

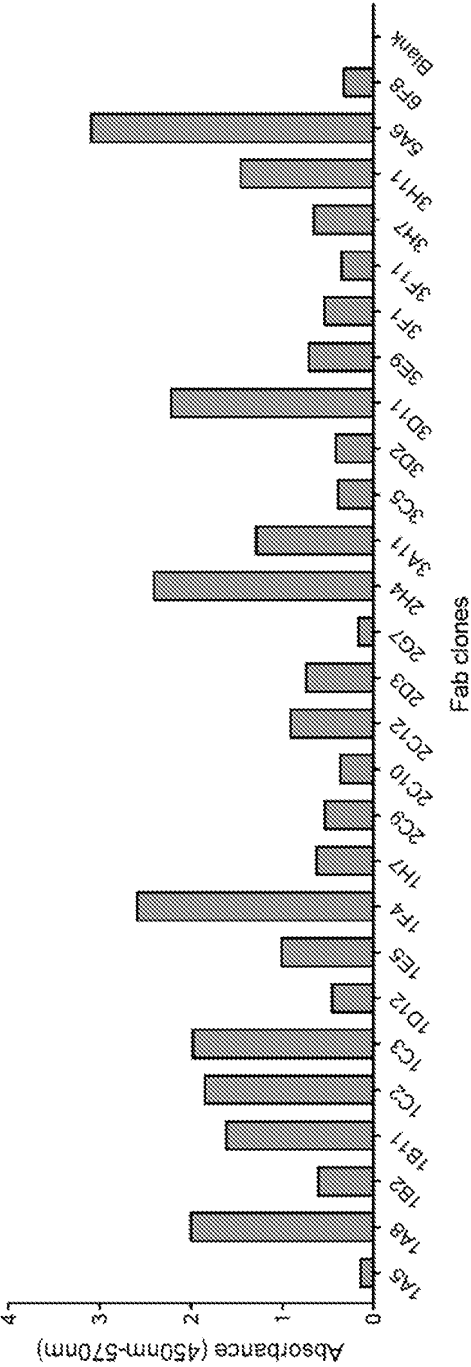


FIG. 1

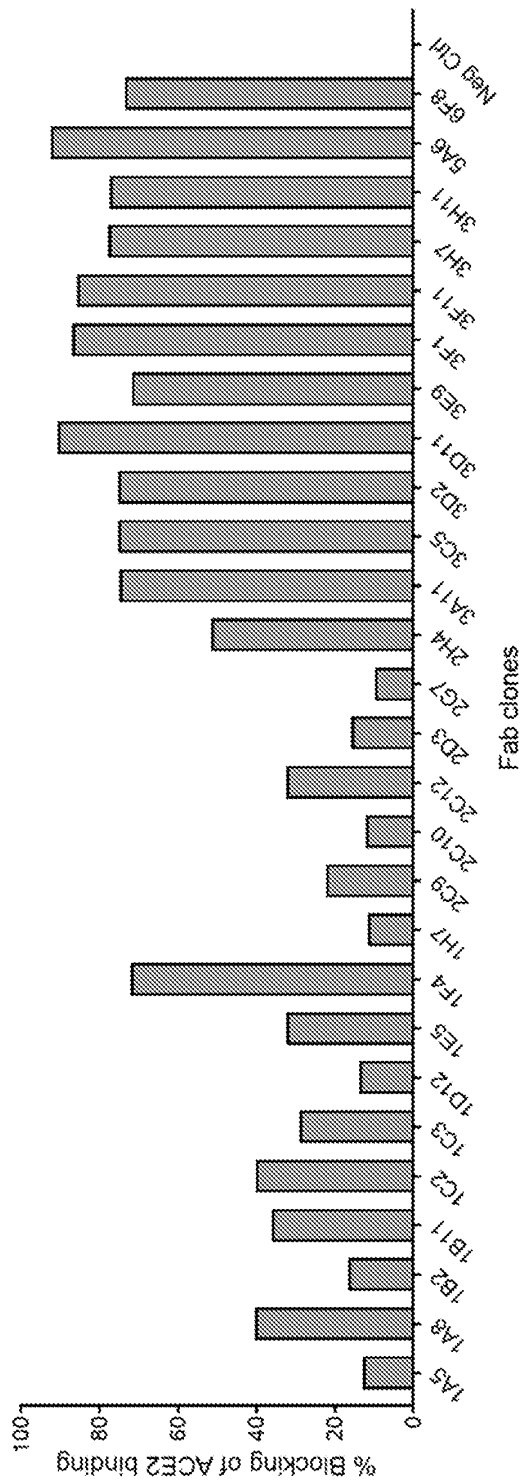


FIG. 2

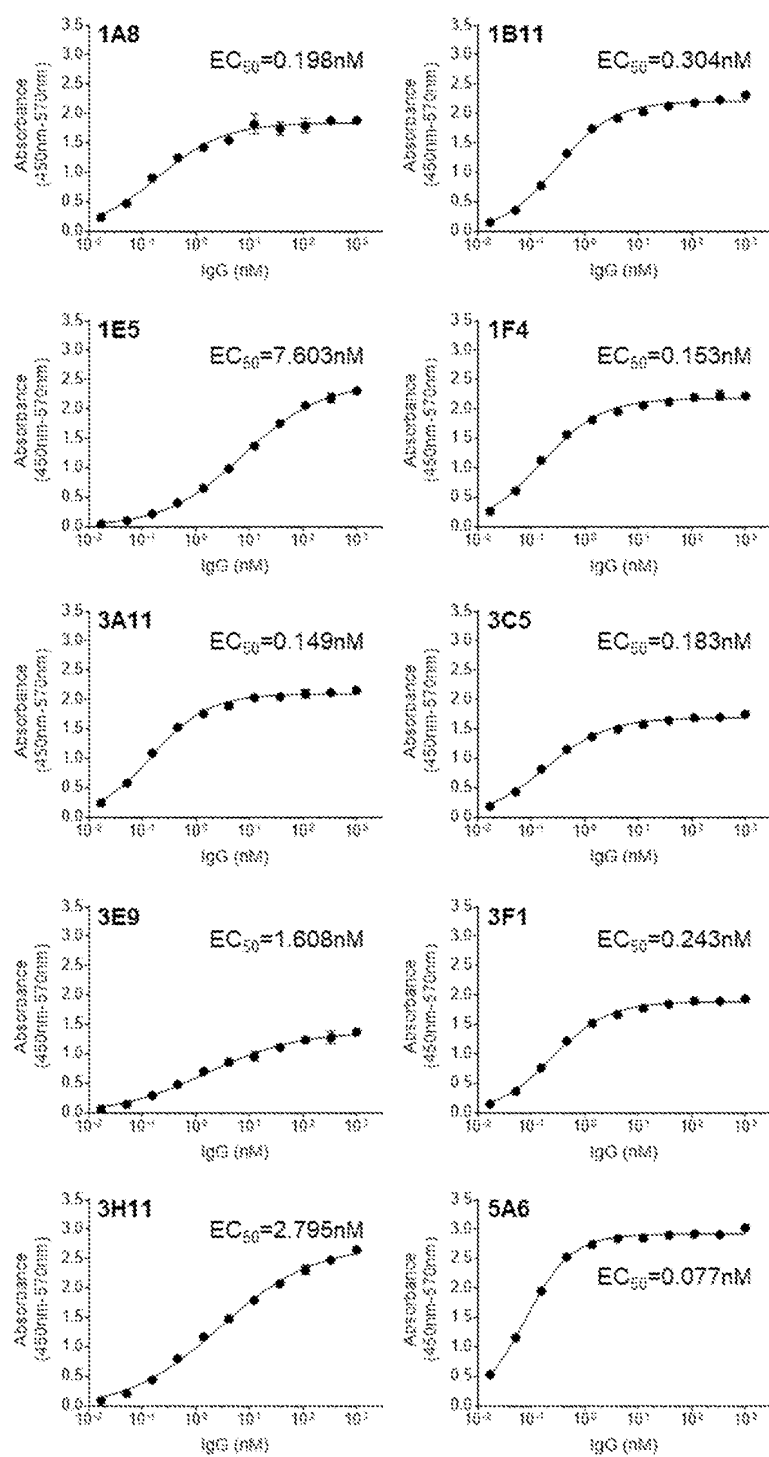


FIG. 3 (continued)

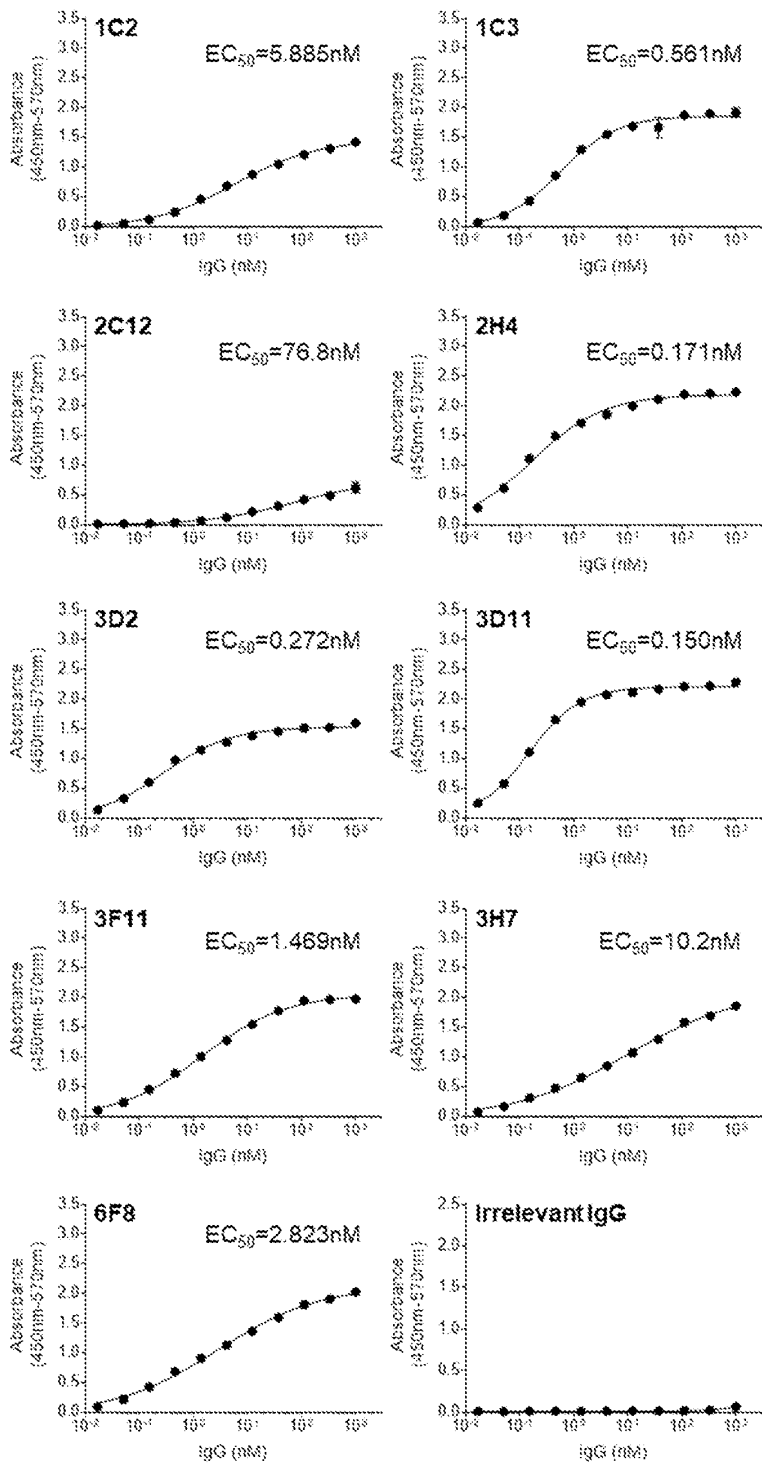


FIG. 3

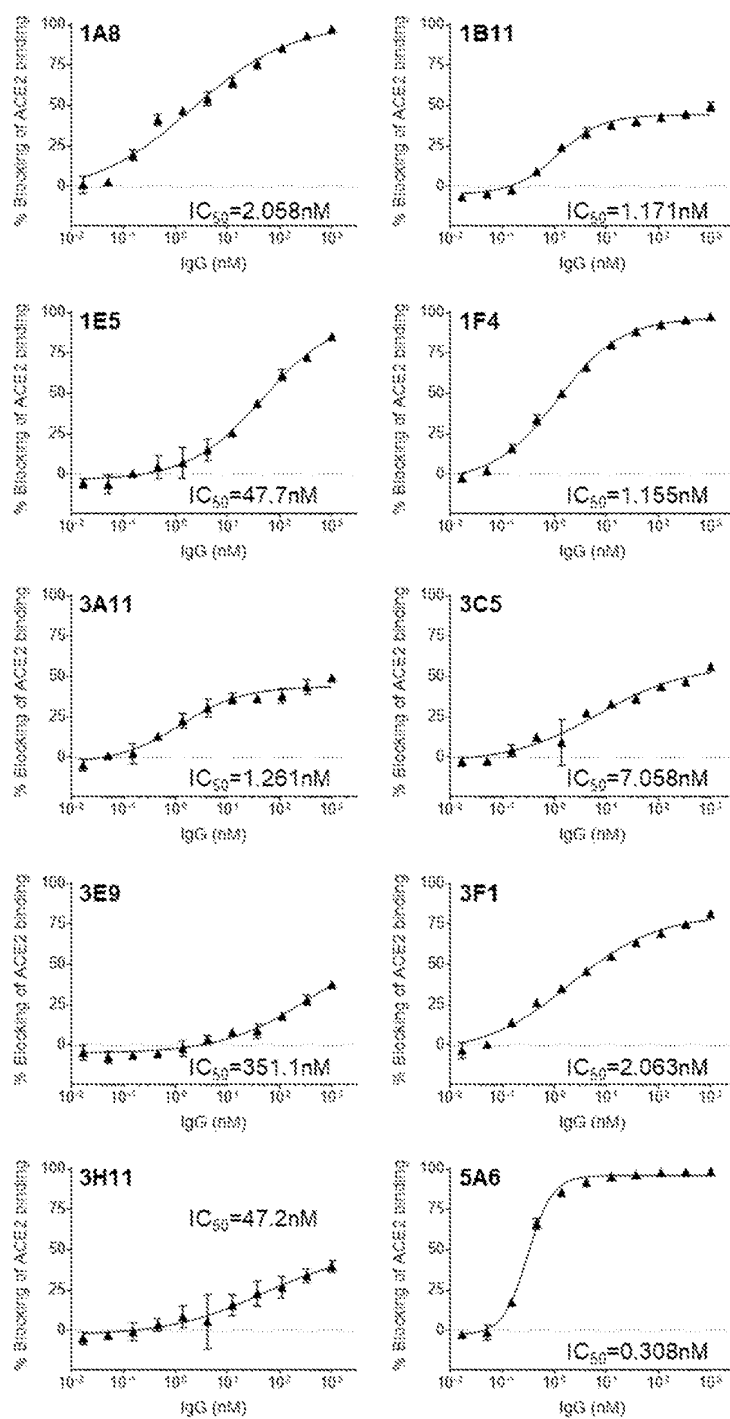


FIG. 4 (continued)

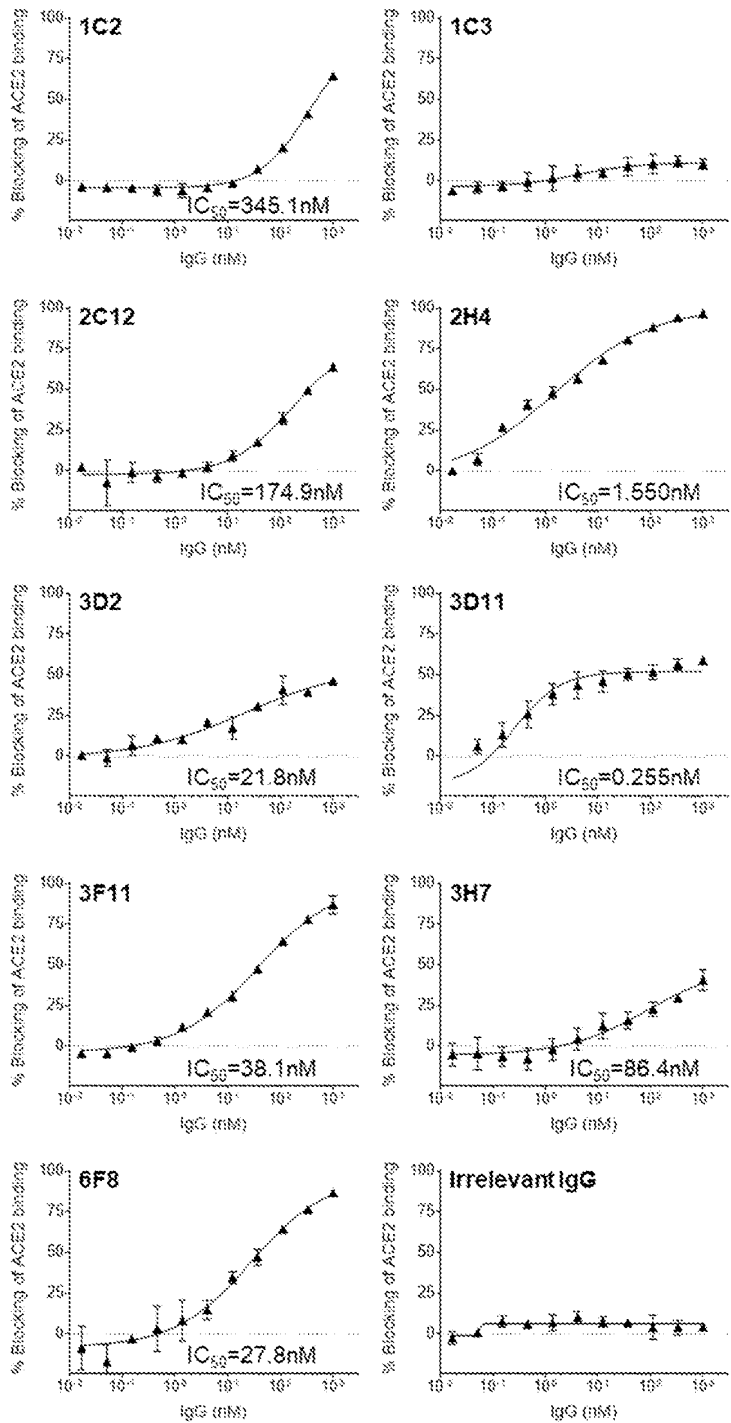


FIG. 4

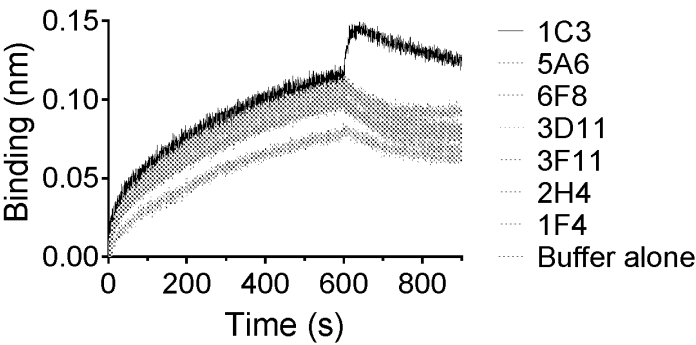


FIG. 5

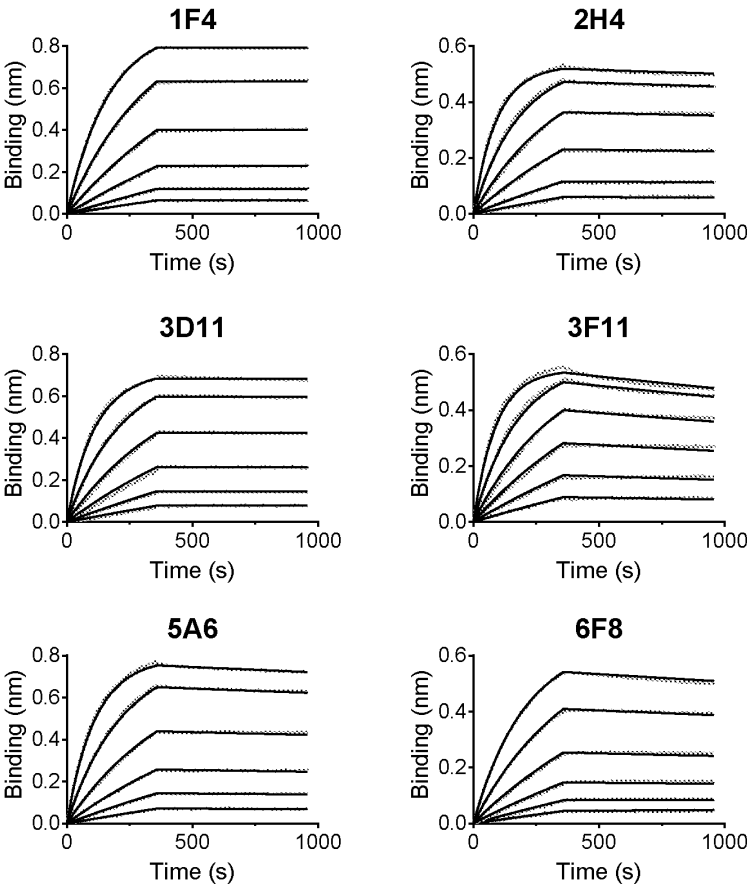


FIG. 6

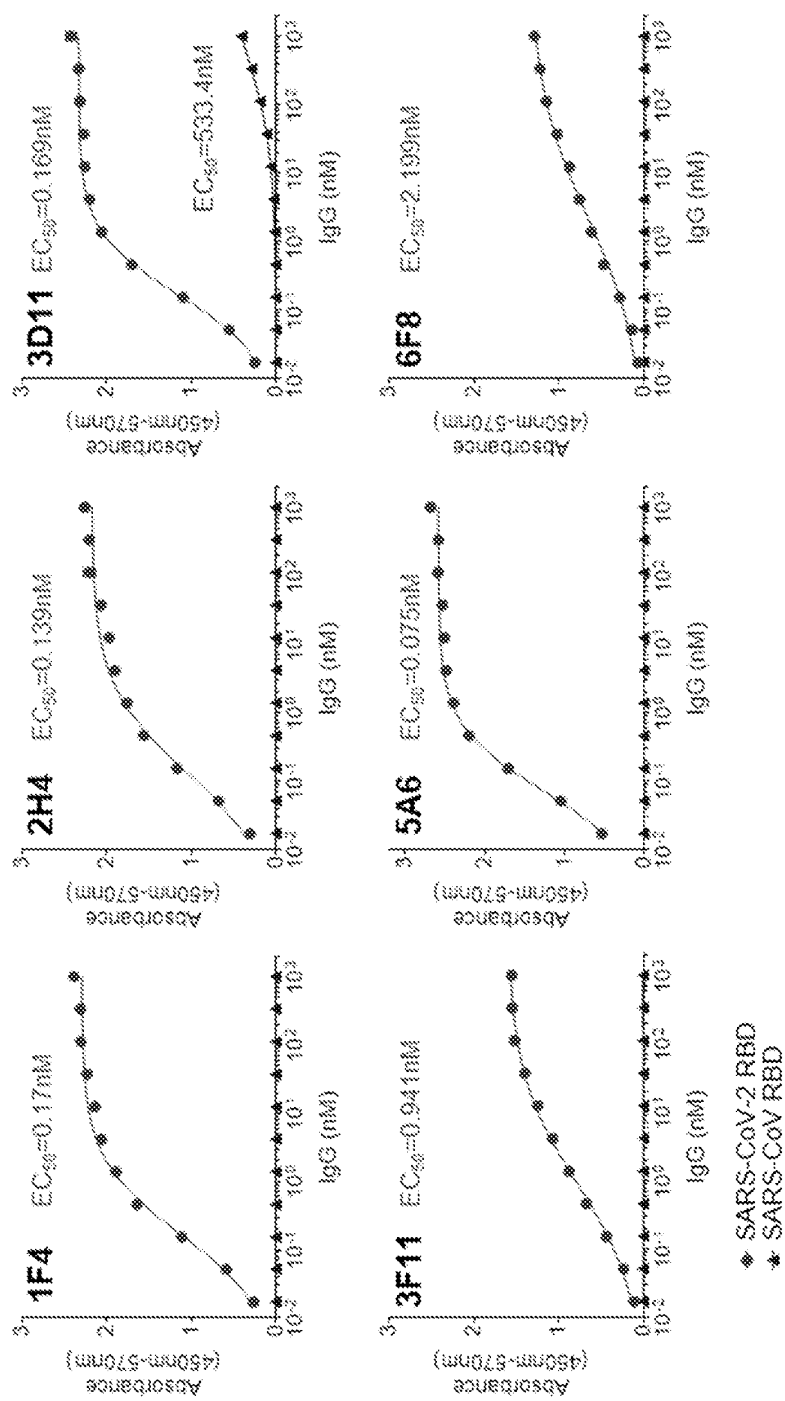


FIG. 7

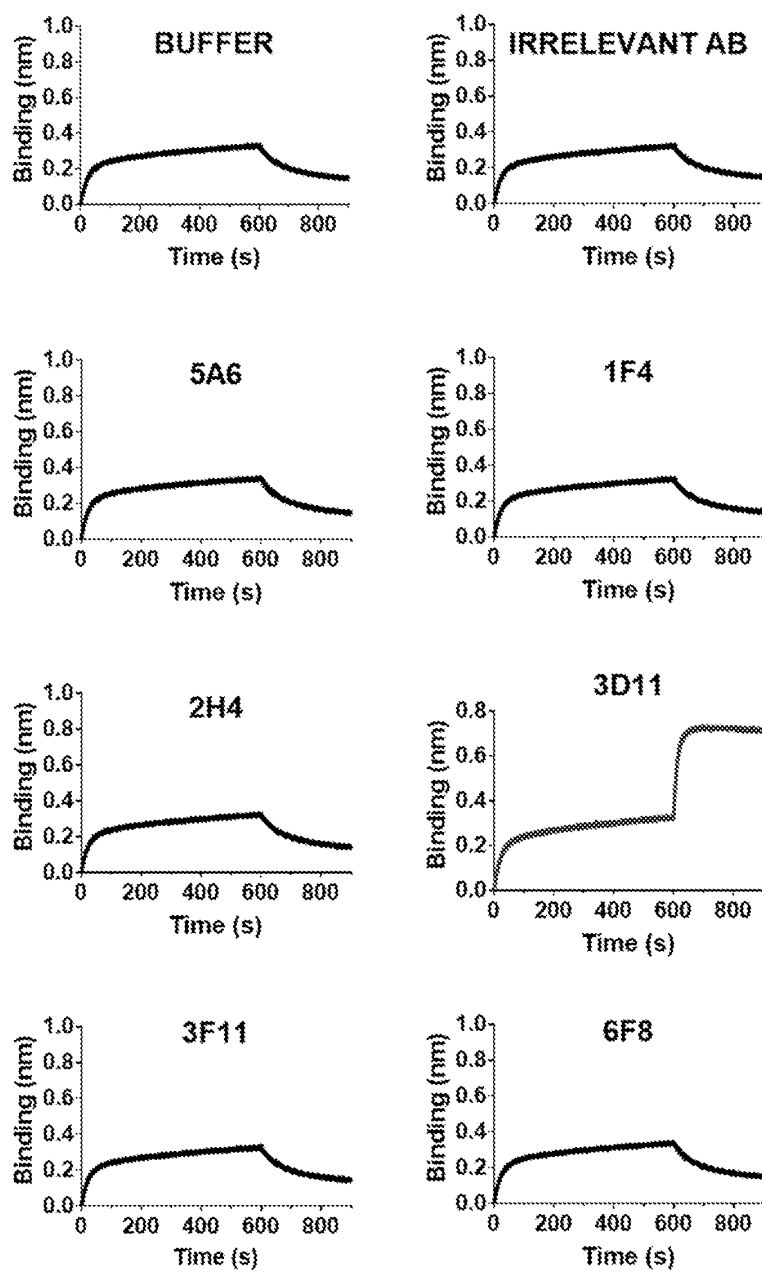


FIG. 8

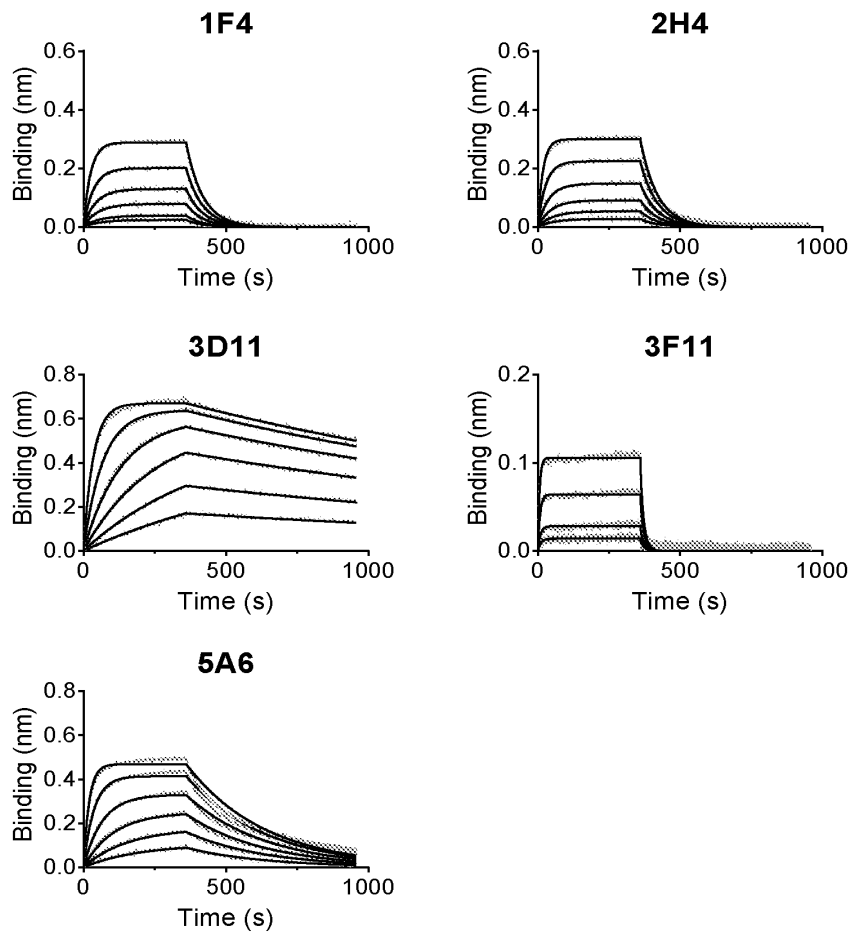


FIG. 9

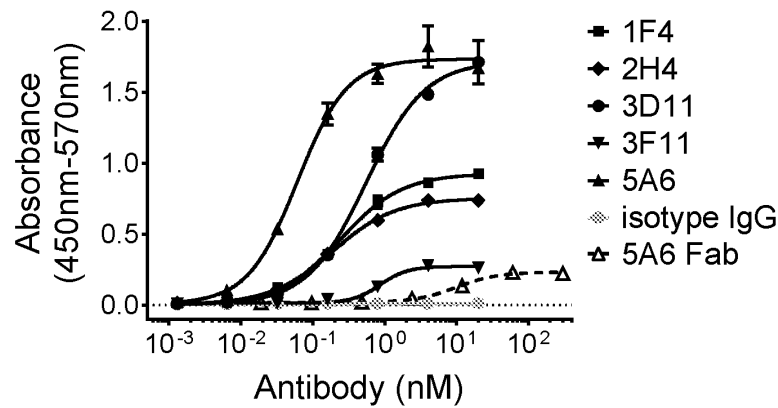


FIG. 10

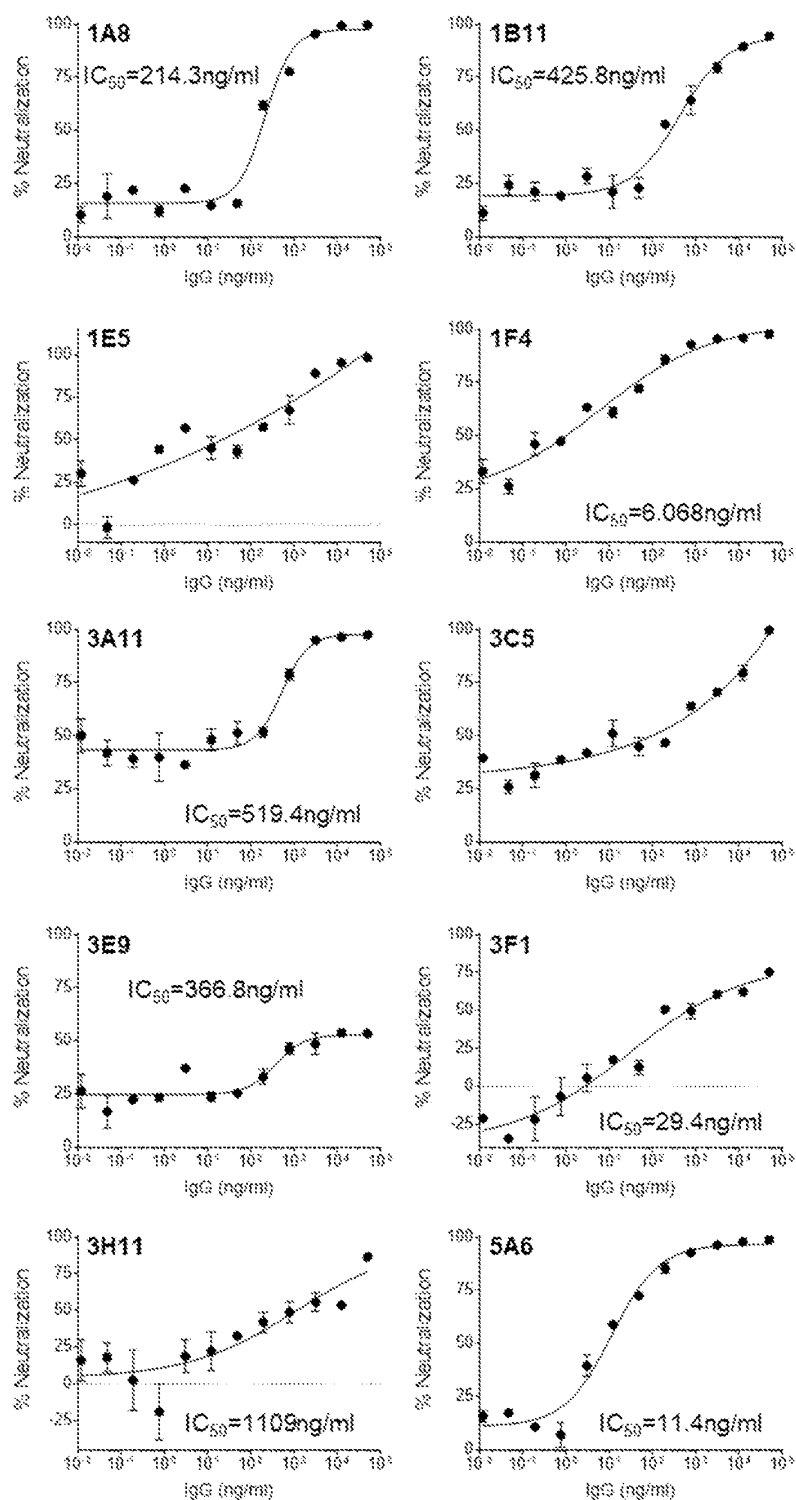


FIG. 11 (continued)

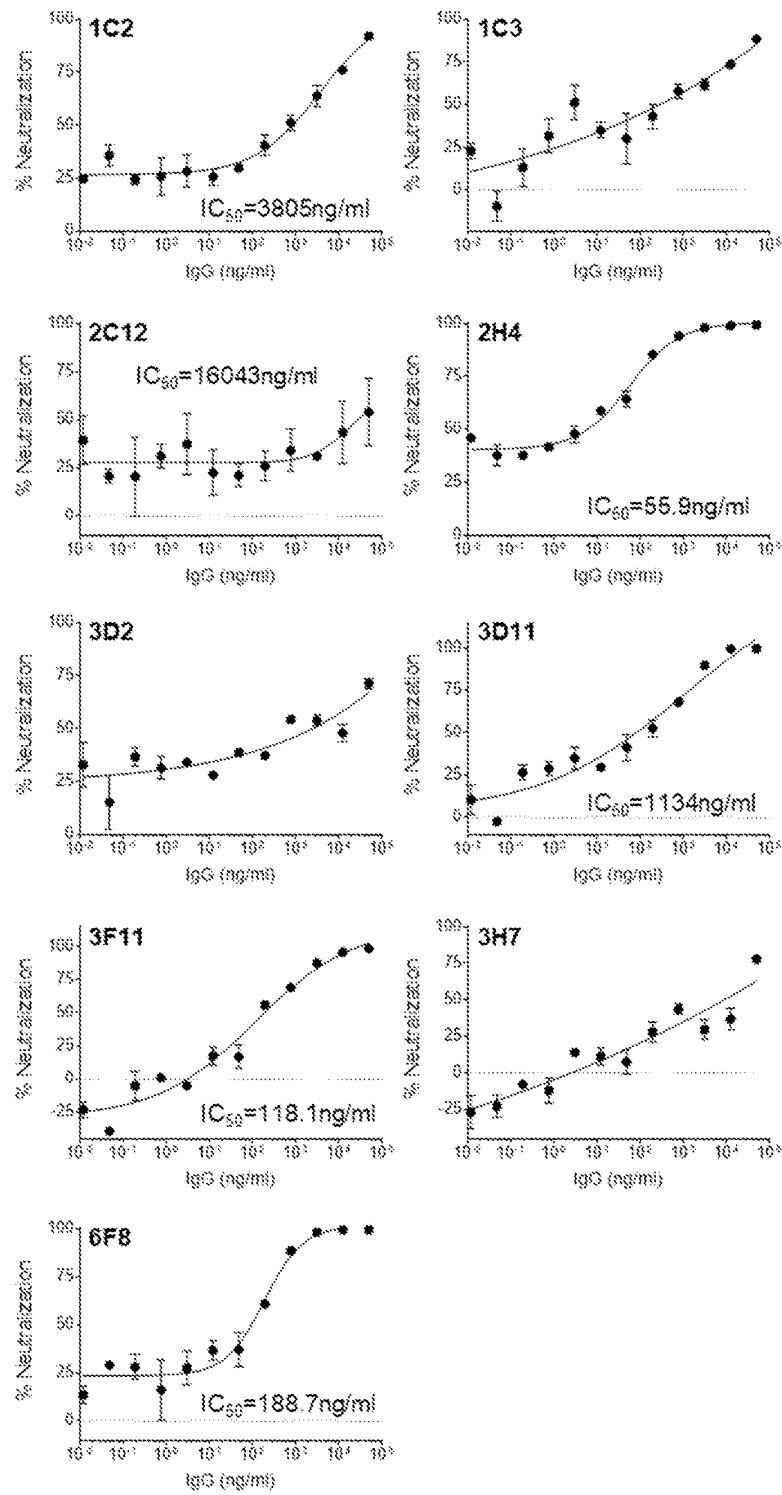


FIG. 11

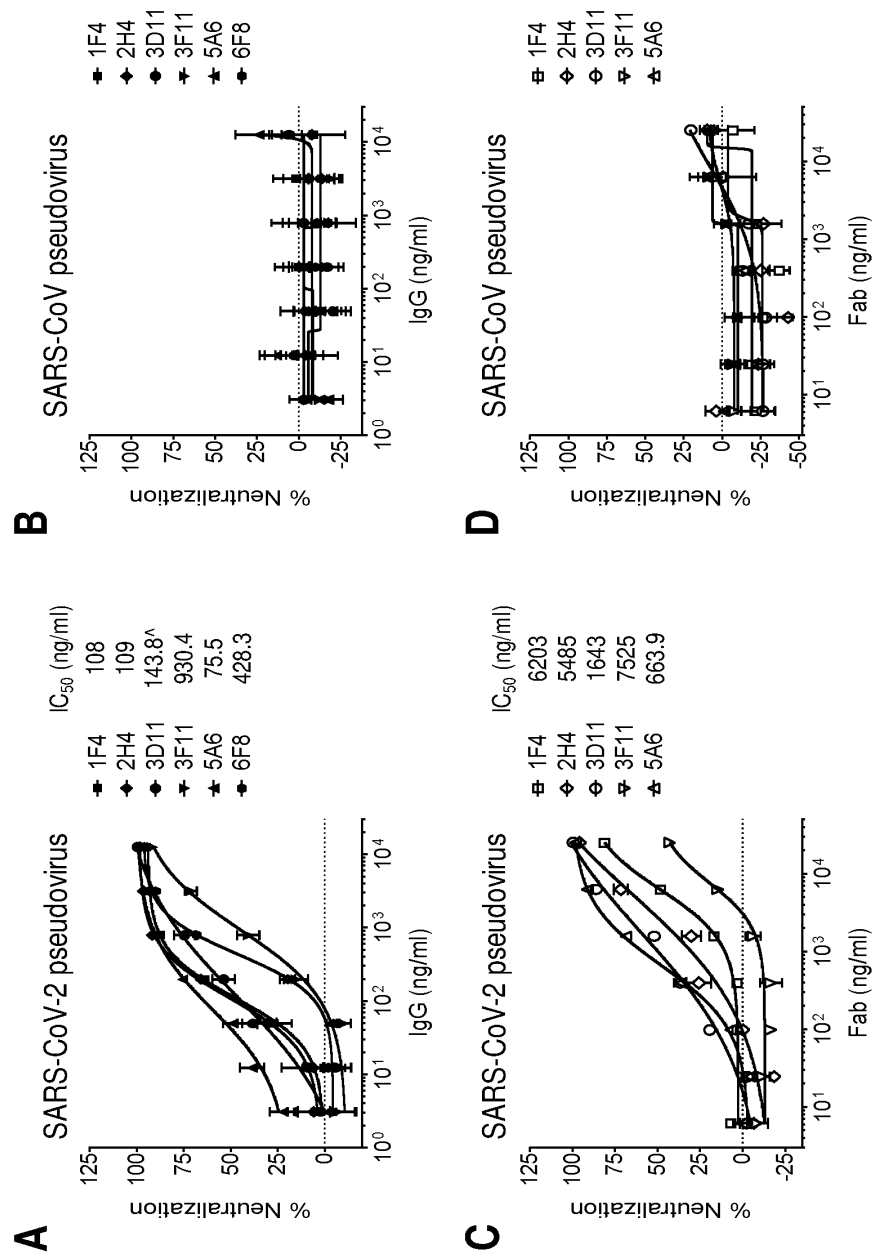


FIG. 12

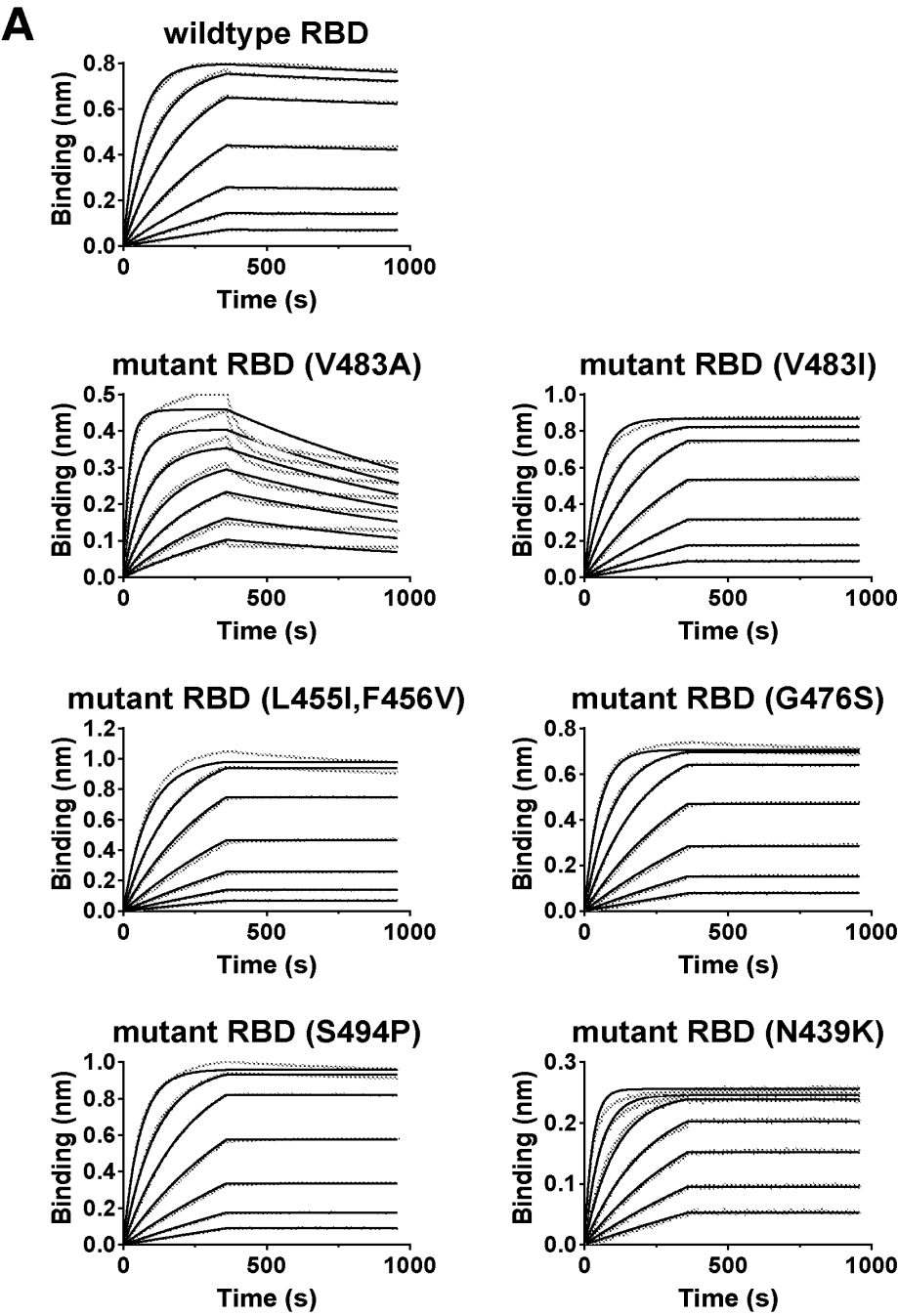


FIG. 13A

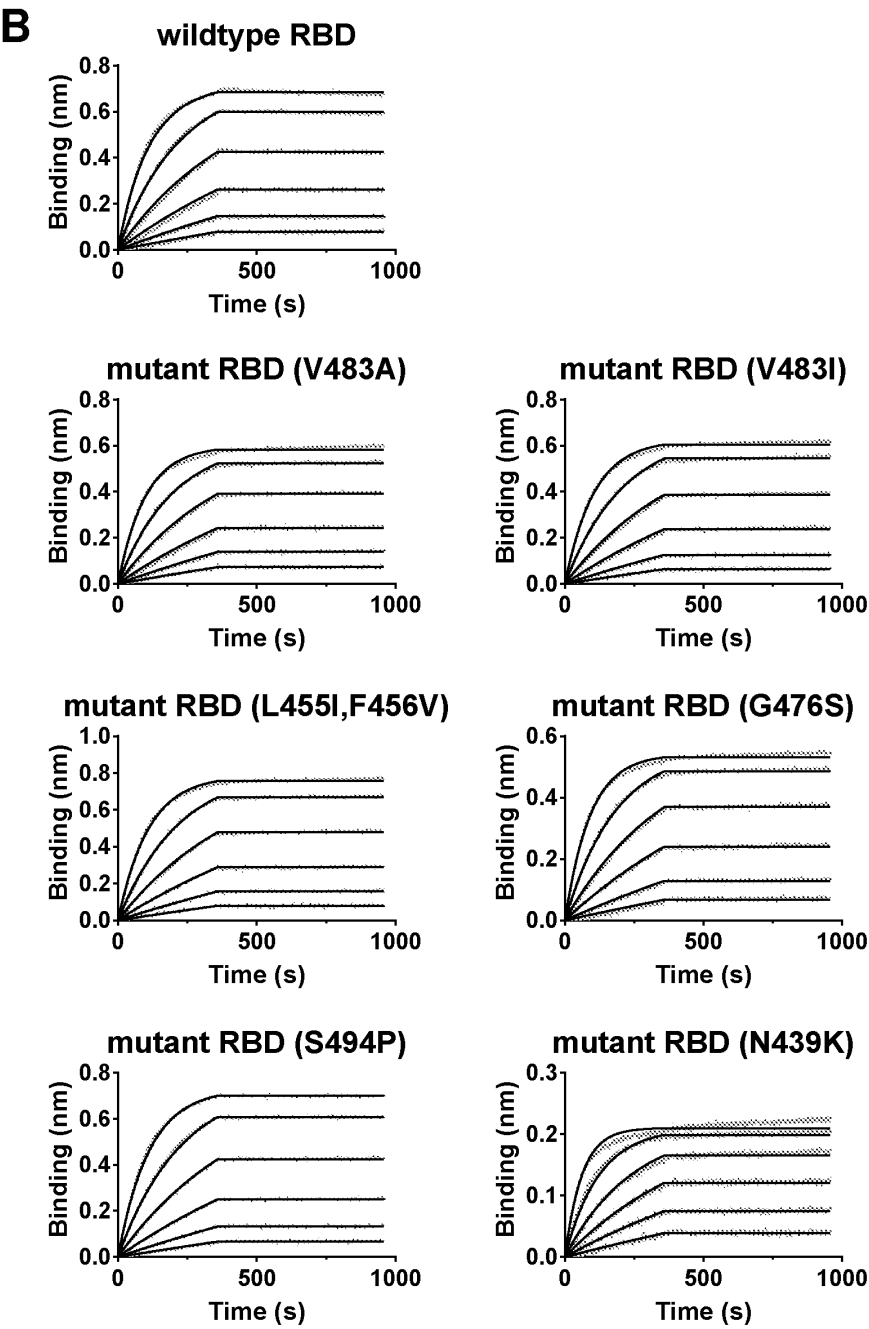


FIG. 13B

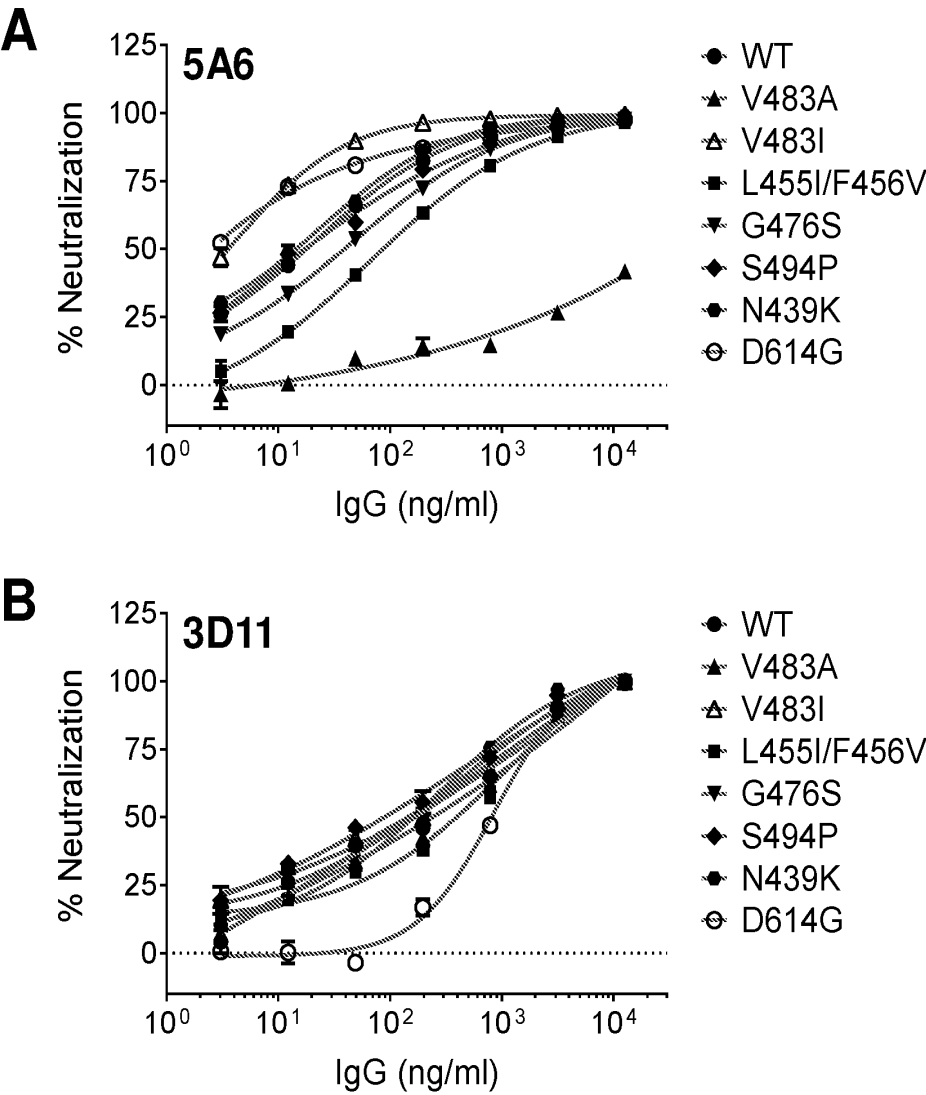


FIG. 14

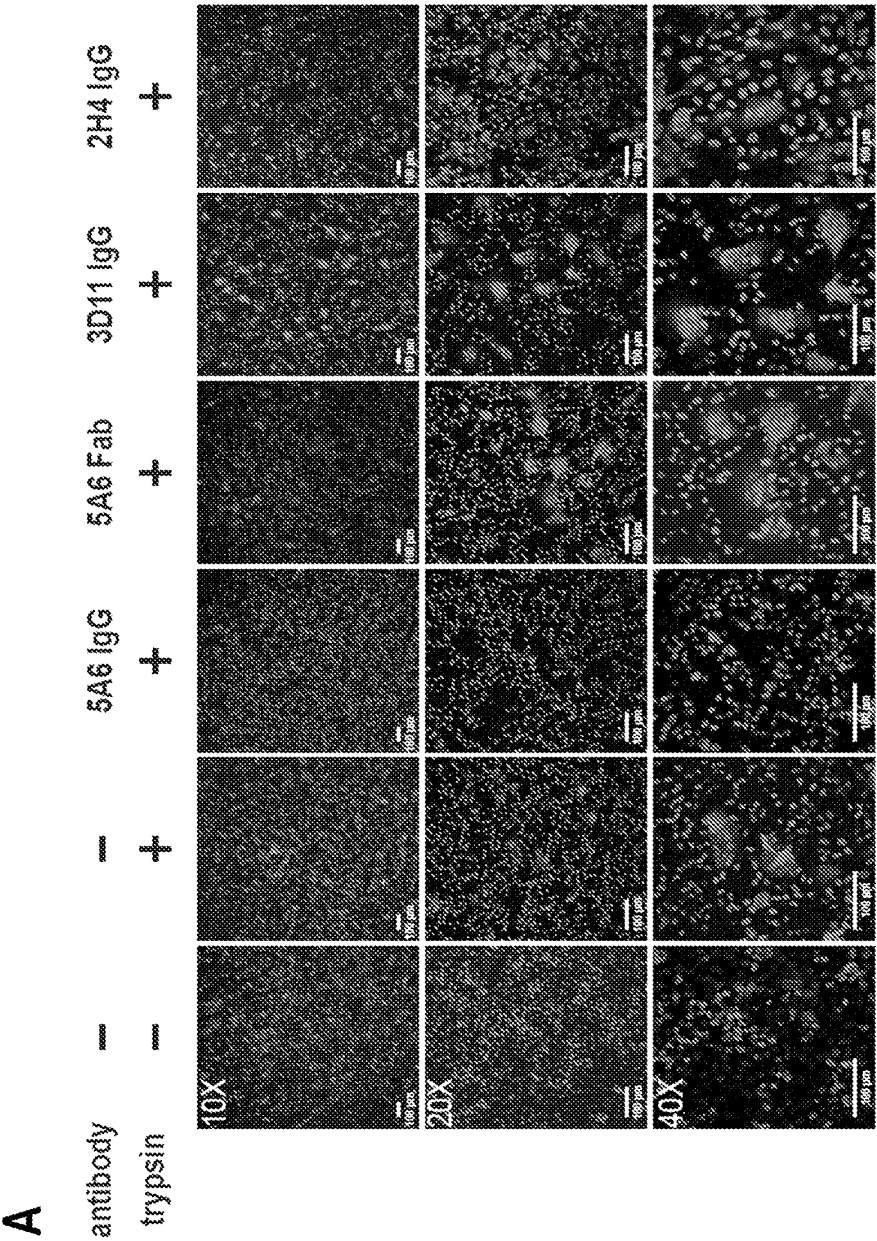


FIG. 15A

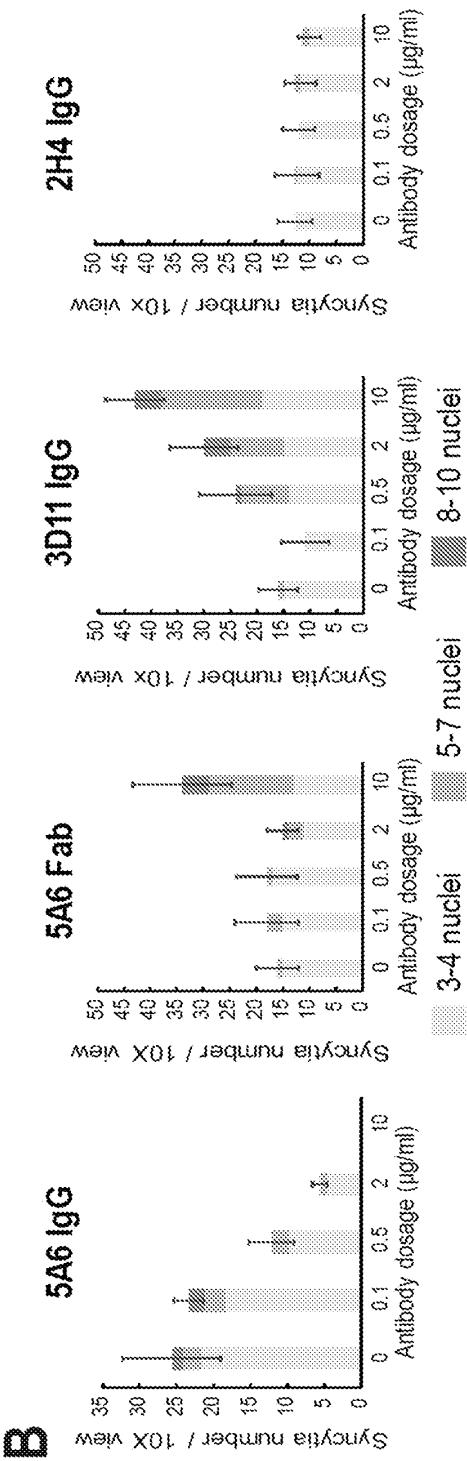


FIG. 15B

I. Amino-acid sequences

CDRs are in shaded and identified consecutively as CDR1 (first shaded region), CDR2 (second shaded region) and CDR3 (third shaded region).

I.1. Light chain variable domain sequences for human IgG1**1A5**

NFMLTQPHSVSESPGKTVAISCTGNSGSIASHYVQWFQQRPGSAPTTVIYEDNQRP SGVPDRFS
GSIDRSSNSASLTISGLKSEDEADYYCQSYGSGFVVFGGGTK

1A8

EIVLTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYNASTRESGV
PDRFSGSGSGTDFTLTISLQAEDVAVYYCQYYGTPYTFGQGTK

1B2

NFMLTQPHSVSESPGKTVTISCTGSGGRIATNYVQWYQQRPGSAPTTVIYEDNKRPSGVPHRFS
GSIDASSNSASLTISGLETEDEADYYCQSHDTSRQAVFGGGTK

1B11

DVVMTQSPPLSLPVTGPGEPAISCRSSQSLLYSNGYNYLDWYLQKPGQSPQLLIYIGSNRASGVP
DRFSGSGSGTDFTLKISRVEADVGVYYCMQALQTPYTFGQGTK

1C2

DVVMTQSPPLSLPVTGPGEPAISCRSSQSLHLSNGFTYLDWYLQKPGLSPLQLLIYIGSNRAPGVP
DRFSGSGSGTDFTLKISRVEADVGVYYCMQGIQTPYTFGQGTK

1C3

NFMLTQPHSVSESPGKTVTISCTRSSGSIASYVQWYQQRPGSSPTTVIYEDNQRP SGVPDRFS
GSIDSASNSASLTISGLQTEDEADYYCQSFDSSTQHVVFGGGTQ

1D12

NFMLTQPHSVSESPGKTVTISCTGSSGSIASNYVHWYQQRPGSAPTTVIYEDNQRP SGVPDRFS
GSIDSSNSASLTISGLKTEDEADYYCQSYDGSAAVVFGGGTK

1E5

NFMLTQPHSVSESPGKTLTISCTRSSGRIASNYVQWYQQRPGSAPTTVIYEDNQRP SGVPDRFS
GSIDSSNSASLTISGLKTEDEADYYCQSFDSGNQRVVFGGGTK

1F4

QSVLTQPPSVSGTPGQRTVITSCGSSSNIGRNFVSWYQQLPGAAPRLLMYEDNQRP SGVPDRFS
GSESATSASLAITGLQPEDEADYYCQSYDNSLFVVFGGGTK

1H7

NFMLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQRPGSSPTTVIYEDNQRP SGVPDRFS
GSVDSSNSASLTISGLKTEDEADYYCQSYDENIRVFGGGTK

2C9

EIVLTQSPGTLSSSPGERATLSCTASQTVGGSYLAWYQQKRGQPPRLIYGASTRAPGIPERFS
GSGSGTDFTLTISTLEPEDFAVYFCQYASSRTFGQTR

2C10

QSVVTQPPSASGSPGQSVTISCSGSSSTIGTNYVAWYQQLPGTAPKLLIYEDNKRPSGIPDRFS
GWRSGTSATLVISGLQTGDEADYYCGTWDSRLSVGVVFGGGTK

2C12

DIQMTQSPSSLSASIGDRVITICRASQSIINIYLNWYQQKPGKAPKLLIYAAASLQSGVPSRFSG
SGSATDFTLTISLQPEDFATYYCQSYITPQTFGQGTK

FIG. 16 (continued)

2D3

NFMLTQPHSVSESPGKTVTISCTGSSGSIASNYVQWYQQRPGSAPTTIIYEDNQRP SGVPDRFS
GSVDSSSNSASLTISGLKTEDEADYYCQSYDSSNWFVGGGTK

2G7

NFMLTQPHSVSESPGKTITISCTRSGGTIGSNYVQWYQQRPGSSPTTVIYEDNQRP SGVPDRFS
GSIDSSSNSASLTISGLKTEDEADYYCQSYDSSNRVFGGGTK

2H4

ETTLTQSPAFVSAAPGDKVISCKASEFIGDDVNWYQKPGEAPVFIIQEPVVRGIPPRFSG
SGYGTDFTLTIDDIQSEDSAFYFCLOYDSFPLTFGQGTK

3A11

QSALTQPASVSGSPGQAITMPCTGTSSDVGTINYVSWYQHFP GKAPKLLIYDVSHRPAGISDRF
SGSKSGNTASLTISGLQAEDEADYYCASFSSSSTLLVFGGGTK

3C5

NFMLTQPHSVSESPGKTVTISCTGSSGSIASNYVQWYQQRPGSAPTTVIYEDNQRP SGVPDRFS
GSIDSSSNSASLTISGLKTEDEADYYCQSYDSSNWFVGGGTK

3D2

NFMLTQPHSVSESPGKTVTISCTGSSGSIARNYVHWYQQRPGSAPTTVIYEDNQRP SGVPDRFS
GSIDSSSNSASLTISGLKTEDEADYYCQSYDRINKRVFGGGTR

3D11

NFMLTQPHSVSASPGKTVTIPCTGSSGNIASNYVQWYQQRPGSAPTTVIYEDNQRP SGVPDRFS
GSIDSSSNSASLTISGLKTEDEADYYCQSYDNNIQVFGGGTK

3E9

NFMLTQPHSVSESPGKTVTISCTGSSGSIASNYVQWYQQRPGSAPTTVIYEDNQRP SGVPDRFS
GSIDSSSNSASLTISGLKTEDEADYYCQSYDSSNLQWVFGGGTK

3F1

NFMLTQPHSVSESPGKTVTISCTASGGSIADNFVQWYQQRPGSAPTTIIYEDNRRPYGVDRFS
GSIDRSSNASLTVSGLMTEDEADYYCQSYDISNPVFGGGTK

3F11

ETTLTQSPGTLSSLPGESATLSCRASHSDGRNYIAWYQQTGQAPRLLVYDTSNRAAGVPDRFR
GSGSGTDFTLTISRLEPEDFAVYFCHQFRRSVSTFGQGTK

3H7

NFMLTQPHSVSESPGKTVTISCTRSTDSIASNYVQWYQQRPGSAPTTVIYEDNQRP SGVPDRFS
GSIDSSSNSASLTISGLKTEDEADYYCQSYDGVNRGVIFGGGTK

3H11

NFMLTQPHSVSESPGKTVTISCTRSSGNIASYYVQWYQQRPGSSPTTVIYEDNQRP SGVPDRFS
GSIDSSSNSASLTISGLQTEDEADYYCQSYDRPNEVFGGGTR

5A6

DIQLTQSPSSLSASVGHVRTITCRASQSISSYLNWYQKP GKAPKLLIYAASSLQSGVPSRFSG
GSGGTDFTLTISSLQPEDFATYYCQOSYNLPRIFGGGTK

6F8

EIVLTQSPGTLSSLSPGERATLSCTASQTINNNYLAWYQKP GQGPSLLIYDASSRATGVDRFS
GSGSGTDFTLTISRLEPEDFAVYYCQOYGSSPRTFGQGTK

FIG. 16 (continued)

I.2. Heavy chain variable domain sequences for human IgG1
--

1A5

QVQLQESGGGLVQP GGSRLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSV
KGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDYFRWLWGQGTL

1A8

QVQLQESGPGLVKPS ETL SLTCTVSGVSISRSDHWGVRQPPGKGLEWIGSISYSGSTYYNPS
LKSRTISVDTSKNQLSLKLSSVTAADTAVYYCARLASLYSTFDI WGHGTL

1B2

QVQLVQSGAEVKKPGASVKVSKASGYTFTSYMHVVRQAPGQGLEWMGII NPSGGSTSYAQKF
QGRVTMTRDTSTSTVYME LSSLRSED TAVYYCAIGEMAGDFDYWGQGTL

1B11

EVQLVQSGAEVKKPGSSVKVSKASGGTFSSYAI SWVRQAPGQGLEWMGGIPIFGTANYAQKF
QGRVTITADESTSTAYME LSSLRSED TAVYYCARDNPGYSSWSFNWEDFWGQGTL

1C2

EVQLVQSGAEVKKPGASVKVSKASGYTFTSYMHVVRQAPGQGLEWMGII NPSGGSTSYAQKF
QGRVTMTRDTSTSTVYME LSSLRSED TAVYYCASSAGTFYFDYWGQGTL

1C3

EVQLVQSGAEVKKPGASVKVSKASGYPFSTYYIHWVRQAPGQGLEWMGII DPSSGGSTSYAQKF
QGRVTMTRDTSTSTVYME LRLSRDDTAVFYCARVAEQHLDYFDYWGQGTL

1D12

EVQLVQSGAEVKKPGSSVKVSKASGGTFSSYAI SWVRQAPGQGLEWMGWI SAYNGNTNYAQKL
QGRVTMTDTSTSTAYME LRLSRSED TAVYYCARLEWLRGAFD YWGQGT

1E5

EVQLVQSGAEVKKPGSSVKVSKASGGTFSSYAI SWVRQAPGQGLEWMGGIPIFGTANYAQKF
QGRVTITADESTSTAYME LSSLRSED TAVYYCARALVGKWLRLRGFD YWGQGT

1F4

QVQLQQSGPGLVKPSQ TSLTCAISGDSVSSNSAAWN WIRQSPSRGLEWLGRFTYRISKWYNDYA
VSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCAREKGI EGPAFDYWGQGT

1H7

QVQLQQWGAGLLKPSETLPLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGETNHSGSTNYNPSLK
SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGRWLRGAFD YWGQGT

2C9

QVQLVQSGAEVKKPGSSVKVSKASGGTFSSYAI SWVRQAPGQGLEWMGRIPIILGTANYAQKF
QGRVTITADKSTSTAYME LSSLRSED TAVYYCARHGGVGATTGYYYMDYWGKGTT

2C10

QVQLQQWGAGLLKPSETL SLTCGVYGGSFSGYYWSWIRQSPGKGLEWIGETNYRGNTNYNPSLK
SRVTISVDTSKNQFSLNVNSVTAADTAVYYCARWDGGNSVDH YWGQGT

2C12

QVQLVESGGGVVQPG RSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYADSV
KGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGGRFHYYYAMD YWGQGT

2D3

EVQLVQSGAEVKKPGSSVKVSKASGGTFSSYAI SWVRQAPGQGLEWMGGIPIFGTANYAQKF
QGRVTITADESTSTAYME LSSLRSED TAVYYCASSGWLRGAFD YWGQGT

FIG. 16 (continued)

2G7

QVQLQQWGAGLLKPSSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYPNPSLK
SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARQKWLRGAFDYGWGQGT

2H4

QVQLVQSGAEVTKPGASVKVSCASGYTFSGYYIHWVRQAPGQGLEWMGRVNPNSGGTKYAQKF
QDRVTLTTRDTSISTAYMELTSLRSDDTAMYFCARGGRLPLAAGYIDYWGQGT

3A11

EVQLVQSGAEVKKPGASVKVSCASGYTFSTYDISWVRQAPGQGLEWMGWISTYNGDTNYAQKF
QGRVTMTTDTSTSTIYMELRSLRSDDTAVYYCARGDSSVGYEYFQHWGQGT

3C5

QVQLQQWGAGLLKPSSETLSLTGCVYGGSLSGYYWSWIRQPPGKGLEWIGEINHSGSTNYPNPSLK
SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARPWWLRGAFDYGWGQGT

3D2, 3D11

QVQLQQWGAGLLKPSSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYPNPSLK
SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARPWWLRGAFDYGWGQGT

3E9

EVQLVQSGAEVKKPGASVKVSCASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKL
QGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARGITMTISDYWGQGT

3F1

QVQLVQSGGGVVQPGRLRLSCLASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADSV
KGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDGSGGMDYWGQGT

3F11

EVQLVQSGAEVKKPGASVKVSCASGYTFSSSGISWVRQAPGQGLEWMGWISTYNGNTNYAQNF
QGRVTMTTDTSTSTVYMELRGLTSDDTAVYYCATSIYVAGIDYWGQGT

3H7

QVQLVQSGGGVVQPGRLRLSCLASGFTFSSNYGMHWVRQAPGKGLEWVAVINHDGNTKYYADSV
KGRFTVSRDN SKNTLYLQMDTLRAEDTAVYYCVRDQAGVWNGYSYWGQGT

3H11

QVQLVQSGAEVKKPGASVKVSCASGYTFTSYIMHWVRQAPGQGLEWMGISTNPSSGGSISYAQKF
QGRVTMTTRDTSTNTVYMELSLRSDDTAVYYCASSVVPAAIYDYVYGMDYWGQGT

5A6

QVQLQESGGGLVQPGGSLRLSCLASGFTFSSYEMNWVRQAPGKGLEWVAVISYDGSNKYYADSV
KGRFTISRDN AKNSLYLQMNSLRAEDTAVYYCARLITMVRGEDYWGQGT

6F8

QVQLVESGGGLVQPGGSLRLSCLASGFTVSSNYMSWVRQAPGKGLEWVSVISGGGSITYYADSVK
GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDYGDYFDYWGQGT

FIG. 16

II. Nucleotide sequences

CDRs are in shaded and identified consecutively as CDR1 (first shaded region), CDR2 (second shaded region) or CDR3 (third shaded region).

II.1. Light chain variable domain sequences for human IgG1**1A5**

AATTTTATGCTGACTCAGCCCCACTCTGTGTCGGAGTCTCCGGGGAAGACGGTAGCCATCTCCT
GCACCGGCAACAGTGGCAGCATTGCCAGCCACTATGTGCAGTGGTTCCAACAGCGCCCGGGCAG
TGCCCCCACTACTGTGATCTATGAAGATAACCAAAGACCCTCTGGGGTCCCTGATCGGTTCTCT
GGCTCCATCGACAGGTCGTCCAACCTCTGCCTCCCTCACCATCTCTGGACTTAAGAGTGAGGACG
AGGCTGACTATTACTGTCAGTCTTATGGCAGCGGGCTTTGTGGTCTTCGGCGGAGGGACCAAG

1A8

GAAATTGTGTTGACGCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCA
ACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCTTGGTATCA
ACAGAAAACCAGGACAGCCTCCTAAGTTGCTCATTACCTGGGCTCTACCCGGGAATCCGGGGTC
CCTGACCGATTAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGG
CTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATGGTACTCCGTACACTTTTGGCCAGGG
GACCAAG

1B2

AATTTTATGCTGACTCAGCCCCACTCTGTGTCGGAGTCTCCGGGGAAGACCGTAACCATCTCCT
GCACCGGCAGCGGTGGCAGGATTGCCACCAACTATGTGCAGTGGTACCAGCAGCGCCCGGGCAG
TGCCCCCACTACTGTGATCTATCAGGATAATAAAAGACCCTCTGGGGTCCCTCATCGGTTCTCT
GGCTCCATCGACGCCTCCTCCAATTCTGCCTCCCTCACTATCTCTGGACTGGAGACTGAGGACG
AGGCTGACTACTACTGTCAGTCTCATGATACCAGCGTCAGGCGGTCTTCGGCGGCGGGACCAA
G

1B11

GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCATCT
CCTGCAGGTCTAGTCAGAGCCTCCTGTATAGTAATGGATACAACCTATTTGGATTGGTACCTGCA
GAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTGGGTTCTAATCGGGCCTCCGGGGTCCCT
GACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGAGGCTG
AGGATGTTGGGGTTTATTACTGCATGCAAGCTCTACAAACCCCGTACACTTTTGGCCAGGGGAC
CAAG

1C2

GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCATCT
CCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATTACCTATTTGGATTGGTACCTGCA
GAAGCCAGGGCTGTCTCCACAGCTCCTGATCTACTGGGTTCTAATCGGGCCCCCGGGGTCCCT
GACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGAGGCTG
AGGATGTTGGGGTTTATTACTGCATGCAAGGTATACAAACCCCGTACACTTTTCGGCGGGGGGAC
CAAG

FIG. 17 (continued)

1C3

AATTTTATGCTGACTCAGCCCCACTCTGTGTCGGAGTCTCCGGGGAAGACGGTAACCATCTCCT
GCACCCGAGCAGCGGCAGCATTGCCAGCTACTATGTGCAGTGGTACCAGCAGCGCCCGGGCAG
TTCCCCACCACTGTGATCTATGAGGATGACCAAAGACCCTCTGGGGTCCCTGATCGGTTCTCT
GGCTCCATCGACAGTGCCTCCAACCTCAGCCTCCCTCACCATCTCTGGCCTGCAGACTGAGGACG
AGGCTGACTACTACTGTGAGTCTTTTGATAGCAGCATTCAACATGTGGTCTTCGGCGGAGGGAC
CCAG

1D12

AATTTTATGCTGACTCAGCCCCACTCTGTGTCGGAGTCTCCGGGGAAGACGGTAACCATCTCCT
GCACCCGAGCAGTGGCAGCATTGCCAGCAATTATGTGCATTGGTACCAGCAGCGCCCGGGCAG
TGCCCCACCACTGTGATCTATGAGGATAACCAAAGACCCTCTGGGGTCCCTGATCGGTTCTCA
GGCTCCATCGACAGCTCCTCCAACCTCTGCCTCCCTCACCATCTCTGGACTGAAGACTGAGGACG
AGGCTGACTACTACTGTGAGTCTTTTGATGGCAGCGCTTGGGTCTTCGGCGGAGGGACCAAG

1E5

AATTTTATGCTGACTCAGCCCCACTCTGTGTCGGAGTCTCCGGGGAAGACGGTAAACCATCTCCT
GCACCCGAGCAGTGGCAGGATTGCCAGCAACTATGTGCAGTGGTACCAGCAGCGCCCGGGCAG
TGCCCCACCACTGTGATCTATGAGGATAACCAAAGACCCTCTGGGGTCCCTGATCGGTTCTCT
GGCTCCATCGACAGCTCCTCCAACCTCTGCCTCCCTCACCATCTCTGGACTGAAGACTGAGGACG
AGGCTGACTACTACTGTGAGTCTTTTGATAGCGGCAATCAACGGGTGGTTTCGGCGGAGGGAC
CAAA

1F4

CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGGGACCCCGGGCAGAGGGTCACCATCTCTT
GCTCTGGAAGCAGCTCCAACATCGGACGTAATTTTGTATCCTGGTACCAGCAGCTCCCAGGAGC
GGCCCCAGACTCCTCATGTATAGGAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCT
GGCTCCGAGTCTGCCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGCCTGAGGATGAAGCTG
ATTATTACTGCCAGTCTTATGACAACAGCCTGTTTGTGGTATTTCGGCGGAGGGACCAAG

1H7

AATTTTATGCTGACTCAGCCCCACTCTGTGTCGGAGTCTCCGGGGAAGACGGTAACCATCTCCT
GCACCCGAGCAGTGGCAGCATTGCCAGCAACTATGTGCAGTGGTACCAGCAGCGCCCGGGCAG
TTCCCCACCACTGTGATCTATGAGGATAACCAAAGACCCTCTGGGGTCCCTGATCGGTTCTCT
GGCTCCGTCGACAGCTCCTCCAACCTCTGCCTCCCTCACCATCTCTGGACTGAAGACTGAGGACG
AGGCTGACTACTACTGTGAGTCTTTTGATGAAAACATTGGGGTCTTCGGCGGAGGGACCAAG

2C9

GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTCGTCTCCTGGGGAGAGAGCCACCCTCT
CCTGCACGGCCAGCCAGACTGTGGCGGCAGCTACTTAGCCTGGTACCAGCAAAAACGTGGCCA
GCCTCCCAGGCTCCTCATCTATGGTGGGTCCACTAGGGCCCCCTGGCATCCCAGAGAGATTTAGT
GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCACCCCTGGAGCCTGAAGATTTTGAG
TGTATTCTGTGAGCAGTATGCCAGTTACGGACGTTTCGGCCAAGGGACCAGG

FIG. 17 (continued)

2C10

CAGTCTGTCGTGACGCAGCCGCCCTCCGCGTCCGGGTCTCCTGGACAGTCAGTCACCATCTCCT
GTTCTGGAAGCAGCTCCACCATTGGAACATAATTATGTGGCCTGGTACCAGCAGCTCCAGGAAC
AGCCCCAACTCCTCATTATGACAATTATAAGCGACCCTCGGGAATTCCTGACCGATTCTCT
GGCTGGAGGTCTGGCACGTTCAGCCACCCTGGTCATCAGCGGACTCCAGACCGGGGACGAGGCCG
ATTATTACTGCGGAACGTGGGATAGTAGGCTGAGTGTGGCGTGTTCGGCGGAGGGACCAAG

2C12

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTATAGGAGACAGAGTCACCATCA
CTTGCCGGGCAAGTCAGAGCATTAACTCTATTAAATTGGTATCAGCAGAAACCAGGGAAAGC
CCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCAGTGGC
AGTGGATCTGCGACAGATTTCACTCTCACCATCAGCAGTCTGCAGCCTGAAGATTTTGCAACTT
ACTACTGTCAACAGAGTTACATTACCCCTCAGACGTTTCGGCCAAGGGACCAAG

2D3

AATTTTATGCTGACTCAGCCCCACTCTGTGTGCGAGTCTCCGGGGAAGACGGTAACCATCTCCT
GCACCGGCAGCAGTGGCAGCATTGCCAGCAACTATGTGCAGTGGTACCAGCAGCGCCCGGGCAG
TGCCCCCACCCTATTATCTATGAGGATAACCAAAGACCCTCTGGGGTCCCTGATCGGTTCTCT
GGCTCCGTCGACAGCTCCTCCAACCTCTGCCTCCCTCACCATCTCTGGACTGAAGACTGAGGACG
AGGCTGACTACTACTGTGAGTCTTATGATAGCAGCAATTGGGTGTTTCGGCGGAGGGACCAAG

2G7

AATTTTATGCTGACTCAGCCCCACTCTGTGTGCGAGTCTCCGGGGAAGACGATAACCATCTCCT
GCACCCGCAGCGGTGGCACCATTGGCAGCAACTATGTGCAGTGGTACCAGCAGCGCCCGGGCAG
TTCCCCCACCCTGTGATCTATGAGGATAACCAAAGACCCTCTGGGGTCCCTGATCGGTTCTCT
GGCTCCATCGACAGCTCCTCCAACCTCTGCCTCCCTCACCATCTCTGGACTGAAGACTGAGGACG
AGGCTGACTACTACTGTGAGTCTTATGATAGCAGCAATGGGTGTTTCGGCGGAGGGACCAAG

2H4

GAAACGACACTCACGCAGTCTCCAGCATTCTGTGTGCGCGGCTCCCGGAGACAAAGTGTCATCT
CCTGCAAAGCCAGTGAATTCATTGGAGATGATGTGAAGTGGTACCAACAGAAACCAGGAGAGGC
TCCTGTTTTTCATCATTCAAGAGGCTCGTGTTCCCGTTCTGTGAATCCACCCCGATTCAAGTGGC
AGCGGCTATGGAACAGATTTTACCCTCACAATTGATGACATACAATCTGAGGATTCTGCATTTT
ACTTCTGTCTGCAATATGATTCTTTCCCTCTCACTTTTGGCCAGGGGACCAAG

3A11

CAATCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGGCGATCACCATGCCCT
GCACTGGAACCAGCAGTGACGTTGGTACTTATAACTATGTCTCCTGGTATCAACACTTCCCAGG
CAAAGCCCCAACTCTTGATTTATGATGTGAGTCATCGGCCCGCGGGGATTTCTGATCGCTTC
TCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGCCTCCAGGCTGAGGACGAAG
CTGACTATTACTGCGCTTCATTTTCATCCAGCAGCACTCTCTTAGTGTTCGGCGGAGGGACCAAG

G

FIG. 17 (continued)

3C5

AATTTTATGCTGACTCAGCCCCACTCTGTGTCGGAGTCTCCGGGGAAGACGGTAACCATCTCCT
GCACCGGCAGCAGTGGCAGCATTGCCAGCAACTATGTGCAGTGGTACCAGCAGCGCCCGGGCAG
TGCCCCCACCCTGTGATCTATGAGGATAACCAAAGACCCTCTGGGGTCCCTGATCGGTTCTCT
GGCTCCATCGACAGCTCCTCCAACCTCTGCCTCCCTCACCATCTCTGGACTGAAGACTGAGGACG
AGGCTGACTACTACTGTGAGTCTTATGATAGCAGCAATTGGGTCTTCGGCGGAGGGACCAAG

3D2

AATTTTATGCTGACTCAGCCCCACTCTGTGTCGGAGTCTCCGGGGAAGACGGTAACCATCTCCT
GCACCGGCAGCAGTGGCAGCATTGCCGCAACTATGTGCATTGGTACCAGCAGCGCCCGGGCAG
TGCCCCCACCCTGTGATCTATGAGGATAACCAAAGACCCTCTGGGGTCCCTGATCGGTTCTCT
GGCTCCATCGACAGCTCCTCCAACCTCTGCCTCCCTCACCATCTCTGGACTGAAGACTGAGGACG
AGGCTGACTACTACTGTGAGTCTTATGATAGGACCAATAAGAGGGTTTCGGCGGAGGGACCAAG
G

3D11

AATTTTATGCTGACTCAGCCCCACTCTGTGTCGGCGTCTCCGGGGAAGACGGTAACCATCCCT
GCACCGGCAGCAGTGGCAACATTGCCAGCAACTATGTGCAGTGGTACCAGCAGCGCCCGGGCAG
TGCCCCCACCCTGTGATCTATGAGGATAACCAAAGACCCTCTGGGGTCCCTGATCGGTTCTCT
GGCTCCATCGACAGCTCCTCCAACCTCTGCCTCCCTCACCATCTCTGGACTGAAGACTGAGGACG
AGGCTGACTACTACTGTGAGTCTTATGATAATAACATTGAGGTCTTCGGCGGAGGGACCAAG

3E9

AATTTTATGCTGACTCAGCCCCACTCTGTGTCGGAGTCTCCGGGGAAGACGGTAACCATCTCCT
GCACCGGCAGCAGTGGCAGCATTGCCAGCAACTATGTGCAGTGGTACCAGCAGCGCCCGGGCAG
TGCCCCCACCCTGTGATCTATGAGGATAACCAAAGACCCTCTGGGGTCCCTGATCGGTTCTCT
GGCTCCATCGACAGCTCCTCCAACCTCTGCCTCCCTCACCATCTCTGGACTGAAGACTGAGGACG
AGGCTGACTACTACTGTGAGTCTTATGATAGCAGCAACCTTCACTGGGTCTTCGGCGGAGGGAC
CAAG

3F1

AATTTTATGCTGACTCAGCCCCACTCTGTGTCGGAGTCTCCGGGGAAGACGGTCACCATCTCCT
GCACCGCCAGCGGTGGCAGCATTGCCGACAACTTTGTGCAGTGGTACCAGCAGCGCCCGGGCAG
TGCCCCCACCCTCTGATCTATGACTATAGTCGAAGACCCTATGGGGTCCCAGATCGGTTCTCT
GGCTCCATCGACAGGTCTCTCAATTCTGCCTCCCTCACCCTCTCTGGACTGATGACTGAGGACG
AGGCTGACTACTATTGTGAGTCTTATGATATCAGCAATCCGGTCTTCGGCGGAGGGACCAAG

3F11

GAAACGACACTCACGCAGTCTCCAGGCACCCTGTCCTTGTCTCCAGGGGAAAGCGCCACCCTCT
CCTGCAGGGCCAGTCACAGTGATGGCAGGAATTACATTGCCTGGTACCAGCAGACACCTGGCCA
GGCTCCCAGGCTCCTCGTTTATGATACGTGGAACAGGGCCGCTGGCGTCCCAGACAGGTTTCTAGA
GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAGGATTTTTCAG
TTTATTTCTGTGATCAATTTCCGAGGTCCGTGTCCTTTTGGCCAGGGGACCAAA

FIG. 17 (continued)

3H7

AATTTTATGCTGACTCAGCCCCACTCTGTGTCTGGAGTCTCCGGGGAAGACGGTAACCATCTCCT
 GCACCCGCAGCAGTGGCAACATTGCCAGTTACTATGTGCAGTGGTACCAGCAGCGCCCGGGCAG
 TGCCCCACCACTGTGATCTATGAAGATAACCAAAGACCCTCTGGGGTCCCTGATCGGTTCTCT
 GGCTCCATCGACAGCTCCTCCAACCTCAGCCTCCCTCACCATCTCTGGACTGAAGACTGAGGACG
 AGGCTGACTACTACTGTCAGTCTTATGATGGCGTCAATCGCGGCGTGATTTTCGGCGGAGGGAC
 CAAG

3H11

AATTTTATGCTGACTCAGCCCCACTCTGTGTCTGGAGTCTCCGGGGAAGACGGTAACCATCTCCT
 GCACCCGCAGCAGTGGCAACATTGCCAGTTACTATGTGCAGTGGTACCAGCAGCGCCCGGGCAG
 TTCCCCACCACTGTGATCTATGAGGATAACCAAAGACCTTCTGGGGTCCCTGATCGGTTCTCT
 GGCTCCATCGACAGCTCCTCCAACCTCTGCCTCCCTCACCATCTCTGGACTGCAGACTGAGGACG
 AGGCTGACTACTACTGTCAGTCTTATGATCGTCCCAATCATGTGGTCTTCGGCGGCGGGACCAG
 G

5A6

GACATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGACACAGAGTCACCATCA
 CTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGC
 CCCTAAGCTCCTGATTTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTGAGCGGC
 AGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCGACTT
 ACTACTGTC AACAGAGTTACAATCTTCCGCGCACTTTCGGCGGAGGGACCAAG

6F8

GAAATTGTGCTGACTCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCT
 CCTGCACGGCCAGTCAGACTATTAACAACAACCTACTTAGCCTGGTACCAGCAGAAACCTGGCCA
 GGGTCCCAGCCTCCTCATCTATGATGCATCCAGCAGGGCCACTGGCGTCCCAGACAGGTTCACT
 GGCAGTGGGTGCGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCGAG
 TGTATTACTGTCAGCAGTATGGAAGCTCGCCTCGGACCTTCGGCCAAGGGACCAAG

II.2. Heavy chain variable domain sequences for human IgG1

1A5

CAGGTGCAGCTGCAGGAGTCGGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCT
 GTGCAGCCTCTGGATTACCTTTAGCAGCTATGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAA
 GGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCAGACTCCGTG
 AAGGGCCGTTTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCC
 TGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAAAGATTACTTCAGGTGGTTATGGGGCCA
 GGAACCTG

1A8

CAGGTGCAGCTGCAGGAGTCGGGCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCT
 GCACTGTCTCTGGTGTCTCCATCAGCAGTAGAAGTGACCACTGGGGCTGGGTCCGCCAGCCCC
 AGGGAAGGGGCTGGAGTGGATTGGAAGTATCTCTTATAGTGGGAGAACCTACTACAACCCGTCC
 CTCAAGAGCCGAGTCACCATATCCGTAGACACCTCCAAGAACCACCTCTCCCTGAAGCTGAGCT
 CTGTGACCGCCGAGACACGGCTGTCTATTACTGTGCGAGACTCGCTTGCCTTTATCTACTTT
 TGATATCTGGGGCCACGGCACCCCTG

FIG. 17 (continued)

1B2

CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCT
GCAAGGCATCTGGATACACCTTCACCAGCTACTATATGCACTGGGTGCGACAGGCCCCCTGGACA
AGGGCTTGAGTGGATGGGAATAATCAACCCTAGTGGTGGTAGCACAAGCTACGCACAGAAGTTC
CAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCC
TGAGATCTGAGGACACGGCCGTGTATTACTGTGCGACTGGGGAGATGGCAGGGGATTTTGACTA
TGGGGCCAGGGCACCCCTG

1B11

GAAGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCT
GCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCCCCTGGACA
AGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACGCACAGAAGTTC
CAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACATGGAGCTGAGCAGCC
TGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACAACCCCGGGTATAGCAGCAGCTG
GTCCCCCAACTGGTTGACCCCTGGGGCCAGGGAACCCTG

1C2

GAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCT
GCAAGGCATCTGGATACACCTTCACCAGCTACTATATGCACTGGGTGCGACAGGCCCCCTGGACA
AGGGCTTGAGTGGATGGGAATAATCAACCCTAGTGGTGGTAGCACAAGCTACGCACAGAAGTTC
CAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCC
TGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGCTCTTCGGCTGGTACGTTCTACTTTGA
CTACTGGGGCCAGGGCACCCCTG

1C3

GAGGTCCAGCTGGTACAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCT
GCAAGGCATCTGGATACCCCTTCAGCACTTACTATATACACTGGGTGCGACAGGCCCCCTGGACA
AGGGCTTGAGTGGATGGGAATAATCGACCCTAGTGGTGGTAGCACAAGCTACGCACAGAAGTTC
CAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGGAGCC
TAAGATCTGACGACACGGCCGTGTTTTACTGTGCGAGAGTTGCCGAGCAACACCTGGACTACTA
CTTTGACTACTGGGGCCAGGGAACCCTG

1D12

GAGGTCCAGCTGGTACAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCT
GCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCCCCTGGACA
AGGGCTTGAGTGGATGGGATGGATCAGCGCTTACAATGGTAACACAAACTATGCACAGAAGCTC
CAGGGCAGAGTCACCATGACCACAGACACATCCACGAGCACAGCCTACATGGAGCTGAGGAGCC
TGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGGCTTGAGTGGCTACGTGGTGGTTTGA
TATCTGGGGCCAAGGGACCACG

1E5

GAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCT
GCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCCCCTGGACA
AGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACGCACAGAAGTTC
CAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACATGGAGCTGAGCAGCC
TGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGCGTTAGTCGGAAAAGTGGTTATTACT
ACGGGGCTTTGACTACTGGGGCCAGGGAACCCTG

FIG. 17 (continued)

1F4

CAGGTACAGCTGCAGCAGTCAGGTCCAGGACTGGTGAAGCCCTCGCAGACCCTCTCACTCACCT
GTGCCATCTCCGGGGACAGTGTCTCTAGCAACAGTGTGCTTGGAACTGGATCAGGCAGTCCCC
ATCGAGAGGCCTTGAGTGGCTGGGAAGGACATACTACAGGTCCAAGTGGTATAATGATTATGCA
GTATCTGTGAAAAGTCGAATAACCATCAACCCAGACACATCCAAGAACCAGTTCTCCCTGCAGC
TGAACCTCTGTGACTCCCGAGGACACGGCTGTGTATTACTGTGCAAGAGAAAAGGGCATCGAAGG
GCCTGCGTTCCGACCCCTGGGGCCAGGGAACCCTG

1H7

CAGGTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGCCCCCTCACCT
GCGTGTCTATGGTGGGTCCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCCCCAGGGAA
GGGGCTGGAGTGGATTGGGGAAATCAATCATAGTGGAAAGCACCAACTACAACCCGTCCCTCAAG
AGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGA
CCGCCGCGGACACGGCTGTGTATTACTGTGCGAGAGGGAGGTGGCTGCGGGGTGCTTTTGATAT
CTGGGGCCAAGGGACAATG

2C9

CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCTCGGTGAAGGTCTCCT
GCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCCTGGACA
AGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCCTTGGTATAGCAAACTACGCACAGAAGTTC
CAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACATGGAGCTGAGCAGCC
TGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGACATGGGGGGGTGGGAGCTACTACGGG
TTACTACTACATGGACGTCTGGGGCAAAGGGACCACG

2C10

CAGGTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACCT
GCGGTGTCTATGGTGGGTCCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGTCCCCAGGGAA
GGGGCTGGAGTGGATTGGGGAAATCAATTATAGAGGAAACACCAACTACAACCCGTCTCTCAAG
AGTCGAGTCACCATATCGGTAGACACGTCCAAAACCAGTTCTCCCTAAACGTGAACCTCTGTGA
CCGCCGCGGACACGGCTGTGTATTATTGTGCGAGATGGGACGGTGGTAACTCCGTGGACCACTG
GGGCCAGGGAACCCTG

2C12

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCT
GTGCAGCCTCTGGATTACCTTCAGTAGCTATGCTATGCACTGGGTCCGCCAGGCTCCAGGCAA
GGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAAGTAATAAACTATGCAGACTCCGTG
AAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAAATGAACAGCC
TGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGGGGGACGATTCCACTACTACTACTA
TGCCATGGACGTCTGGGGCCAAGGGACCACG

2D3

GAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCTCGGTGAAGGTCTCCT
GCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCCTGGACA
AGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACGCACAGAAGTTC
CAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACATGGAGCTGAGCAGCC
TGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGCAGTGGCTGGTTAAGGGGTGCTTTTGA
TATCTGGGGCCAAGGGACAATG

FIG. 17 (continued)

2G7

CAGGTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACCT
GCGTGTCTATGGTGGGTCCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCCCCAGGGAA
GGGGCTGGAGTGGATTGGGGAAATCAATCATAGTGGGAAGCACTACAACCCGTCCCTCAAG
AGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGA
CCGCCGCGACACGGCTGTGTATTACTGTGCGAGAGGGAAATGGTTACGGGGTGCTTTTGATAT
TGGGGCCAAGGGACAATG

2H4

CAGGTCCAGCTGGTACAGTCTGGGGCTGAGGTGACGAAGCCTGGGGCCTCAGTGAAGGTCTCCT
GCAAGGCTTCTGGATACACCTTCAGCGGCTACTATATACACTGGGTGCGACAGGCCCTGGACA
AGGGCTTGAGTGGATGGGGCGGGTCAACCTTAATAGTGGTGGCACAAAGTATGCACAGAAGTTT
CAGGACAGGGTCACGTTGACCAGGGACACGTCCATCAGTACTGCCACATGGAATTGACCAGTC
TGAGATCTGACGACACGGCCATGTATTTCTGTGCGAGAGGTGGCAGGCGCGGTTTACCTGCAGC
TGGCTATATTGACTACTGGGGCCAGGGCACCCCTG

3A11

GAGGTCCAGCTGGTACAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCT
GCAAGGCTTCTGGTTACACGTTTAGCACCTATGATATCAGCTGGGTGCGACAGGCCCTGGACA
AGGGCTTGAGTGGATGGGATGGATCAGCACTTACAATGGTGACACAAGTATGCACAGAAGTTC
CAGGGCAGAGTCACCATGACCACAGACACGTCCACGAGCACAATCTACATGGAGCTGAGGAGCC
TGAGATCTGACGACACGGCCGTCTATTACTGTGCGAGGGGAGATAGCAGTGTGGGGTACGAATA
CTTCCAAACACTGGGGCCAGGGAACCCTG

3C5

CAGGTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACCT
GCGGTGTCTATGGTGGGTCCCTTAAGTGGTTACTACTGGAGCTGGATCCGCCAGCCCCCAGGGAA
GGGGCTGGAGTGGATTGGGGAAATCAATCATAGTGGGAAGCACTACAACCCGTCCCTCAAG
AGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGA
CCGCCGCGACACGGCTGTGTATTACTGTGCGAGACGGTGGTGGCTACGAGGTGCTTTTGATAT
TGGGGCCAAGGGACCACG

3D2, 3D11

CAGGTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACCT
GCGTGTCTATGGTGGGTCCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCCCCAGGGAA
GGGGCTGGAGTGGATTGGGGAAATCAATCATAGTGGGAAGCACTACAACCCGTCCCTCAAG
AGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGA
CCGCCGCGACACGGCTGTGTATTACTGTGCGAGACGGTGGTGGCTACGAGGTGCTTTTGATAT
TGGGGCCAAGGGACCACG

FIG. 17 (continued)

3E9

GAAGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCT
GCAAGGCTTCTGGTTACACCTTTACCAGCTATGGTATCAGCTGGGTGCGACAGGCCCCCTGGACA
AGGGCTTGAGTGGATGGGATGGATCAGCGCTTACAATGGTAACACA AACTATGCACAGAAGCTC
CAGGGCAGAGTCACCATGACCACAGACACATCCACGAGCACAGCCTACATGGAGCTGAGGAGCC
TGAGATCTGACGACACGGCCGTGTATTACTGTGCCAGAGGCATTATTACTATGATATCGGACTA
TGGGGCCAGGGAACCCCTG

3F1

CAGGTGCAGCTGGTGC AATCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCT
GTGCAGCCTCTGGATTACCTTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAA
GGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAAGTAATAA TACTATGCAGACTCCGTG
AAGGGCCGATTACCATCTCCAGAGACAATCCAAGAACACGCTGTATCTGCAAAATGAACAGCC
TGAGAGCTGAGGACACGGCTGTGTATTACTGTGCCAGAGACGCTGGGGGAGGTATGGACGCTCTG
GGCCAAGGGACCACG

3F11

GAGGTCCAGCTGGTACAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCT
GCAAGGCTTCTGGTTACACCTTTAGCAGCTCTGGTATCAGCTGGGTGCGACAGGCCCCCTGGACA
AGGGCTTGAGTGGATGGGATGGATCAGCACTTACAATGGTAACACA AACTATGCACAGAATTTT
CAGGGCAGAGTCACCATGACCACAGACACGTCCACGAGCACAGTCTACATGGAGTTGAGGGGCC
TGACATCTGACGACACGGCCGTGTATTACTGTGCTACGAGTATAGCGGTGGCTGGTATTGACTA
TGGGGCCAGGGCACCCCTG

3H7

CAGGTGCAGCTGGTGC AATCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTGTCTCT
GTGCAGCGTCTGGATTACCTTTCAGTAACCTATGGCATGCACTGGGTCCGCCAGGCTCCGGGCAA
GGGGCTGGAGTGGGTGGCAGTTATATGGCATGATGGAAACCAATAA TACTATGCAGACTCCGTG
AAGGGCCGATTACCGTCTCCAGAGACAATTCGAAGAACACTCTGTATTGCAAAATGGACACTC
TGAGAGCCGAGGACACGGCTGTGTATTACTGTGTGAGAGATCAGGGGGCCGGTGTGTTGGAATGG
TTATTCCCTACTGGGGCCAGGGAACCCCTG

3H11

CAGGTGCAGCTGGTGC AATCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCTCT
GCAAGGCATCTGGATACACCTTTCACCAGCTACTATATGCACTGGGTGCGACAGGCCCCCTGGACA
AGGGCTTGAGTGGATGGGAATAATCAACCTAGTGGTGGTAGACA AGCTACGCACAGAAGTTC
CAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAACACAGTCTACATGGAGCTGAGCAGCC
TGAGATCTGAGGACACGGCCGTGTATTACTGTGCCAGCTCAGTAGTACCAGCTGCTATTTACGA
CTACTACTACGGTATGGACGCTCTGGGGCCAAGGGACCACG

FIG. 17 (continued)

5A6

CAGGTGCAGCTGCAGGAGTCGGGGGAGGCTTGGTACAGCCTGGAGGGTCCCTGAGACTCTCCT
GTGCAGCCTCTGGATTACCTTCAGTAGTTATGAAATGAACTGGGTCCGCCAGGCTCCAGGCAA
GGGGCTGGAGTGGGTGGCAGTTATATCATATGATGCAAGCAATAAA TACTACGCAGACTCCGTG
AAGGGCCGATTACCATCTCCAGAGACAATGCCAAGAACTCACTGTATCTGCAAATGAACAGCC
TGAGAGCCGAGGACACGGCTGTGTATTACTGT GCGAGACTGATTACTATGGTTCGGGGAGAGGA
CTAC TGGGGCCAGGGCACCCCTG

6F8

CAGGTGCAGCTGGTGGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCT
GTGCAGCCTCTGGGTTCACCGTCAGTAGCAACTACATGAGCTGGGTCCGCCAGGCTCCAGGGAA
GGGGCTGGAGTGGGTCTCAGTTATTTATAGCGGTGGTAGCACA TACTACGCAGACTCCGTGAAG
GGCCGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGA
GAGCCGAGGACACGGCCGTGTATTACTGT GCGAGAGACTACGGTGACTATTACTTTGACTACTG
GGGCCAGGGCACCCCTG

FIG. 17