTTCACT
CTCACCATCACCAGTCTGCAACCTGAGGATTTTGGAACTTACTACTGTCAACAGACTTACAGTATGATTTAC
ACTTTTGGCCAGGGGACCAGGGTGGACATCAAAC

SEQ ID NO: 75> 10/50_9B1
CAGGTCCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGAGAGTCTCTAAAGATCTCTTGTAAGGCC
TCTGGATACATCTTTACCAGCTACTGGATCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTAGAGTGGATG
GGGATTATCTATCCTGGTAACTCTGACCCCAGATACAGCCCGTCCTTCCAGGGCCAGGTCACCATCTCAGCC
GACAAGTCCAGCAGTACCGCCTACCTGCAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATATATTACTGT
TCGAGACTCGACCACTACTTCTACTACGGTATGGACCTCTGGGGCCAGGGGACCACGGTCACCGTCTCCTCA
SEQ ID NO: 76> 10/50_9B1
GATGTTGTGATGACTCAGTCTCCAGGCGCCCTGTCTCTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG
GCCAGTCAGACTTTTAGCAGCATCTACTTATCCTGGTTCCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTC
ATTTATGGTGCATCCAACAGGGCCGATGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTC
ACTCTCATCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTTTATTATTGTCAGCACTATGACAACTCCTTC
TTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAAC

SEQ ID NO: 77> 10/50_9E2
CAGGTGCAGCTGGTGCAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGTAGCC

TCTGGATTCACCCTCAGAAGCTATGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTC
TCATCTATTAGTGATAGTGATGATAGCACATACTACGCAGACTCCGTGAAGGGCCGCTTCACCATCTCCAGA
GACGATTCCAAGAACACGCTGTATCTGCAAATGAGCAGCCTGAGAGCCGAGGACACGGCCGTATTTTTCTGT
GCGACGACAAACTGGGGTGTTTCGGTCAAGCCGGGTACTTTTGATATCTGGGGCCAAGGGACAGTGATCACC
GTCTCTTCA

SEQ ID NO: 78> 10/50_9E2
GACATCCAGTTGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGTCGG
GCGAGTCAGGGTATTAGCAGCTACTTAGCCTGGTATCAGCAGAAGCCAGGGAAAGCCCCTAAGCTCCTGATC
TTTGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGCTCTGGGACAGATTTCACT
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ACGTTCGGCCCAGGGACCAAGGTGGAAATCAAAC

SEQ ID NO: 79> 10/50_11E1
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TCAGTCATTTTTAACGGAGGTAGTAGTACATACTATGCAGACTCCGTGAAGGGCCGGTTCACCATTTCCAGA
GATAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGT
GCGAAATTTGCGGCCCCGCCGAGTGGCTGGTGTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
G

SEQ ID NO: 80> 10/50_11E1
CCCTGTCTGCATCTGTGGGAGACAGAGTCACCATCACTTGCCGGGCCAGTCAGAGTGTTAGTAACTGGTTGG
CCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAACTCCTGATCTATAAGGCGTCCACTTTAGAAAGTGGGG
TCCCATCAAGGTTCAGCGGCAGCGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAGCCTGATG
ATTTTGCAACTTATTACTGCCAACAGTCTGGGACATTCGGCCAAGGGACCAAGGTGGAAATCAAAC

SEQ ID NO: 81> 1st_BASE_973574_A3_3M2_D3_H_2_1146
GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCGGCCGGGGGGGTCCCTGAGACTCTCCTGTGTGGGC
TCTGGATTCAATTTTGGGAGGCATTGGATAAGCTGGGTCCGCCAGGCTCCAGGGAACGGGCTGGAGTGGGTG
GCCAATATAAAAGAAGACGGAAGTGCGAAGTACTATGTGGAGTCTGTGAAGGGCCGATTCACCATCGTCAGA
GACAACGCCAAAAATTCGCTGTTTCTGCAAATGAGCAGCCTGAGAGCCGAGGACACGGCAGTATATTACTGT
GCGAGAGAGTCTTGTACTGGTGTTACCTGCCAAGGTTTCCTAGACTTCTGGGGCCAAGGAACCCTGGTCACC
GTCTCCTCAG

SEQ ID NO: 82> 1st_BASE_945681_A3-3M2-D3_Ck516
AGTCTCCATCCTCCCTGTCTGCATCTATAGGAGACAGAGTCACCATCGCTTGCCGGGCAAGTCAGAACATTG
GCATCTTTTTGAACTGGTATCACCACAAACCAGGGGAAGCCCCTAAACTCCTGATCTATGCTGCATCCACTT
TGCAAACTGGGGTCCCATCAAGGTTCAGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAGTC
TGGAACGTGAAGATTTTGCAACTTACTACTGTCAGCAGACTTACAGTATGTTCTATAGTTTTGGCCAGGGGA
CCAACCTGGTGATCAAAC

SEQ ID NO: 83> 1st_BASE_892549_A3-3M2-F5_PWCgamma
AGGTGCAGCTGTTGGAGTCGGGCCCAGGACTGGTGAAGCCTGCGGGGACCCTGTCCCTAAATTGCGCTGTGT
CTGGTGGCTCCATCAGCACCAGTAACTGGTGGAGTTGGCTTCGTCAGTCCCCAGGGAAGGGACTGGAGTGGA
TTGGAGAAATTCATCATAGTGGGAACACCAACTACAACCCGTCCCTCAAGAGTCGACTCACCATATCAGTAG
ACACCTCCAAGAACCAGTTCTCCCTGAAACTGACGTCTGTGACCGCCGCGGACACGGCCGTCTATTACTGTG
GGAGGACCGGGGGTGATAGCAACGCCTGGCCAGATTGACTACTGGGGCCAGGGAATCCTGGTCACCGTCTCCT
CAG

SEQ ID NO: 84> 1st_BASE_945687_A3-3M2-F5_Ck516
AGTCTCCATCCTCCCTGTCTGCATCTGTGGGAGACAGGGTCACCATCACTTGCCGGGCAAGTCAGAGCATTA
GCAGATTTTTAAATTGGTATCAGCAGCGACCAGGGAAAGCCCCTAACCTCCTGATCTATGCTGCATCCAATT
TGCAAGGTGGGGTCCCATCAAGATTCAGTGGCTCTGGATCTGGGACAGATTTCACTCTCACCATTAGTAGTC
TGCAACCTGAAGATTTTGCAACCTACTACTGTCAACAGACTTACAGTTCCCCTCCGACGTTCGGCCTAGGGA
CCAAGGTGGAAATCAAAC

SEQ ID NO: 85> 1st_BASE_892571_A3-3M3-C4_PWCgamma
GGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAACCTGGAGGGTCCCTGAGACTATCCTGTGCAGCCTC
TGGAATCACCCTCAGGAATTATGAAGTGAACTGGGTCCGCCAGGCTCCAGGAAAGGGGCTGGAGTGGCTTTC
ATACATCAGTATTAGAGGTAATACCATATACTATGCAGACTCTGCGAAGGGCCGATTCACCGTCTCCAGAGA
CAACGCCGAGAACTCAGTGTTTCTACAAATGAATAGCCTGAGAGCCGAGGACACGGCTGTTTATTACTGTGC

GAGATGGTCCCGTGGTAACTCCGACTCTGGGGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTC
CTCA

SEQ ID NO: 86> 1st_BASE_945760_A3-3M3-C4_Ck516
AGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTA
ACAGCAGGTTCTTAGCCTGGTACCAACAAAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGCTGCATCCT
ACAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGAGACAGACTTCACGCTCACCATCAACA
GACTGGAGCCTGAAGATGTCGCAGTGTATTTCTGTCACCAGTATGGGTTTTCACCTCCGTATGTTTTTGGCC
AGGGGACCAGGCTGGAGATCAAGC

SEQ ID NO: 87> 1st_BASE_896204_A3-2M2-G8_PWCgamma
GGTGCAGCTGTTGGAGTCTGGGGGACGCTTGGTACGGCCAGGAGGGTCCCAGAGACTCTCCTGTACAGCCTC
TGGATTCAGTTTTAGTAGTTATGAAATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTTC
ATACATAAGTAGTAGTGGGACTACCATATACTACGCAGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGA
CAACGCCAAGAACTCACTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTTTATTACTGTGC
GAGACTCCTATTACTATGGTTGGGGGAGACAACGGCAATGGACGGTATGGACGTCTGGGGCCAAGGGACCAC
GGTCACCGTCTCCTCA

SEQ ID NO: 88> 1st_BASE_945551_A3-2M2-G8_Ck516
AGTCTCCATCCTCCCTGTCTGCTTCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGAAGATTA
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TGCAAAGTGGGGTCCCATCAAGGTTCAGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCACCAGTC
TGCAACCTGATGATTTTGCGACTTACTACTGTCAGCAGAGTTACACTTCCCCGCTCACTTTCGGCGGAGGGA
CCAAGGTGGAGATCAAAC

SEQ ID NO: 89> 1st_BASE_878754_A3-3M1-B11_PWCgamma
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCC
TCTGAATTCACCTTCAGTAGCTATGCTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTG
GCAGTTACATCATATGATGGCATTAATACATACTACGTAGACTCCGTGAAGGGCCGATTCACCATCTCCAGA
GACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCGGAGGACACGGCTGTGTATTACTGT
GCGAGAGCCCCCCAGGAACATGATAGCAGTGGTAATCCCCTCGACTACGGTATGGACCTCTGGGGCCAGGGG
ACCACGGTCACCGTCTCCTCA

SEQ ID NO: 90> 1st_BASE_945644_A3-3M1-B11_Ck516
AGTCTCCATCCTTCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCCAGTCAGGGCATTA
GCAGTTCTTTAGCCTGGTATCAGCAAAGACCAGGGGAAGCCCCTAAGCTCCTGATCTATGCTGCATCCACTT
TGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACAATCAGCAGCC
TGCAGCCTGAAGATTTTGCAACTTATTACTGTCAACAGCTGAATAGTTACCTTTTCGGCGGAGGGACCAAGG
TGGAGATCAAAC

SEQ ID NO: 91> 1st_BASE_878760_A3-3M1-D1_PWCgamma
AGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACTCTCCTGTACAGCTT
CTGGATTCACCTTTGGTGATTATGCTATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTAG
GTTTCATTAGAAGCAAAGCTTATGGTGGGACAACAGAATACGCCGCGTCTGTGAAAGGCAGATTCACCATCT
CAAGAGATGATTCCAAAAGCATCGCCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATT
ACTGTACTAGGACGCGCGGCAGCAGCTGGTCCCACTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA
CCACGGTCACCGTCTCCTCA

SEQ ID NO: 92> 1st_BASE_945652_A3-3M1-D1_Ck516
AGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGAGCATTA
GCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTT
TGCAAAGTGGGGTCCCATCAAGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTC
TGCAACCTGAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGTACACTTTTGGCCAGGGGA
CCAAGCTGGAGATCAAAC

SEQ ID NO: 93> 1st_BASE_892606_A3-3M3-G3_PWCgamma
CAGGTGCAGCTGGTGGAGACTGGGCCTGAGGTGAAGAAGCCTGGGACCTCAGTGAAGGTCTCCTGCAAGGCT
TCTGGGTTCACCTTTACTAGTTCTGGTATACAGTGGGTTCGACAGGCTCGTGGACAAAGCCTTGAGTGGATA
GGATGGATCGTCGTCGGCAGTGACATGACAAACTACGCACGGAAGTTGCAGGGAAGGGTCACCATCACCTGG
GACATGTCCACAAGCACAGCCTACATGGAACTAAACAGCCTGCGATCCGAGGACTCGGCCATTTATTACTGT
GCGGCAGTGGGAACTTCGCCTCCGCCATACTTTGACCACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
G

SEQ ID NO: 94> 1st_BASE_945781_A3-3M3-G3_Ck516

AGTCTCCATCCTTCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCCAGTCAGGGCATTT
ACAGTTATTTAGCCTGGTTTCAGCAAAAACCAGGGAAAGCCCCTAAACTCCTGATCTATTCTGTTTCCACTT
TGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGACTTCACTCTCACCATCAACAGCC
TGCAGCCTGAGGATTTTGCAACTTATTATTGTCAACAGCTTAATGGTTACCCCTCCTTCGGCCAAGGGACAC
GACTGGAAATTAGAC

SEQ ID NO: 95> 1st_BASE_904578_A3-2M1-A5_PWCgamma
GGTGCAGCTGTTGGAGTCTGGGGGAGCCTTGGTACAGCCTGGAGGGTCCCTGAGACTCTCCTGTACAGCCTC
TGATTTCACCTTCAGTGATTATGACATGAACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAATGGCTTTC
ATACATTAATTCTAGGGGTGTTACAAAATACTACGCAGACTCTGTGAAGGGCCGGTTCACCATCTCCAGAGA
CAACGCCAAGAACTCACTTTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTCTTTATTACTGTGC
CCGAGGACTCAGAGGGCACGATTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
SEQ ID NO: 96> 1st_BASE_945500_A3-2M1-A5_Ck516
AGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGCCAGAGTGTTA
GCAGCAGGTTCTTAGCCTGGTACCAGCAGAAACCAGGCCAGGCTCCCAGGCTCCTCATCTACGGTGCATCCA
GCAGGGCCTCTGGCATCCCAGATAGGTTCAGTGGCAGTGGGTCTGAGACAGACTTCACTCTCAGCATCAGCA
GACTGGAGCCTGAAGATTTTGCAGTGTATTTCTGTCTGCAGTATGGTTTCTCACCCCCGTACACTTTTGGCC
AGGGGACCAAACTGGAGATCAAAC

SEQ ID NO: 97> 1st_BASE_896206_A3-2M2-H5_PWCgamma
GGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTTCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTC
TGGATTCACCTTTAGCAACTATGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC
AGTTATTTATAACGGTGGCAGTAGCACATACTATGCAGACTCCGTGAAGGGCCGCTTCACCATCTCCAGAGA
TAACTCCAAGAACACACTGTATCTGCGAATGAACAGTCTGCGAGTCGAAGACACGGCCGTATATTACTGCGC
GAAATTCCTCGTGTTGCCAGCAGCTGCTGCCGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
SEQ ID NO: 98> 1st_BASE_945554_A3-2M2-H5_Ck516
AGTCTCCATCCTTCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCCAGTCAGGGCATTA
GCAGTCATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAACTCCTGATCTATGCTGCATCCACTC
TGCACACTGGAGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACAATCACCAGCC
TTCAGCCTGAAGATTTTGCGACTTATTACTGTCAGCAGCCGGGTGCTTTCGGCCCTGGGACCAGACTGGATA
TCAA

SEQ ID NO: 99> 1st_BASE_897923_A3-2M3-C9_PWCgamma
GGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGAAGGTCCCTGAGACTCTCCTGTGCAGCCTC
TGGATTCCCCTTCAGTAGCTATGAAATGAACTGGGTCCGCCAAGCTCCAGGGAAGGGGCTGGAGTGGATTTC
ATATATCAGTAGTACTGGTAGTCCCATCCACTACGCAGACTCTGTGAGGGGCCGATTCACCATCTCCAGAGA
CAACGCCAAGAACTCACTCTATCTGCACATGAACAGCCTGAGAGCCGAGGACACGGCTATTTATTACTGTGC
GGGGGATTTGCTGCTCTGGGTCCCCGAAGCAACAGGTGCTACAGCTGGTACCGGCGGTTTGGACGTCTGGGG
CCAAGGGACCACGGTCACCGTCTCCTCA
SEQ ID NO: 100> 1st_BASE_949089_A3-2M3-C9_Ck516
AGTCTCCATCCTTCCTGTATGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGACCATCA
GTAAATATTTAAATTGGTACCACCAGAAGCCAGGGAAAGCCCCTAATCTCCTGATCTATGCTGCATCAAGTT
TGCAGAGTGGAGTCCCATCGAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTC
TGCAGCCTGAAGACTTTGCAACTTACTACTGTCAACAGAGTTACAGTATCCCTCGGACGTTCGGCCAAGGGA
CCAAGGTGGAAATCAAAC

SEQ ID NO: 101> 1st_BASE_992133_A3-2M3-E9-H-1_Resend_1146_Resend
GAGGTGCAGCTGGTACAGTCTGAAACAGAGGTGAAAGAGCCCGGGCAGTCTCTGAAGATCTCCTGTAAGGGT
TCTGGATACACCTTTACCAACTACTGGATCGGCTGGGTGTGCCAAATGCCCGGGAAAGGCCTGGAGTGGATG
GGGATCATCTATCCTGGTGACTCTGAAACCAGATACAGCCCGTCCTTTCAAGGCCAGGTCACCATCTCAGTC
GACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGTAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGT
GCGAGACTCAAAAATTACTATACTTCGGGGAATTATGTTCCGGTGGGAGGTATGGACGTCTGGGGCCAAGGG
ATCACGGTCACCGTCTCCTCAG
SEQ ID NO: 102> 1st_BASE_949097_A3-2M3-E9_Ck516
AGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGAGCGTTA
GCAACTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAACTCCTGATCTATGCTGCTTCCACTT
TGCAAAGTGGGGTCCCATCAAGATTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCTCCATCAGCAGTC
TGCAACCTGAAGACTTTGCAATATACTACTGTCAACAGACTTACAGTCCCCCTCAGAACACTTTTGGCCAGG
GGACCAAGCTGGAGATCAAAC

SEQ ID NO: 103> 1st_BASE_988416_A3-2M3-F9-H-2_1146
GGCCAGGTGGAGCTGGTGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGGGTCCCTGTCCCTCACCTGCGCT
GTCTCTGGTGGCTCCATCACCAGTAGTAACTGGTGGAGTTGGGTCCGCCAGCCCCCAGGGAAGGGGCTGGAA
TGGATTGGAGAAATCTATCATAGTGGGAGCGCCGACTACAACCCGTCCCTCAAGAGTCGAGTCACCATATCA
GTAGACACCTCCAAGAACCAGTTCTCCCTGAAGCTGAGGTCTGTGACCGCCGCGGACACGGCCGTGTATTAC
TGTGCGAGGGTTGAGGTTATGATTAAGTTTGGGGGAGTTATCCGATACTTTGACTACTGGGGCCTGGGAACC
CTGGTCACCGTCTCCTCAG
SEQ ID NO: 104> 1st_BASE_949101_A3-2M3-F9_Ck516
AGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCGAGTCAGGACATTA
GCAACTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTACTATGCATCCAATT
TGGAAACAGGGGTCCCATCAAGGTTCAGTGGAAGTGGATCTGGGACAGATTTTACTTTCACCATCAGCAGCC
TGCAGCCTGAAGATTTTGCAACATACTACTGTCAACAGTATGATAATCTCCCTCCGCGGTACACTTTTGGCC
AGGGGACCAAGCTGGAGATCAAAC

SEQ ID NO: 105> 1st_BASE_897935_A3-2M3-G3_PWCgamma
GGTGCAGCTGTTGGAGTCTGGGGGAGCCTTGGTACAGCCAGGGCGGTCCCTGAGACTCTCCTGTACAGCTTC
TGGATTCACCTTTGGGGATTTTGCTTTGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTAGG
TGTCATCAGAAGCAAAGGCTATGGTGGGACAACAGAGTACGCCGCGTCTGTGAAAGGCAGATTCAGTATCTC
AAGAGATGATTCCAAATTCATCGCCTATCTGCAAATGAACAGCCTGGAAACCGAGGACACTGCCGTGTACTT
CTGTACCAGCACAACCTTATATTATTTTGTTTCGGGGAGGGCAAAAGACTACGGGATGGACGTCTGGGGCCA
AGGGACCACGGTCACCGTCTCCTCA
SEQ ID NO: 106> 1st_BASE_949103_A3-2M3-G3_Ck516
AGTCTCCATCCTCCCTGTCTGCATCTGTTGGAGACAGTGTCACCATCACTTGCCGGGCAAGTCAGGGCATTA
GAAATGATTTAGGCTGGTATCAGCAGAAAGCAGGTAAAGCCCCTAAGGCCGTGATCTATGCTGTATCCACTT
TACAAAGTGGGGTCCCATCGAGGTTCAGCGGCAGTGGATCTGGCACAGATTTCACTCTCACCATCAGCAGCC
TGCAGCCTGAAGATTTTGCAACTTATTACTGTCTGCAAGATTACAGTTTTCCGTGGACGTTCGGCCAAGGGA
CCAAGGTGGAAATCAAAC

SEQ ID NO: 107> 1st_BASE_988406_A3-2M3-C2-H-3_1146
GAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTC
TCTGGTGGCTCCATCACCAGTAGTAGTTACTACTGGGCCTGGCTCCGCCAGCCCCCAGGGAAGGGGCTGGAG
TGGATTGGGAATATCTATTACAGTGGGAACACCGACTACAACCCGTCCCTCAAGAGTCGAGTCACCATATCC
GCAGACACGTCCATGGACCAATTCTCCCTGAGGCTGAGGTCTATGGCCGCCTCAGACACGGCTGTTTATTAT
TGTGCGAGCGGGCTACAGACCTGGGACGTGACTACGGGTGGTGCGTGGGCCTCCCTCGACTACTGGGGCCAG
GGAACCCTGGTCACCGTCGCCTCAG
SEQ ID NO: 108> 1st_BASE_949084_A3-2M3-C2_Ck516
AGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTA
GCAGCAGTTTCTTAGCCTGGTACCAGCACAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCA
TCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCATTCTCACCATCAGCA
GGCTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTTTGGTAGAACACCTCCAATGTACACTTTTG
GCCAGGGGACCAAGCTGGAGATCAAAC

Ab 10/50 11E-H1L1
heavy chain:
SEQ ID NO: 109> 10/50_11E1
EVQLVESGGGLVKPGGSLRLSCAASGFTFSTYPMSWVRQAPGKGLEWVSVIFNGGSSTYYADSVKGRFTISR
DNSKNTLYLQMNSLRAEDTAVYYCAKFAAPPSGWCDYWGQGTLVTVSS
light chain:
SEQ ID NO: 110> 10/50_11E1
xLSASVGDRVTITCRASQSVSNWLAWYQQKPGKAPKLLIYKASTLESGVPSRFSGSGSGTEFTLTISSLQPD
DFATYYCQQSGTFGQGTKVEIK

Ab 10/50 1B-H1L1
heavy chain:
SEQ ID NO: 111> 10/50_1B1
EVQLVESGPGLVKPSETLSLTCSVSGDSITNYYWAWIRQPPGKRLEWIANLYYTGGTNYNPSLKARLTTSVD
TSKNTFSLKVRSATAADTAVYYCARVTSLSGSEVYGMDVWGQGITVTVSS
light chain:
SEQ ID NO: 112> 10/50_1B1

DVVMTQSPSSLSASVGDRVTITCQASQDISNSLTWFQQKPGKAPRLLMYAASNLQTGVPSRFSGSGSGTDFT
FTISSLQPEDIATYYCQQYDSIPITFGQGTRLELK

Ab 10/50 3H-H1L1
heavy chain:
SEQ ID NO: 113> 10/50_3H1
QVQLQESGGGLVQPGGSLRLSCAASGFNFGDYVMAWVRQAPGKGLEWVSVIYNGGSSTYYADSVKGRFTVSR
DNSRNTVSLHMSSLSAEDTARYYCAKDRQSLHDPGSGSYVALDHWGQGTLVTVSS
light chains
SEQ ID NO: 114> 10/50_3H1
EIVMTQSPSSLPASLGDRVTITCRASQSISGSLNWYQQRPGKAPKLLIFAASRLHSGVPSRFSGSGSGPDFT
LSISSLQPEDFATYYCQQGSTFGGGTKVEFK

Ab 10/50 5A-H1L1
heavy chain:
SEQ ID NO: 115> 10/50_5A1
QVQLQQWGAGLLKPSETLSLTCAVYDGSFSGFSWTWIRQSPGKGLEWIGEINHSGSTNYNPSLKSRLTIALD
TSTNQFSLRLTSVSAADTAIYYCALSLQTLVRGLVYINFDYWGQGSLVTVSS
light chain:
SEQ ID NO: 116> 10/50_5A1
DIQMTQSPASLSASVGDRVTITCRASQAITTYLNWYQQKPGKAPNLLIYAASSLQSGVPSRFTGSGSGTDFT
LTISSLQPGDFATYYCQQSYNLPRTFGHGTKVEIK

Ab 10/50 5D-H6L2
heavy chain:
SEQ ID NO: 117> 10/50_5D6
EVQLVQSGGGLVQPGGSLRHSCVASGFTFTTHAMGWVRQAPGKGLEWVSAISASGDGTYYADSVKGRFTISR
DNSKNTLFLQMNSLTAADTAFYYCATIDWSDKGVFDYWGQGIPVTVSS
light chain:
SEQ ID NO: 118> 10/50_5D2
EIVLTQSPSSVSASVGDRVTITCRASQAVGSLLAWYQQKPGKPPRLLVYTASTLQSGVPSRFSGSGSGTDFT
LTITSLQPEDFATYSCQQAFSFPWTFGQGTKVEIR

Ab 10/50 6E-H1L1
heavy chain:
SEQ ID NO: 119> 10/50_6E1
EVQLVQSGGGLVQPGGSLRLSCVASEFSFSTYAMGWARQAPGKGLEWVSVIYTGGGSTYYADSVRGRFTISR
DNSKNTLYVQMNSLTVDDTAVYYCAGGGIVSTMGAFGFWGQGTMVAVSS
light chain:
SEQ ID NO: 120> 10/50_6E1
ETTLTQSPSFLSASVGDRVTITCRASQEFSSYVAWYQQKPGKAPKLLIYGVSTLHSGVPLRFSGGGSGTEFI
LTISGLQPEDVGTYYCQQTGTFGQGTKVEIK

Ab 10/50 7A-H1L1
heavy chain:
SEQ ID NO: 121> 10/50_7A1
QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYEMNWVRQAPGKGLEWISYISRSGTATYYADSVKGRFTISR
DNAKNSLYLQMNSLRAEDMAVYYCAGEGYFGSAAINYFAFWGQGTLVTVSS
light chain:
SEQ ID NO: 122> 10/50_7A1
ETTLTQSPSSLSASVGDRVTITCRASQTIGTYLHWYQQKPGKAPKLLIFAASSLQSGVPSRFSGSGSGTDFT
LTISSLQPEDFATYYCLQTYSSLYTFGQGTKLEIK

Ab 10/50 7H-H1L1
heavy chain:
SEQ ID NO: 123> 10/50_7H1
EVQLVETGGGLVQPGGSVRLSCAASGFTFSRYWMSWVRQAPGKGLEWVANINQGGSERHYVDSVKGRFTISR
DNARNSFYLEIRNLRVEDTAVYYCAREGMVEVTALSFLDYWGEGNLVAVSS
light chain:
SEQ ID NO: 124> 10/50_7H1

ETAFTQSPSSLSASVGDTVTITCRASQTIGTFLNWYQLKPGKAPKLLIFATSNLQGGVPSRFSGSGSGGDFT
LTITSLQPEDFGTYYCQQTYSMIYTFGQGTRVDIK

Ab 10/50 9B-H1L1
heavy chain:
SEQ ID NO: 125> 10/50_9B1
QVQLVQSGAEVKKPGESLKISCKASGYIFTSYWIAWVRQMPGKGLEWMGIIYPGNSDPRYSPSFQGQVTISA
DKSSSTAYLQWSSLKASDTAIYYCSRLDHYFYYGMDLWGQGTTVTVSS
light chain:
SEQ ID NO: 126> 10/50_9B1
DVVMTQSPGALSLSPGERATLSCRASQTFSSIYLSWFQQKPGQAPRLLIYGASNRADGIPDRFSGSGSGTDF
TLIISRLEPEDFAVYYCQHYDNSFFTFGPGTKVDIK

Ab 10/50 1D-H8L1
heavy chain:
SEQ ID NO: 127> 10/50_1D8
EVQLVQSGGGLVKPGGSLRLSCAASGFTFAPFSLTWVRQAPGKGLEWVSSITPSSNYIFYADSVKGRFTISR
DDGRKSVYLQMNSLRVEDTAVYYCARDPSGTYDYNYYAMDVWGPGTTVTVSS
light chain:
SEQ ID NO: 128> 10/50_1D1
EIVLTQSPGTLSLSPGERATLSCRASQTVGSSYLAWYQQKPGQAPRLLIYGTSTRATGIADRFSGSGSGTDF
TLTISRLEPEDFAVYYCQQYGGSPPITFGQGTRLETK

Ab 10/50 2F-H3L1
heavy chain:
SEQ ID NO: 129> 10/50_2F1
QLVETGAEVKKPGASVKVSCKASGSGYPFSSHGFSWVRQAPGQGLEWMGWTTAYNGETQYAQKFLGRVTMTT
DTSTNTAYMELRSLRSDDTAIYYCYSSGPRWGHFDIWGQGTVVTVSS
light chain:
SEQ ID NO: 130> 10/50_2F3
DIQMTQSPGTLSLSPGERATLSCRASQSVDLAWFQQKPGQAPRLLIYGTSSRATGIPERFSGSGSGTDFTLT
ISRLEPEDFAVYYCHQYDSSPWTFGQGTRVEFK

Ab 10/50 4B-H2L1
heavy chain:
SEQ ID NO: 131> 10/50_4B2
EVQLVQSGPGLVKPSETLSLTCTVSGGSLSSDGHSWGWLRQPPGKGLEWIGNIYYTGTTYYNPSLESRITVS
VDTSKNQFSLKLNSVAAADTAVYYCAAWNAGPSYYFHYWGLGTLVTVSx
light chain:
SEQ ID NO: 132> 10/50_4B1
EIVLTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQRPGQAPRLLIYGASTRATGIPARFSGSGSGTEFT
LTISSLQSEDFAVYYCQQYESWWTFGQGTKVEVK

Ab 10/50 5C-H6L1
heavy chain:
SEQ ID NO: 133> 10/50_5C6
EVQLVESGAEVRRPGASMKVSCKASGYTFSSYYIHWVRQAPGQGLEWVGIINPRGGSASVAQKFQGRVTLTR
DTSTSTVYMELSSLRSEDTALYFCARAGVALFYDSSGYDPTPYDAFEVWGQGTMVTVSS
light chain:
SEQ ID NO: 134> 10/50_5C1
EIVMTQSPATLSVSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIFGASTRATGIPARFSGSGSGTEFT
LTISSLQSEDFAVYYCHQYNHWPRTFGQGTKVEIK

Ab 10/50 6B-H1L2
heavy chain:
SEQ ID NO: 135> 10/50_6B1
EVQLVQSGAEVEKPGASVKISCKASGYTFANNYIHWVRQAPGQGLQWMGVINPRGGSAASAQMFQGRITMTR
DTSTSTVYLDLRSLRSEDTAVYYCARGGRAYYYDSYTTPRDGESWWFDPWGQGTLVTVSS
light chain:
SEQ ID NO: 136> 10/50_6B2

ETTLTQSPSSLSASVGDRVTITCQASQDIRKYLNWYQQKPGKAPKVLIYDASNLKTGVPSRFSGGGSGTDFT
FTISSLQPGDIATYYCQHSDYLPITFGQGTRLEIE

Ab 10/50 6D-H3L1
heavy chain:
SEQ ID NO: 137> 10/50_6D3
QVQLQQSGAEVKKPGASVHLSCKASGYSFTSNYMHWVRQAPGQGLEWMGIINPRGGSTSIAQQFQGRITMTR
DTSTSTVYMELRSLTSEDTAVYYCARAGPALYYDSSGYDPTTYDSFEVWGQGTMVTVSS
light chain:
SEQ ID NO: 138> 10/50_6D1
DVVMTQSPATLSVSPGERATLSCRASQGVRSYLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFT
LTINSLRSEDSAVYYCQQYNHWPRTFGQGTKVEIK

Ab 10/50 7C-H3L1
heavy chain:
SEQ ID NO: 139> 10/50_7C3
EVQLVESGAEVKKPGASVKVSCKASGYTFSNYYIHWVRQAPGQGLEWMGVINPRGGSASSAEKFQGRITMTR
DTSTSTVYMELSSLRSEDTAVFYCARGGWAYYYDSYTTPRDGQSWWFDPWGQGTLVTVSS
light chain:
SEQ ID NO: 140> 10/50_7C1
DVVMTQSPSSLSASVGDRVTITCQASQDIRNFLNWYQHKPGKAPKVLIYDASKLKTGVPSRFSGSGSGTDFT
FTIRSLQPEDIATYYCQQSDNLPITFGQGTRLEIK

Ab 10/50 7E-H1L1
heavy chain:
SEQ ID NO: 141> 10/50_7E1
QVQLQQSGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIHYSGSTNYNPSLKSRVTISVD
TSKNHFSLKLNSVTAADTAVYYCARHDCSDTTCREYFQHWGQGTLVTVSS
light chain:
SEQ ID NO: 142> 10/50_7E1
ETTLTQSPSSLSASVGDRVTITCRASQSISTFLNWYQKKPGKAPELLISAASTLQSGVPSRFSGSGSGTDFT
LTINSLQPGDFATYYCQESYSMMYTFGQGTKVEIK

Ab 10/50 9E-H2L2
heavy chain:
SEQ ID NO: 143> 10/50_9E2
QVQLVQSGGGLVQPGGSLRLSCVASGFTLRSYAMSWVRQAPGKGLEWVSSISDSDDSTYYADSVKGRFTISR
DDSKNTLYLQMSSLRAEDTAVFFCATTNWGVSVKPGTFDIWGQGTVITVSS
light chain:
SEQ ID NO: 144> 10/50_9E2
DIQLTQSPSSVSASVGDRVTITCRASQGISSYLAWYQQKPGKAPKLLIFAASSLQSGVPSRFSGSGSGTDFT
LTISSLQPEDFATYYCQQANSFPWTFGPGTKVEIK

Ab 10/63 1D-H4L1
heavy chain:
SEQ ID NO: 145> 10/63 1D4_001.ab1
QVTLKESGPPLVKPTQTLTLTCTFSGFSLSTSGVNVGWIRQPPGKALEWLALLYWDDDRRYSPSLRSRLTIT
KDTSKNQVVLTMTNMDPVDTATYYCAHRRWEDSTFQHWGQGTLVTVSS
light chain:
SEQ ID NO: 146> 10/63 1D-1_055
DVVMTQSPATLSVSPGERATLSCRASQSVNSNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFT
LTISSLQSEDFAVYYCQHYHNWGTFGQGTKVEIK

Ab 10/63 1E-H3L1
heavy chain:
SEQ ID NO:147> 10/63 1E3_061
EVQLVQSGSELKKPGASVKVSCKASGYTFPTYAINWVRQAPGQGLEWMGWINTNTGNPMYAQGFTRRFVFSW
DTSVSTAYLQISSLKTEDTAVYYCARGRGGFAATAGTDYWGQGTLVTVSS
light chain:
SEQ ID NO: 148> 10/63 1E-1_053

EIVLTQSPSSVSASVGDRVTITCRASQPISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTNFT
LTISSLQPDDFVTYYCQQANSFPYTFGQGTKLEIK

Ab 10/63 5D-H1L2
heavy chain:
SEQ ID NO: 149> 10/63 5D1_037
EVQLVQSGAEVKKPGSSVKVSCKASGGTFSSDSISWVRQAPGQGLEWMGSIIPIFSRANYAQKFQGRVTINA
DESTSTVYMELSSLRSDDTALYFCARTPVTGPDLDYWGQGTLITVSS
light chain:
SEQ ID NO: 150> 10/63 5D-2_070.ab1
EVVLTQSPSSLSASVGDRVTITCRASESISTNLNWFQQKPGKAPTLLIHAASTLQTGVPSRFIGSGSGTDFT
LTVSSLLPEDFATYFCQQTYNTPRTFGQGTRVEIK

Ab 10/63 2A-H5L4
heavy chain:
SEQ ID NO: 151> 10/63 2A5_014
QVQLVQSGAEVKKPGSSVKVSCKASGGSFNNYAIGWVRQAPGQGLEWMGGIITVFGRGNYAQKFQGRVTITA
DESTSTAYMELSSLRPEDTAVYYCVRDYTFVRGVASWEYWGQGTLVTVSS
light chain:
SEQ ID NO: 152> 10/63 2A-4_049
EIVLTQSPSSVSASVGDRVTITCRASQPISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTNFT
LTISSLQLDDFVTYYCQQANSFPYTFGQGTKLEIK

Ab 10/63 2C-H3L2
heavy chain:
SEQ ID NO: 153> 10/63 2C3_006.ab1
QVQLQQSGAEVTRPGSSVKVSCKASGASIGSYTVHWVRQAPGQGLEWIGGINPIFGTVNYAQRFQGRLTISA
DDSTSSAYMEMSSLKSEDTAVYYCARSQRHILTGHYTDYWGPGTLVTVSS
light chain:
SEQ ID NO: 154> 10/63 2C-2_058
DVVMTQSPSSLSASVGDRVSITCQASQDIKNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFS
FTISSLQPEDIATYYCQHYENLPALTFGGGTKVEIR

Ab 10/63 2E-H2L2
heavy chain:
SEQ ID NO: 155> 10/63 2E2_004
EVQLVETGGGVVQPGKSLTLSCAASGFTFSNYGMVWVRQPPGKGLEWVAVISYDAKKQYYADSVKGRFTVSR
DDSEGKVYLQMNSLRGDDAAVYFCAKLQRPDSTVWPFDQWGQGILVIVSP
light chain:
SEQ ID NO: 156> 10/63 2E-2_050
ETTLTQSPSTLSASVGDTVTITCRASQSISMWLAWYQQKPGKAPRLLIYTTSNLRTGVPSRFSGSGSGTEFT
LTISSLQPEDFATYYCQQYKTSWTFGQGTKVDIx

Ab 10/63 2F-H1L1
heavy chain:
SEQ ID NO: 157> 10/63 2F1_031
EVQLVESGGALVQPGGSLRLSCAASGFTFNNFEMSWVRQAPGKGLEWVSAISVSDGNTYYADSVKGRFTISR
DTSRNTLYLQMNSLRAEDTALYYCANVLGYCTPTTCYEDHWGQGTLVTVSS
light chain:
SEQ ID NO: 158> 10/63 2F1_059
DVVMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVSSRFSASGSGTEFT
LTISSLQPEDFATYYCLQHNSFPGSFGQGTKVEIK

Ab 10/63 2G-H2L1
heavy chain:
SEQ ID NO: 159> 10/63 2G2_027.ab1
QVQLVQSGAEVKKAGESLKISCKGSGYTFTTYWIAWVRQVPGKGLEWMGIIYPSDSDTRYSPSFQGQITISA
DKSINTAYLQWTSLKASDTAMYYCARPDDSSGLEAFDIWGQGTMVTVSS
light chain:
SEQ ID NO: 160> 10/63 2G-1_079.ab1

EIVLTQSPSSVSASVGDRVTITCRASQPISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTNFT
LTISSLQPDDFVTYYCQQANSFPYTFGQGTKLEIK

Ab 10/63 3E-H1L2
heavy chain:
SEQ ID NO: 161> 10/63 3E1_030
QVHLVQSGGGLVQPGGSLRLSCAASGFTFSTYWMSWVRQAPGKGLEWVANIKADGRQEYYLQSVTGRFTVSR
DNAKNSLYLEMSSLRAEDTAMYYCVRDVSSYSIIWSDAFEIWGQGTMVTVSP
light chain:
SEQ ID NO: 162> 10/63 3E-2_069
ETTLTQSPSSLSASVGDTVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFT
LTITSLQPEDLATYYCVHHNDYPRTFGQGTKVEIK

Ab 10/63 3F-H1L2
heavy chain:
SEQ ID NO: 163> 10/63 3F1_026
QVQLVQSGAEVKKPGSSVKVSCKASGGTFSTHSINWVRQAPGQGLEWMGGNIPIFGKASYAEKFQDRVTITA
DESTSTAYMELSSLRSEDTAVYYCARFFVKYSGSHYYFDSWGQGTLVTVSS
light chain:
SEQ ID NO: 164> 10/63 3F-2_065
DVVMTQSPSSVSASVGDRVTITCRASQPISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTNFT
LTISSLQPDDFVTYYCQQANSFPYTFGQGTKLEIK

Ab 10/63 4F-H6L1
heavy chain:
SEQ ID NO: 165> 10/63 4F6_020.ab1
EVQLVESGGGLAKPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVGRIKNKIDGETTDYAASVKGRFII
SRDDSKNTVYLQMNSLKTEDTAEYWCTIYFYDRSGYFFDHWGQGTLVTVSS
light chain:
SEQ ID NO: 166> 10/63 4F-1_076
ETTLTQSPATLSLSPGQRATLSCRASQSVSSYLAWYQQKPGQAPRLLIFDASHRATGIPARFSGSGSGTDFI
LTISSLEPEDFAVYYCLQRGKWPSFGQGTRLEIK

Ab 10/63 5A-H6L1
heavy chain:
SEQ ID NO: 167> 10/63 5A6_045.ab1
QVQLQESGGGLVQPGGSLRLSCAASGFTFSDYAMSWVRQAPGKGLEWVSGLSESGHNTYYADSVLDRSAISR
DNSKSTLYLQMNSLTAEDTAVYYCARCWRGYDPLTGYYTGYYFDYWGPGTLVTVSS
light chain:
SEQ ID NO: 168> 10/63 5A-1_074
EIVLTQSPSSLSASIGDRVTITCRASQDISNYLAWYQQRPGKVPKLLIYAASTLQSGVSSRFSGSGSGTDFT
LTISSLQPEDVATYYCQKYNNAPVTFGGGTKVEIK

Ab 10/63 5B-H1L1
heavy chain:
SEQ ID NO: 169> 10/63 5B1_043
QVQLQQSGPGLVRPSETLSLTCSVSGGSISSITPYWGWIRQPPGKGLEWIGSLAYSGDTYYNPSLKSRVTIS
LDTSETQFSLKVNSVTAADTALYFCARHHSSGNALDYWGQGILVTVSS
light chain:
SEQ ID NO: 170> 10/63 5B1_053
ETTLTQSPSSLSASVGDRVTITCRASQGISSYLAWYQQKPGKAPKLLIFGASTLQSGVPSRFSGSGSGTDFT
LTISSLQPEDFATYYCQQLNNYVLTFGGGTKVEIK

Ab 10/63 5C-H2L1
heavy chain:
SEQ ID NO: 171> 10/63 5C2_041
EVQLVQSGAEMEKPGSSVKVSCKSSGGTFNNYAISWVRQAPGQGLEWMGGINPLFRTVNYAQKFQGRVTITA
DESTSTAYMELSSLRSDDTAVYYCAGAYCSATSCSSGQWLVYWGQGTLVTVSS
light chain:
SEQ ID NO: 172> 10/63 5C1_049.ab1

DVVMTQSPDSLAVSLGERATINCKSSQSVFHSSNNKNYLAWYQQKPGQPPRLLIYWASTRESGVPDRFSGSG
SGTEFTLTISSLQAEDVAVYYCQQYYSSPPVFTFGPGTKVDVK

Ab 10/63 5H-H3L1
heavy chain:
SEQ ID NO: 173> 10/63 5H3_044
QVQLQESGPGLVKPSETLSLTCTVSGGSINNSNYYWSWIRQSPGRGLEWIGGIYFSGTTYYNPSLQSRVTIS
IDTSKNQFSLKLSSVTAADTAIYYCVRQMNYYHLGSSVGFDPWGQGALATVSS
light chain:
SEQ ID NO: 174> 10/63 5H-1_095
DVVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPSLLIYEASTRATGIPARFSGSGSGTDFT
LTISSLQSEDFAIYYCQQYNDWLWTFGQGTKVEIR

Ab 10/63 6C-H8L1
heavy chain:
SEQ ID NO: 175> 10/63 6C8_036
QVQLQESGAEVKKPGSSVKVSCKASGDTLNTYTLSWVRQAPGQGLEWLGGIIHPFGTENYAQKFQGRLTITA
DESTSTAYMELRSLTSEDMAVYFCARHHRHILTGERTDYWGQGTLVTVSS
light chain:
SEQ ID NO: 176> 10/63 6C-1_091
EIVLTQSPSSLSASVGDRVTITCQASQDIRNSLNWYQQKPGKAPILLIYDASNLKTGVPSRFSGSGSGTDFT
FTISSLQPEDIATYFCQHYDNLPLFTFGPGTKVDIK

Ab 10/63 6E-H6L1
heavy chain:
SEQ ID NO: 177> 10/63 6E6_034
QVQLVQSGAEVKKPGSSVKVSCKSSGGTLNSYTISWVRQAPGQGLEWMGGINPIFGTTNNAQKFQGRVTITA
DKSTNTVYMELSSLRSDDTAVYYCARGGHHILTGRYIDDWGQGTLVTVSS
light chain:
SEQ ID NO: 178> 10/63 6E1_058
DVVMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKAGKGPKLLIYDASNLETGVPSRFSGSGSGTDFT
FTISSLQPEDVATYYCQQYDNLPRHTFGQGTKLEIK

Ab 10/63 7E-H1L1
heavy chain:
SEQ ID NO: 179> 10/63 7E1_061
EVQLVETGGGVVQPGRSLKLSCAASGFNFNEYGMHWVRQAPGKGLEWVAVVAYDGINKYYEDSVKGRFTISR
DNSKNTLSLQMNSLQPEDTAVYFCAKSAGSTLKTVISLLQPFDIWGQGTMVTVSS
light chain:
SEQ ID NO: 180> 10/63 7E-1_087
DVVMTQSPATLSVSPGERATLSCRASQSVSSNLGWYQQKPGQAPRLLIYDASTRATGIPPRFSGSGSGTEFT
LTISSLQSEDFAVYYCQQYHDWPPYTFGQGTKLEIK

Ab 10/63 7G-H1L1
heavy chain:
SEQ ID NO: 181> 10/63 7G1_055
EVQLVESGGGLAKPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVGRIKNKIDGETTDYAASVKGRFII
SRDDSKNTVYLQMNSLKTEDTAEYWCTIYFYDRSGYFFDHWGQGTLVTVSS
light chain:
SEQ ID NO: 182> 10/63 7G-1_081
DVVMTQSPATLSLSPGQRATFSCRASQSVSSYLAWYQQKPGQAPRLLIFDASHRATGIPARFSGSGSGTDFI
LTISSLEPEDFAVYYCLQRGKWPSFGQGTRLEIK

Ab 10/63 7H-H1L1
heavy chain:
SEQ ID NO: 183> 10/63 7H-1_060
QVQLVQSGGGLAKPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVGRIKNKIDGETTDYAASVKGRFII
SRDDSKNTVYLQMNSLKTEDTAEYWCTIYFYDRSGYFFDHWGQGTLVTVSS
light chain:
SEQ ID NO: 184> 10/63 7H-1_038

EIVLTQSPATLSLSPGQRATLSCRASQSVSSYLAWYQQKPGQAPRLLIFDASHKTTGIPARFSGSGSGTDFI
LTISSLEPEDFAVYYCLQRGKWPSFGQGTRLEIK

Ab 10/63 8F-H1L1
heavy chain:
SEQ ID NO: 185> 10/63 8F1_051
EVQLVQSGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGGIYYTGTTYYNPSLNSPVTIS
IDMSKNHFSLELTSVTAADTAVYYCARQAVFAEATGTTIGAIDYWGQGTLVVVSS
light chain:
SEQ ID NO: 186> 10/63 8F-1_036
DVVMTQSPSSVSASVGDRVIITCRASQSFNNWLAWYQQKPGKAPKLLIYGASTLQSGVPSRFSGSGSGTDFT
LTISSLQPEDFATYYCQQASSFPWTFGQGTKVEIK

Ab 10/63 3D-H2L2
heavy chain:
SEQ ID NO: 187> 10/63 3D
GTHIEWLVLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIAYDGINKYYADFVKGRFTISRDNSKNTVYL
QMISLGPEDTAVYYCAREYCSSTTCINSFLTPDYWGQGTLVIVSS
light chain:
SEQ ID NO: 188> 10/63 3D-2_071.ab1
EIVLTQSPSSVSASVGDRVTITCRASQPISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTNFT
LTISSLQPDDFVTYYCQQANSFPYTFGQGTKLEIK

SEQ ID NO: 189> 1st_BASE_945644_A3-3M1-B11_Ck516
xSPSFLSASVGDRVTITCRASQGISSSLAWYQQRPGEAPKLLIYAASTLQSGVPSRFSGSGSGTEFTLTISS
LQPEDFATYYCQQLNSYLFGGGTKVEIK
SEQ ID NO: 190> 1st_BASE_945644_A3-3M1-B11_Ck516
xSPSFLSASVGDRVTITCRASQGISSSLAWYQQRPGEAPKLLIYAASTLQSGVPSRFSGSGSGTEFTLTISS
LQPEDFATYYCQQLNSYLFGGGTKVEIK

SEQ ID NO: 191> 1st_BASE_878760_A3-3M1-D1_PWCgamma
xVQLLESGGGLVQPGRSLRLSCTASGFTFGDYAMSWVRQAPGKGLEWVGFIRSKAYGGTTEYAASVKGRFTI
SRDDSKSIAYLQMNSLKTEDTAVYYCTRTRGSSWSHYYYYGMDVWGQGTTVTVSS
SEQ ID NO: 192> 1st_BASE_945652_A3-3M1-D1_Ck516
xSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPYTFGQGTKLEIK

SEQ ID NO: 193> 1st_BASE_973574_A3_3M2_D3_H_2_1146
EVQLVESGGGLVRPGGSLRLSCVGSGFNFGRHWISWVRQAPGNGLEWVANIKEDGSAKYYVESVKGRFTIVR
DNAKNSLFLQMSSLRAEDTAVYYCARESCTGVTCQGFLDFWGQGTLVTVSS
SEQ ID NO: 194> 1st_BASE_945681_A3-3M2-D3_Ck516
xSPSSLSASIGDRVTIACRASQNIGIFLNWYHHKPGEAPKLLIYAASTLQTGVPSRFSGSGSGTEFTLTISS
LEREDFATYYCQQTYSMFYSFGQGTNLVIK

SEQ ID NO: 195> 1st_BASE_892549_A3-3M2-F5_PWCgamma
xVQLLESGPGLVKPAGTLSLNCAVSGGSISTSNWWSWLRQSPGKGLEWIGEIHHSGNTNYNPSLKSRLTISV
DTSKNQFSLKLTSVTAADTAVYYCGRTGVIATPGQIDYWGQGILVTVSS
SEQ ID NO: 196> 1st_BASE_945687_A3-3M2-F5_Ck516
xSPSSLSASVGDRVTITCRASQSISRFLNWYQQRPGKAPNLLIYAASNLQGGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQTYSSPPTFGLGTKVEIK

SEQ ID NO: 197> 1st_BASE_892571_A3-3M3-C4_PWCgamma
xVQLLESGGGLVQPGGSLRLSCAASGITLRNYEVNWVRQAPGKGLEWLSYISIRGNTIYYADSAKGRFTVSR
DNAENSVFLQMNSLRAEDTAVYYCARWSRGNSDSGGMDVWGQGTTVTVSS
SEQ ID NO: 198> 1st_BASE_945760_A3-3M3-C4_Ck516
xSPGTLSLSPGERATLSCRASQSVNSRFLAWYQQKPGQAPRLLIYAASYRATGIPDRFSGSGSETDFTLTIN
RLEPEDVAVYFCHQYGFSPPYVFGQGTRLEIK

SEQ ID NO: 199> 1st_BASE_892606_A3-3M3-G3_PWCgamma
QVQLVETGPEVKKPGTSVKVSCKASGFTFTSSGIQWVRQARGQSLEWIGWIVVGSDMTNYARKLQGRVTITW

DMSTSTAYMELNSLRSEDSAIYYCAAVGTSPPPYFDHWGQGTLVTVSS

SEQ ID NO: 200> 1st_BASE_945781_A3-3M3-G3_Ck516
xSPSFLSASVGDRVTITCRASQGIYSYLAWFQQKPGKAPKLLIYSVSTLQSGVPSRFSGSGSGTDFTLTINS
LQPEDFATYYCQQLNGYPSFGQGTRLEIR

SEQ ID NO: 201> 1st_BASE_904578_A3-2M1-A5_PWCgamma
xVQLLESGGALVQPGGSLRLSCTASDFTFSDYDMNWVRQAPGKGLEWLSYINSRGVTKYYADSVKGRFTISR
DNAKNSLYLQMNSLRAEDTALYYCARGLRGHDYGMDVWGQGTTVTVSS

SEQ ID NO: 202> 1st_BASE_945500_A3-2M1-A5_Ck516
xSPGTLSLSPGERATLSCRASQSVSSRFLAWYQQKPGQAPRLLIYGASSRASGIPDRFSGSGSETDFTLSIS
RLEPEDFAVYFCLQYGFSPPYTFGQGTKLEIK

SEQ ID NO: 203> 1st_BASE_896204_A3-2M2-G8_PWCgamma
xVQLLESGGRLVRPGGSQRLSCTASGFSFSSYEMSWVRQAPGKGLEWVSYISSSGTTIYYADSVKGRFTISR
DNAKNSLYLQMNSLRAEDTAVYYCARLLLLWLGETTAMDGMDVWGQGTTVTVSS

SEQ ID NO: 204> 1st_BASE_945551_A3-2M2-G8_Ck516
xSPSSLSASVGDRVTITCRASQKINRFLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTEFTLTITS
LQPDDFATYYCQQSYTSPLTFGGGTKVEIK

SEQ ID NO: 205> 1st_BASE_896206_A3-2M2-H5_PWCgamma
xVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSVIYNGGSSTYYADSVKGRFTISR
DNSKNTLYLRMNSLRVEDTAVYYCAKFLVLPAAAADYWGQGTLVTVSS

SEQ ID NO: 206 1st_BASE_945554_A3-2M2-H5_Ck516
xSPSFLSASVGDRVTITCRASQGISSHLAWYQQKPGKAPKLLIYAASTLHTGVPSRFSGSGSGTEFTLTITS
LQPEDFATYYCQQPGAFGPGTRLDIx

SEQ ID NO: 207> 1st_BASE_897923_A3-2M3-C9_PWCgamma
xVQLLESGGGLVQPGRSLRLSCAASGFPFSSYEMNWVRQAPGKGLEWISYISSTGSPIHYADSVRGRFTISR
DNAKNSLYLHMNSLRAEDTAIYYCAGDLLLWVPEATGATAGTGGLDVWGQGTTVTVSS

SEQ ID NO: 208> 1st_BASE_949089_A3-2M3-C9_Ck516
xSPSFLYASVGDRVTITCRASQTISKYLNWYHQKPGKAPNLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSIPRTFGQGTKVEIK

SEQ ID NO: 209> 1st_BASE_992133_A3-2M3-E9-H-1_Resend_1146_Resend
EVQLVQSETEVKEPGQSLKISCKGSGYTFTNYWIGWVCQMPGKGLEWMGIIYPGDSETRYSPSFQGQVTISV
DKSISTAYLQWSSLKASDTAMYYCAR

SEQ ID NO: 210> 1st_BASE_949097_A3-2M3-E9_Ck516
xSPSSLSASVGDRVTITCRASQSVSNYLNWYQQKPGKAPKLLIYAASTLQSGVPSRFSGSGSGTDFTLSISS
LQPEDFAIYYCQQTYSPPQNTFGQGTKLEIK

SEQ ID NO: 211> 1st_BASE_988416_A3-2M3-F9-H-2_1146
GQVELVESGPGLVKPSGSLSLTCAVSGGSITSSNWWSWVRQPPGKGLEWIGEIYHSGSADYNPSLKSRVTIS
VDTSKNQFSLKLRSVTAADTAVYYCARVEVMIKFGGVIRYFDYWGLGTLVTVSS

SEQ ID NO: 212> 1st_BASE_949101_A3-2M3-F9_Ck516
xSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYYASNLETGVPSRFSGSGSGTDFTFTISS
LQPEDFATYYCQQYDNLPPRYTFGQGTKLEIK

SEQ ID NO: 213> 1st_BASE_897935_A3-2M3-G3_PWCgamma
xVQLLESGGALVQPGRSLRLSCTASGFTFGDFALSWVRQAPGKGLEWVGVIRSKGYGGTTEYAASVKGRFSI
SRDDSKFIAYLQMNSLETEDTAVYFCTSTTLYYFVSGRAKDYGMDVWGQGTTVTVSS

SEQ ID NO: 214> 1st_BASE_949103_A3-2M3-G3_Ck516
xSPSSLSASVGDSVTITCRASQGIRNDLGWYQQKAGKAPKAVIYAVSTLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCLQDYSFPWTFGQGTKVEIK

SEQ ID NO: 215> 1st_BASE_988406_A3-2M3-C2-H-3_1146
EVQLQESGPGLVKPSETLSLTCTVSGGSITSSSYYWAWLRQPPGKGLEWIGNIYYSGNTDYNPSLKSRVTIS
ADTSMDQFSLRLRSMAASDTAVYYCASGLQTWDVTTGGAWASLDYWGQGTLVTVAS

SEQ ID NO: 216> 1st_BASE_949084_A3-2M3-C2_Ck516
xSPGTLSLSPGERATLSCRASQSVSSSFLAWYQHKPGQAPRLLIYGASIRATGIPDRFSGSGSGTDFILTIS
RLEPEDFAVYYCQQFGRTPPMYTFGQGTKLEIK