

**Ms1\_VH** SEQ ID NO: 1

EIQLOQSGPELVKPGASVKVSKASGYAYTRYNMYWVKQSHGKSLEWIGYIDPYNGGTNYN  
QKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARGGYYGNAMDYWGQGTSVTVSS

|          |          |              |
|----------|----------|--------------|
| GYAYTRYN | IDPYNGGT | ARGGYYGNAMDY |
| SEQ:47   | SEQ:48   | SEQ:49       |

**Ms1\_VL** SEQ ID NO: 2

DIVMTQSPSSLTVTAGEKVTMSCKSSQSLNLSGNOKNYLTWYQKPGQPPKLLIYWASTRES  
GVPRFTGSGSGTDFTLTISVQAEDLSIYYCQSNYYPFTFGAGTTLELQ

|              |        |          |
|--------------|--------|----------|
| QSLNLSGNOKNY | WAS    | QSNYYPFT |
| SEQ:50       | SEQ:51 | SEQ:52   |

**Ms2\_VH** SEQ ID NO: 3

QVQLKESGPGLVAPSQSLITCTVSGFSLTSYGVHWVRQPPGKGLEWLGVIWAGGSTNYNSA  
LMSRLSISKDNSKSQVFLKMNSLQTDITAMYYCARDFTTATGFEDYWGQGTTLTVSS

|          |         |               |
|----------|---------|---------------|
| GFSLTSYG | IWAGGST | ARDFTTATGFEDY |
| SEQ:53   | SEQ:54  | SEQ:55        |

**Ms2\_VL** SEQ ID NO: 4

DIVMTQSPSSLVSAGEKVTMSCKSSQSLNLSGNOKNYLAWYQKPGQPPKLLIYGASTRES  
GVPRFTGSGSGTDFTLTISVQAEDLAVYYCQNDHSYPFTFGSGTKLEIK

|              |           |           |
|--------------|-----------|-----------|
| QSLNLSGNOKNY | GAS       | QNDHSYPFT |
| SEQ ID:56    | SEQ ID:57 | SEQ ID:58 |

**Ms3-VH1** SEQ ID NO: 5

EVMLVESGGGIVKPGGSLKLSAASGFTLSSYTMWVRQTPERRLEWVATIIIIGGSYTYYPDS  
VKGRFTISRDNKNTLYLQMSSLRSEDITAMYYCARQGYGNSFPYWGQGTLLTVSA

|           |           |             |
|-----------|-----------|-------------|
| GFTLSSYT  | IIIIGGSYT | ARQGYGNSFPY |
| SEQ ID:59 | SEQ ID:60 | SEQ ID:61   |

**Ms3\_VL** SEQ ID NO: 6

DIVMTQSPSSLTVTAGEKVTMSCKSSQSLNLSGNOKNYLTWYQKPGQPPKLLIYWASTRES  
GVPRFTGSGSGTDFTLTISVQAEDLAVYYCQNDYSYPFTFGSGTKLEIK

|              |           |           |
|--------------|-----------|-----------|
| QSLNLSGNOKNY | WAS       | QNDYSYPFT |
| SEQ ID:62    | SEQ ID:63 | SEQ ID:64 |

FIG. 1

**Ms4\_VH** SEQ ID NO: 7

EVQLQQSGPELEKPGASVKISKASGYSTGYNMNWVKQSNQKSLEWIGNIDPYYGGTRYN  
QKFKGKATLTVDSSSTAYMQLKSLTSEDSAVYYCARLGLGNAMDYWGQGTSVTVSS

|           |           |             |
|-----------|-----------|-------------|
| GYSFTGYN  | IDPYYGGT  | ARLGLGNAMDY |
| SEQ ID:65 | SEQ ID:66 | SEQ ID:67   |

**Ms4\_VL** SEQ ID NO: 8

DIVMTQSPSFLTVTAGEKVTMSCKSSQSLNLSGNQKSYLTWYQQKPGQPPKLLIYWASTRES  
GVPDRFTGSGSGTDFTLTISVQAEDLAVYYCQNDYYYPTFGSGTELEIK

|              |           |           |
|--------------|-----------|-----------|
| QSLNLSGNQKSY | WAS       | QNDYYYPT  |
| SEQ ID:68    | SEQ ID:69 | SEQ ID:70 |

**Ms5\_VH** SEQ ID NO: 9

QVQLQQPGAELVKPGASVKLSCKASGYTFTRYLMHWVKQRPQGGLWIGEINPSNGRTNYN  
EKFKSKAALTVDKSSSTAYMQLSSLTSEDSAVYYCARLAYGYGNAVDYWGQGTSVTVSS

|           |           |               |
|-----------|-----------|---------------|
| GYTFTRYL  | INPSNGRT  | ARLAYGYGNAVDY |
| SEQ ID:71 | SEQ ID:72 | SEQ ID:73     |

**Ms5\_VL** SEQ ID NO: 10

DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNLSGNQKNYLAWYQQKPGQPPKLLIYGASTRES  
GVPDRFTGSGSGTDFTLTISVQAEDLAVYYCQNDHSYPLTFGAGTKLELK

|              |           |           |
|--------------|-----------|-----------|
| QSLNLSGNQKNY | GAS       | QNDHSYPLT |
| SEQ ID:74    | SEQ ID:75 | SEQ ID:76 |

**Ms6\_VH** SEQ ID NO: 11

QVQLQQSGAELAKPGASVKMSCRASGYTFTSYLMHWIKQRPQGALEWIGYINPTTDYTEYN  
QKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCGRLGYYKRNAMDHWGQGTSTVSS

|           |           |               |
|-----------|-----------|---------------|
| GYTFTSYL  | INPTTDYT  | GRLGYYKRNAMDH |
| SEQ ID:77 | SEQ ID:78 | SEQ ID:79     |

**Ms6\_VL** SEQ ID NO: 12

DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNLSGNQKNYLAWYQQKPGQPPKLLIYGASTRES  
GVPDRFTGSGSGTDFTLTISVQAEDLAVYYCQNDHFYPLTFGAGTKLELK

|              |           |           |
|--------------|-----------|-----------|
| QSLNLSGNQKNY | GAS       | QNDHFYPLT |
| SEQ ID:80    | SEQ ID:81 | SEQ ID:82 |

FIG. 1 cont.

**Ms7.2\_VH1** SEQ ID NO: 13

EVKLVESGGDLVQPGGSLRLSCTTPGETSFDFYMEWVVRQPPGKRLEWIAASRNKANDYTTTE  
 NSASVKGRFIVSRDTSQSILYLQMNALRAEDTAIYYCARDACPWDWFAYWGQGLTVSA

|           |            |              |
|-----------|------------|--------------|
| GFTSFDFY  | SRNKANDYTT | ARDACPWDWFAY |
| SEQ ID:83 | SEQ ID:84  | SEQ ID:85    |

**Ms7.2\_VL** SEQ ID NO: 14

DIVMTQSPSSLTVTAGEKVTMSCKSSQSLNLSGNQKNYLTWYQKPGQPPKLLIYWASTRES  
 GVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPFTFGSGTKLEIK

|              |           |           |
|--------------|-----------|-----------|
| QSLNLSGNQKNY | WAS       | QNDYSYPFT |
| SEQ ID:86    | SEQ ID:87 | SEQ ID:88 |

**Ms8\_VH** SEQ ID NO: 15

EIQLQQSGPELVKPGASVKVSCKASDYAFTRYNMYWVKQSHGKSLEWIGYIDPYNGGTNYN  
 QKFQKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARGGYGNAMDYWGQGTSTVTVSS

|           |           |             |
|-----------|-----------|-------------|
| DYAFTRYN  | IDPYNGGT  | ARGGYGNAMDY |
| SEQ ID:89 | SEQ ID:90 | SEQ ID:91   |

**Ms8\_VL** SEQ ID NO: 16

DIVMTQSPSSLTVTAGEKVTMSCKSSQSLNLSGNQKNYLTWYQKPGQPPQLLIYWASTRES  
 GVPDRFTGSGSGTDFTLTISSVQAEDLSIYYCQSNYIYPFTFGAGTTLELQ

|              |           |           |
|--------------|-----------|-----------|
| QSLNLSGNQKNY | WAS       | QSNYIYPFT |
| SEQ ID:92    | SEQ ID:93 | SEQ ID:94 |

**Ms9\_VH** SEQ ID NO: 17

QVQLQQPGAEPVKPGASVKLSCKASGYTFTSYLIHWVKXRPQGQLEWIGEIIPSNNGRTITYNE  
 KFKTKASLTVDKSSSTAYMQLSSLTSEDSAVYYCARLAYGYGNAVDYWGQGTSTVTVSS

|           |           |               |
|-----------|-----------|---------------|
| GYTFTSYL  | IIPSNNGRT | ARLAYGYGNAVDY |
| SEQ ID:95 | SEQ ID:96 | SEQ ID:97     |

**Ms9\_VL** SEQ ID NO: 18

DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNLSGNQKNYLAWYQKPGQPPKLLIYGASTRDS  
 GVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHTYPLTFGAGTKLELK

|              |           |            |
|--------------|-----------|------------|
| QSLNLSGNQKNY | GAS       | QNDHTYPLT  |
| SEQ ID:98    | SEQ ID:99 | SEQ ID:100 |

FIG. 1 cont.

**Ms10\_VH** SEQ ID NO: 19

EVQLQQSGPELEKPGASVKISKASGYSTGYKMNWVKQSNQKSLEWIGHIDPYYGGPRYN  
KKFMGKATLTVDSSSTAYMQLKSLTSEDSAVYYCARLDYGNSFAYWGQGTLVTVSA

|            |            |             |
|------------|------------|-------------|
| GYSFTGYK   | IDPYYGGP   | ARLDYGNSFAY |
| SEQ ID:101 | SEQ ID:102 | SEQ ID:103  |

**Ms10\_VL** SEQ ID NO: 20

DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNLSGNQKNYLAWYQQKPGQPPKLLIYGASTRES  
GVPDRFTGSGSGTDFTLTISVQAEDLAVYYCQNDHSPFTFGGGTKLEIK

|              |            |            |
|--------------|------------|------------|
| QSLNLSGNQKNY | GAS        | QNDHSPFT   |
| SEQ ID:104   | SEQ ID:105 | SEQ ID:106 |

**Ms11\_VH** SEQ ID NO:21

QVQLQQSGAELVKPGASVKMSCKAFGYTFTTYSIEWMKQNHGKSLEWIGNFRPYNDDTKC  
NEKFKGKAKLTVEKSSSTVYLELSRLTSDSSAVYYCARGSYGNSFAYWGQGTLVTVSA

|            |            |             |
|------------|------------|-------------|
| GYTFTTYS   | FRPYNDDT   | ARGSYGNSFAY |
| SEQ ID:107 | SEQ ID:108 | SEQ ID:109  |

**Ms11\_VL** SEQ ID NO:22

DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNLSGNQKNYLAWYQQKPGQPPKLLIYGASTRES  
GVPDRFTGSGSGTDFTLTISVQAEDLAVYYCQNDHSPFTFGSGTKLEIK

|              |            |            |
|--------------|------------|------------|
| QSLNLSGNQKNY | GAS        | QNDHSPFT   |
| SEQ ID:110   | SEQ ID:111 | SEQ ID:112 |

**Ms12\_VH** SEQ ID NO: 23

EIQLQQSGPELVKPGASVKVSKASGYAFASYKMYWVKQSHGKSLEWIGYIDPYNGVTISYN  
QKFRGKATLTVDKSSSTAYMHLNLSLTSEDSAVYYCARGAYYGNSFDYWGQGTLTVSS

|            |            |              |
|------------|------------|--------------|
| GYAFASYK   | IDPYNGVT   | ARGAYYGNSFDY |
| SEQ ID:113 | SEQ ID:114 | SEQ ID:115   |

**Ms12\_VL** SEQ ID NO: 24

DIVMTQSPSSSLTVTAGEKVTMSCKSSQSLNLSGNQKNYLTWYQQQPGQPPKLLIYWASTRES  
GVPDRFTGSGSGTDFTLTISVQAVDLAVYYCQSAYSFPYTFGGGTKLEVK

|              |            |            |
|--------------|------------|------------|
| QSLNLSGNQKNY | WAS        | QSAYSFPYT  |
| SEQ ID:116   | SEQ ID:117 | SEQ ID:118 |

FIG. 1 cont.

**Ms13\_VH** SEQ ID NO: 25

EVQLQQSGPELVKPGASVKMSCKASGYTFTRYIMHWVKQKPGQGLEWIGYFNPYNDDSKTS  
EKFKGKATLTSDKSSSTAYMEINSLTSEDSAVYYCAKLRQERIAIWGQGTLVTVSA

|            |            |            |
|------------|------------|------------|
| GYTFTRYI   | FNPYNDDS   | AKLRQERIAI |
| SEQ ID:119 | SEQ ID:120 | SEQ ID:121 |

**Ms13\_VL** SEQ ID NO: 26

DIQMNQSPSSLSASLGDITITICHASQNIQVWLSWYQQKPGNFPKLLIYKASNLHTGVPSRFSGSGSGTG  
FTLTISLQPEDATYYCQQGQSYPLTFGAGTKLELK

|            |            |            |
|------------|------------|------------|
| QNIQVW     | KAS        | QQGQSYPLT  |
| SEQ ID:122 | SEQ ID:123 | SEQ ID:124 |

**Ms14\_VH** SEQ ID NO: 27

EVQLQQSGPELVKPGASVKMSCKASGYTFTRYIMHWVKQKPGQGLEWIGYFNPYNDDSKNN  
EKFKGKATLTSDKSSSTAYMEISLTSSEDSAVYYCAKLRQERIAIWGQGTLVTVSA

|            |            |            |
|------------|------------|------------|
| GYTFTRYI   | FNPYNDDS   | AKLRQERIAI |
| SEQ ID:125 | SEQ ID:126 | SEQ ID:127 |

**Ms14\_VL** SEQ ID NO: 28

DIQMNQSPSSLSASLGDITITICHVSQNIQVWLSWYQQKPGNIPKLLIYKASNLHTGVPSRFSGSGSGTG  
FTLTISLQPEDATYYCQQGQSYPLTFGAGTKLELK

|            |            |            |
|------------|------------|------------|
| QNIQVW     | KAS        | QQGQSYPLT  |
| SEQ ID:128 | SEQ ID:129 | SEQ ID:130 |

**Ms15\_VH** SEQ ID NO: 29

EVQLQQSGPELVKPGASVKMSCKASGYTFTRYIMHWVKQKPGQGLEWIGYFNPYNDGTYKN  
EIFKDKATLTSDKSSSTAYMELRSLTSEDSAVYYCAKLRQERIAIWGQGTLVTVSA

|            |            |            |
|------------|------------|------------|
| GYTFTRYI   | FNPYNDGT   | AKLRQERIAI |
| SEQ ID:131 | SEQ ID:132 | SEQ ID:133 |

**Ms15\_VL** SEQ ID NO: 30

DIQMNQSPSSLSASLGDITITICHVSQNIQVWLSWYQQKPGNIPKLLIYKASNLHTGVPSRFSGSGSGTG  
FTLTISLQPEDATYYCQQGQSYPLTFGAGTKLELK

|            |            |            |
|------------|------------|------------|
| QNIQVW     | KAS        | QQGQSYPLT  |
| SEQ ID:134 | SEQ ID:135 | SEQ ID:136 |

FIG. 1 cont.

**Ms16\_VH** SEQ ID NO: 31

QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWIKORPGQGLEWIGVINPGSGGTNYNE  
 KLKGKATLTADKSSSTAYMQLSSLTSGDSAVYFCARYVKGNALDYWGQGTSTVTVSS

|            |               |             |
|------------|---------------|-------------|
| GYAFTNYL   | INPGSGGT      | ARYVKGNALDY |
| SEQ ID:137 | SEQ<br>ID:138 | SEQ ID:139  |

**Ms16\_VL** SEQ ID NO: 32

DIVMTQSPSSLTIVTAGEKVTLSCKSSQSLFNSGNQKNYLTWYQQKPGQPPKLLIYWASTRESQVPDRFT  
 GSGSGTDFLTITSSVQAEDLAIYYCQNSYSFPLTFGAGTKLELT

|              |            |            |
|--------------|------------|------------|
| QSLFNSGNQKNY | WAS        | QNSYSFPLT  |
| SEQ ID:140   | SEQ ID:141 | SEQ ID:142 |

**Ms17\_VH** SEQ ID NO: 33

EVQLQQSGPELVKPGASVKMSCKASGYTFTNYIIHWVKQKPGQGLEWIGYFNPYNDGIEYSE  
 KFKGKATLTSDKSSSTAYMELSSLTSEDSAVYYCSKLRQERFAYWGQGTSLTVSA

|            |            |            |
|------------|------------|------------|
| GYTFTNYI   | FNPYNDGI   | SKLRQERFAY |
| SEQ ID:143 | SEQ ID:144 | SEQ ID:145 |

**Ms17\_VL** SEQ ID NO: 34

DIQMNQSPSSLSASLGDTITITICHASQININWLSWYQQKPGNIPKLLIYKASNLHTGVPSRFSGSGSGTG  
 FLTITSSLPEDIATYYCQQGQSYPLTFGAGTKLELK

|            |            |            |
|------------|------------|------------|
| QNINW      | KAS        | QQGQSYPLT  |
| SEQ ID:146 | SEQ ID:147 | SEQ ID:148 |

**Ms18\_VH** SEQ ID NO: 35

QVQLKESGPGLVAPSQSLITCTVSGFSLISYGVHWVRQPPGKGLEWLGVIWAGGNTNYNSA  
 LMSRLSISKDNSKSQVFLKMNSLTDDTAMYYCARVYYGNSFDYWGQGTTLTVSS

|               |               |             |
|---------------|---------------|-------------|
| GFSLSISYG     | IWAGGNT       | ARVYYGNSFDY |
| SEQ<br>ID:149 | SEQ<br>ID:150 | SEQ ID:151  |

**Ms18\_VL** SEQ ID NO: 36

DIVMTQSPSSLTIVTAGEKVTMSCKSSQSLNSGNQKNYLTWYQQKPGQPPKLLIYWASTRQSGVPDRF  
 TGSGSGTDFSLTSSVQAEDLAVYYCHNDYTYPLTFGAGTKLELK

|             |            |            |
|-------------|------------|------------|
| QSLNSGNQKNY | WAS        | HNDYTYPLT  |
| SEQ ID:152  | SEQ ID:153 | SEQ ID:154 |

FIG. 1 cont.

**Ms19\_VH** SEQ ID NO: 37

EVQLQQSGPELVKPGASVKMSCKASGYTFTSYVIHWVKQKPGQGLEWIGYINPYNDGSKYN  
EKFKGKATLTSDKSSSTAYMELSSLTSEDSAVYYCAREGYGKRNALDYWGQGTSTVTVSS

|            |            |               |
|------------|------------|---------------|
| GYTFTSYV   | INPYNDGS   | AREGYGKRNALDY |
| SEQ ID:155 | SEQ ID:156 | SEQ ID:157    |

**Ms19\_VL** SEQ ID NO: 38

DIVMTQSPSSLVSAGERVTMSCKSSQSLNLSGNQKNYLAWYQQKPGQPPKLLIYGASTRESGVDPDRFT  
GSGSGTDFTLIISVQVEDLAVYYCQNDHFYPLTFGAGTKLELK

|              |            |            |
|--------------|------------|------------|
| QSLNLSGNQKNY | GAS        | QNDHFYPLT  |
| SEQ ID:158   | SEQ ID:159 | SEQ ID:160 |

**Ms20\_VH** SEQ ID NO: 39

EIQLQQSGPELMKPGASVKISCKASGYSTSYMHVWKQSHGKSLEWIGYFDPYNGGTNYN  
QKFKGKATLTADKSSSTAYMHLSSLTSEDSAVYYCACYRFFAVWGAGTTVTVSS

|            |            |            |
|------------|------------|------------|
| GYSTSY     | FDPYNGGT   | ACYRFFAV   |
| SEQ ID:161 | SEQ ID:162 | SEQ ID:163 |

**Ms20\_VL** SEQ ID NO: 40

DIVMTQSPSSLTVTAGEKVTMSCKSSQSLNLSGNQKNYLTWYQQKPGQPPKLLIYWASTRESGVDPDRF  
TGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLELK

|              |            |            |
|--------------|------------|------------|
| QSLNLSGNQKNY | WAS        | QNDYSYPLT  |
| SEQ ID:164   | SEQ ID:165 | SEQ ID:166 |

**Ms21\_VH** SEQ ID NO: 41

DVQLVESGGGLVQPGGSRKLSCAASGFTFSTFGMHVVRQAPKGLEWVAFINGDSSSIYYA  
DTVKGRFTISRDNPNILFLQMTSLRSEDAMYYCARFARGNSFDYWGQGTTLTVSS

|            |            |             |
|------------|------------|-------------|
| GFTFSTFG   | INGDSSSI   | ARFARGNSFDY |
| SEQ ID:167 | SEQ ID:168 | SEQ ID:169  |

**Ms21\_VL** SEQ ID NO: 42

DIVMTQSPSSLTVTAGEKVTMSCKSSQSLFNSGNQKNYLTWYQQKPWQPPKLLIYWASTRESGVDPDRF  
TGSGSGTDFTLTIISVQTEDLAVYYCQIGYTYPLTFGAGTKLELK

|              |            |            |
|--------------|------------|------------|
| QSLFNSGNQKNY | WAS        | QIGYTYPLT  |
| SEQ ID:170   | SEQ ID:171 | SEQ ID:172 |

FIG. 1 cont.

**Ms22\_VH** SEQ ID NO: 43

QVQLKESGPGLVAPSQSLSTICTVSGESLTSNGVHWVRQPPGKGLEWLGVIWAGGSTNYN~~SALMSRLSI~~  
SKDNSKSQVFLKMNSLQTHDTAMYYCARDKYDGTGFDYWGQGTTLTVSS

|            |            |              |
|------------|------------|--------------|
| GFSLTSNG   | IWAGGST    | ARDKYDGTGFDY |
| SEQ ID:173 | SEQ ID:174 | SEQ ID:175   |

**Ms22\_VL** SEQ ID NO: 44

QIVLTQSPAIMSASPGEKVTMTCSASSSVSNMYWYQQKPGSSPRLLIYDTSN~~LASGVPVRFSGSGSGTS~~  
YSLTISRMEAEDAATYYCQQWSSYPYTFGGGTKLEIK

|            |            |            |
|------------|------------|------------|
| SSVSN      | DTS        | QQWSSYPYT  |
| SEQ ID:176 | SEQ ID:177 | SEQ ID:178 |

**Ms23\_VH** SEQ ID NO: 45

EIQ~~LQQSGPELVKPGASVKV~~SCKASGYAFTRYNMYWVKQSHGKSLEWIGYIDPYNGGTN~~YN~~  
QKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARDGGYYGNAMDYWGQGTSTVTVSS

|            |            |              |
|------------|------------|--------------|
| GYAFTRYN   | IDPYNGGT   | ARGGYYGNAMDY |
| SEQ ID:179 | SEQ ID:180 | SEQ ID:181   |

**Ms23\_VL** SEQ ID NO: 46

DIVMTQSPSSSLTVTAGEKVTMSCKSSQSLNSGNQKNYLTWYQQKPGQP~~PKLLIYWASTRES~~  
GVPDRFTGSGSGTDFTLTIS~~SVQAEDLSIYYCQSNYIYPFTFGAGTTLELQ~~

|             |            |            |
|-------------|------------|------------|
| QSLNSGNQKNY | WAS        | QSNYIYPFT  |
| SEQ ID:182  | SEQ ID:183 | SEQ ID:184 |

FIG. 1 cont.

**Hu-1** VH SEQ ID NO: 185

QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMYWVRQAPGKGLEWVAVIWDGSNKNYADSVK  
GRFTISRDNKNTLNLMNSLRAEDTAVYYCARRGYDILTGYYGMDVWGQGTTVTVSA

|            |            |                  |
|------------|------------|------------------|
| GFTFSNYG   | IWYDGSNK   | ARRGYDILTGYYGMDV |
| SEQ ID:221 | SEQ ID:222 | SEQ ID:223       |

**Hu-1** VL SEQ ID NO: 186

QIVVTQEPSPFSVSPGGTVTLTCGLSGSVSTSYYPSPWYQQTPGQAPRTLIYRTNTRSSGVPDRFSGSILG  
NKAALTISGAQAPDESNYVCVLYMGSGIWVFGGGTKLTVL

|            |            |            |
|------------|------------|------------|
| SGSVSTSY   | RTN        | VLYMGSGIWV |
| SEQ ID:224 | SEQ ID:225 | SEQ ID:226 |

**Hu-2** VH SEQ ID NO: 187

QLRLQESGPGLVKPSETLSLTCAVSGGSISSRSYWGWIROPKGLIGSIYYSGSTYYNPSLKSRVTI  
SVDTSKNQFSLKLTSTVATIDTAVYYCARQTLRYFDWLSFPDYWGQGTLLTVSS

|            |            |                  |
|------------|------------|------------------|
| GGSISSRSY  | IYYSGST    | ARQTLRYFDWLSFPDY |
| SEQ ID:227 | SEQ ID:228 | SEQ ID:229       |

**Hu-2** VL SEQ ID NO: 188

EIVMTQSPATLSLSPGERATLSCRASQSVRSNYLSWYQQKPGQAPRLIYGTSTRATGIPARFSGSGSGT  
DFLTISSLQPEDFAVYFCQODYNLPIIFGQGTGLEIK

|            |            |            |
|------------|------------|------------|
| QSVRSNY    | GTS        | QODYNLPI   |
| SEQ ID:230 | SEQ ID:231 | SEQ ID:232 |

**Hu-3** VH SEQ ID NO: 189

QLQLQESGPGLVKPSETLSLTCTVSDGPISSRYYWGWIROPKGLWIGSFHYSGSTYYNPSLKSRVT  
ISADTSKNQFSLKLSVTAADTAVYYCARLVRLRYFDWLGFFDLWGRGTLTVSS

|            |            |                   |
|------------|------------|-------------------|
| DGPISSRYY  | FHYSGST    | ARLVRLRYFDWLGFFDL |
| SEQ ID:233 | SEQ ID:234 | SEQ ID:235        |

**Hu-3** VL SEQ ID NO: 190

EIVMTQSPAILSLSPGERAALSCRASQSVRSSYLSWYQQKPGQAPRLIYGTSTRATGIPARFSGSGSGTD  
FTLTISSLQPEDFAVYYCQODYNLPIIFGQGTGLEIK

|            |            |            |
|------------|------------|------------|
| QSVRSSY    | GTS        | QODYNLPI   |
| SEQ ID:236 | SEQ ID:237 | SEQ ID:238 |

FIG. 2

**Hu-4** VH SEQ ID NO: 191

QVQLVESGGGVVQPGRSLRLSCAASGFTFSFYGMHWVRQAPGKGLEWVAVIWIYDGSNKNYVDSVKG  
 RFTISRDNKNTLYLQMNSLRAEDTAVYYCARRNYDILTGRDYYGMDVWGQGTTTVTVSS

|            |            |                    |
|------------|------------|--------------------|
| GFTFSFYG   | IWIYDGSNK  | ARRNYDILTGRDYYGMDV |
| SEQ ID:239 | SEQ ID:240 | SEQ ID:241         |

**Hu-4** VL SEQ ID NO: 192

QTVVTQEPFSVSPGGTVTLTCGLNSGSVSTSYYPSTWYQQTPGQAPRTLIYSTINTRSSGVPDRFSGSILG  
 NKAALITGAQADDDSDYYCVLYMGSGIWIWVFGGGTKLTVL

|            |            |              |
|------------|------------|--------------|
| SGSVSTSY   | STN        | VLYMGSGIWIWV |
| SEQ ID:242 | SEQ ID:243 | SEQ ID:244   |

**Hu-5** VH SEQ ID NO: 193

QVQLVQSGAEVKKPGASVKVSCEASGYTFTSSYMIHWVRQAPGQGLEWMGHIINPSGGRTNYAQKFQG  
 RVTIMTRDTSTSTVYMESSLRSEDYAVYYCARDHYDIFTTYYPRGMDVWGQGTTTVTVSS

|            |            |                    |
|------------|------------|--------------------|
| GYTFTSSY   | INPSGGRT   | ARDHYDIFTTYYPRGMDV |
| SEQ ID:245 | SEQ ID:246 | SEQ ID:247         |

**Hu-5** VL SEQ ID NO: 194

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPKAPKRLIYAASSLQSGVPSRFSGSGSGTE  
 FTLTISSLQPEDFTTYCLQHNSFPFTFGQGLEIR

|            |            |            |
|------------|------------|------------|
| QGIRND     | AAS        | LQHNSFPFT  |
| SEQ ID:248 | SEQ ID:249 | SEQ ID:250 |

**Hu-6** VH SEQ ID NO: 195

QMQLRESGPGLVKPSETLSLTCTVSNGPISSSRYWGWIRQPPGKGLEWIGSFHYSGSTYYKPSLKSRLV  
 TISADTSKNQLSLELSSVTAADTAVYYCARLVLRVFDWLGDFDLWGRGTLTVTVSS

|            |            |                  |
|------------|------------|------------------|
| NGPISSSRY  | FHYSGST    | ARLVLRVFDWLGDFDL |
| SEQ ID:251 | SEQ ID:252 | SEQ ID:253       |

**Hu-6** VL SEQ ID NO: 196

EFVMTQSPATLSLSPGERATLSCRASQSIRSNYLSWYQQKPKQAPRLIYGASTRATAIPARFSGSGSGT  
 DFTLTISSLQPEDFAVYYCQQDYNLPITFGQGTREIK

|            |            |            |
|------------|------------|------------|
| QSIRSNY    | GAS        | QQDYNLPIT  |
| SEQ ID:254 | SEQ ID:255 | SEQ ID:256 |

FIG. 2 cont.

**Hu-7\_VH1** SEQ ID NO: 197

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYVMSWVRQAPGKGLEWVSTISGSGGSTYYADSVKDRF  
TISRDN SKNTLYLQMNSLRAEDTAVYYCGKPLLGGTGLWDYWGQGT LTVSS

|            |            |               |
|------------|------------|---------------|
| GFTFSSYV   | ISGSGGST   | GKPLLGGTGLWDY |
| SEQ ID:257 | SEQ ID:258 | SEQ ID:259    |

**Hu-7\_VL** SEQ ID NO: 198

EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDSSNRATGVPARFSGSGSGTD  
FTLTISLEPEDFAVYYCQQRSNWPLTFGGGTKVEIK

|            |            |            |
|------------|------------|------------|
| QSVSSY     | DSS        | QQRSNWPLT  |
| SEQ ID:260 | SEQ ID:261 | SEQ ID:262 |

**Hu-8\_VH** SEQ ID NO: 199

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWDGSGNKKYADSVKGR  
RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRYDVLTAYPYYFYNNMDVWGPGT TTVSS

|            |            |                      |
|------------|------------|----------------------|
| GFTFSSYG   | IWYDGSNK   | ARRYDVLTAYPYYFYNNMDV |
| SEQ ID:263 | SEQ ID:264 | SEQ ID:265           |

**Hu-8\_VL** SEQ ID NO: 200

QTVVTQEPSPFSVSPGGTVTLTCGLNSGSVSTSYYPSSWYQQTPGQAPRTLIIYSTNTRSSGVPDRFSGSILG  
NKAALITGAQADDES DYCYLYMGSGIWWFGGGTKLTVL

|            |            |            |
|------------|------------|------------|
| SGSVSTSY   | STN        | VLYMGSGIWW |
| SEQ ID:266 | SEQ ID:267 | SEQ ID:268 |

**Hu-9\_VH** SEQ ID NO: 201

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEAMTWVRQAPGKGLEWVSSLSGSGRSTYYA  
ASMKGRTISRDN SKNTLYLQMNSLRAEDTAIYYCAKSLSYHYHYFDYWGQGT LTVTS

|            |            |               |
|------------|------------|---------------|
| GFTFSSEA   | LSGSGRST   | AKSLSYHYHYFDY |
| SEQ ID:269 | SEQ ID:270 | SEQ ID:271    |

**Hu-9\_VL** SEQ ID NO: 202

DIQLTQSPSFLSASVGD RVPITCRASQGISNFLAWYQQKPGKAPELLIHSASTLQSGVPSRFSGS  
GSGTEFTLTISNLQPQDFATYYCQQVNSYPLTFGGGTKVEIK

|            |            |            |
|------------|------------|------------|
| QGISNF     | SAS        | QQVNSYPLT  |
| SEQ ID:272 | SEQ ID:273 | SEQ ID:274 |

FIG. 2 cont.

**Hu-10\_VH** SEQ ID NO: 203

EVQLSESGGALVQPGESLRLSCAASGFTFSYAMTWVRQAPGKGLEWVSSLSGSGRSTYYA  
 ASI~~K~~GRFTISRDNSKNTLYLQMSSLRAEDTAIYYCAKSLSYHYFDYWGQGT~~L~~TVSS

|            |            |             |
|------------|------------|-------------|
| GFTFSYA    | LSGSGRST   | AKSLSYHYFDY |
| SEQ ID:275 | SEQ ID:276 | SEQ ID:277  |

**Hu-10\_VL** SEQ ID NO: 204

DIQLTQSPSFLSASVGDRVPITCRASQDISNYLAWYQKPGKAPKLLIYAS~~A~~TLQSGVPSRFSG  
 SSGSTEFTLTISLQPEDFASYHCQ~~Q~~VKTYPLTFGGG~~T~~KVEIK

|            |            |            |
|------------|------------|------------|
| QDISNY     | SAS        | QQVKTYPLT  |
| SEQ ID:278 | SEQ ID:279 | SEQ ID:280 |

**Hu-11\_VH** SEQ ID NO: 205

QVHLVQSGAEVKKPGASVKVSCKASGYTFTSYIHVVRQAPGQGLEWMGIINPSGGNTIYA  
 QKFQGRVTMTRDTSTTTVYVELSSLRSEDTAVYYCARDHYDILTGYYP~~L~~YGM~~D~~VWGQGT  
 TVTVSS

|            |            |                                               |
|------------|------------|-----------------------------------------------|
| GYTFTSY    | INPSGGNT   | ARDHYDILTGYYP <del>L</del> YGM <del>D</del> V |
| SEQ ID:281 | SEQ ID:282 | SEQ ID:283                                    |

**Hu-11\_VL** SEQ ID NO: 206

SYELTQPLSVSVALGQTARITCGGNNIGSKNVHWYQKPGQAPVLVIYRDSNRPSGIPERFSG  
 SKSGNTATLTISRAQAGDEADYYCQVWDSSTAVFGGGTQLTAL

|            |            |            |
|------------|------------|------------|
| NIGSKN     | RDS        | QVWDSSTAV  |
| SEQ ID:284 | SEQ ID:285 | SEQ ID:286 |

**Hu-12\_VH** SEQ ID NO: 207

EVRLLES~~G~~GLVQPGGSLRLSCIASGFTFSYVMSWVRQAPGKGLEWVSGISGSGGSTYYAD  
 SVKGRFTISRDNSKNTLYLQISSLRAEDTAVYYCTKAPTLWWFFDLWGRGTLTVSS

|            |            |              |
|------------|------------|--------------|
| GFTFSYV    | ISGSGGST   | TKAPTLWWFFDL |
| SEQ ID:287 | SEQ ID:288 | SEQ ID:289   |

**Hu-12\_VL** SEQ ID NO: 208

DIQVTQSPSFLSASVGDRVTITCRASQGIRSYLAWYQKPGKAPKLLIYAAS~~T~~LQSGVPSRFSG  
 SSGSTEFTLTISLLPEDFATYYCQQLNSYPLTFGGG~~T~~KVEIK

|            |            |            |
|------------|------------|------------|
| QGIRSY     | AAS        | QQLNSYPLT  |
| SEQ ID:290 | SEQ ID:291 | SEQ ID:292 |

FIG. 2 cont.

**Hu-13\_VH** SEQ ID NO: 209

EVQLLESGGGLVQPGGSLRVACAASGFPLRSYAMSWVRQAPGKGLEWVSVTSGSGGSTYY  
 ADSVKGRFTISRDNSKSTVYLQMNSLRAEDTAVYYCAKDRGYDILTGYDYFYGMDVWGQ  
 GTTVTVSS

|            |            |                      |
|------------|------------|----------------------|
| GFPLRSYA   | TSGSGGST   | AKDRGYDILTGYDYFYGMDV |
| SEQ ID:293 | SEQ ID:294 | SEQ ID:295           |

**Hu-13\_VL** SEQ ID NO: 210

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWFQQKPGKAPKRLIYAASSLQSGVPSRFS  
 GSGSGTEFTLTISSLQPEDFATYYCLQHNSYPYTFGQGTKLEIK

|            |            |            |
|------------|------------|------------|
| QGIRND     | AAS        | LQHNSYPYT  |
| SEQ ID:296 | SEQ ID:297 | SEQ ID:298 |

**Hu-14\_VH** SEQ ID NO: 211

EVQLLESGGGLVQPGGSLRLSCAASGITFSSYAMSWVRQVPGKGLEWVSVISGSGGSTYYAD  
 SVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDRGYDILTTYYDYFYGMDVWGQPEF  
 QHTGG

|            |            |                       |
|------------|------------|-----------------------|
| GITFSSYA   | ISGSGGST   | AKDRGYDILTTYYDYFYGMDV |
| SEQ ID:299 | SEQ ID:300 | SEQ ID:301            |

**Hu-14\_VL** SEQ ID NO: 212

DIQMTQSPSSLSASVGDRVIITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFS  
 GSGSGTEFTLTISSLQPEDLASYYCLQHNSYPYTFGQGTKLEIK

|            |            |            |
|------------|------------|------------|
| QGIRND     | AAS        | LQHNSYPYT  |
| SEQ ID:302 | SEQ ID:303 | SEQ ID:304 |

**Hu-16\_VH** SEQ ID NO: 215

EVQLLESGGGVVQPGGSLRLSCAASGLIFSSYAMSWVRQAPGKGLEWVSVIGGSGSNTFYAD  
 SVKGRFTISRDNSKNTLFLQMNSLRAEDTAVYYCAKDRGYDILTGYNNYYYGMDVWGQGI  
 TTVTVSS

|            |            |                       |
|------------|------------|-----------------------|
| GLIFSSYA   | IGGSGSNT   | AKDRGYDILTGYNNYYYGMDV |
| SEQ ID:311 | SEQ ID:312 | SEQ ID:313            |

**Hu-16\_VL** SEQ ID NO: 216

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFS  
 GSGSGTEFTLTISSLQPEDFATYYCLQHNSYPYTFGQGTKLEIK

|            |            |            |
|------------|------------|------------|
| QGIRND     | AAS        | LQHNSYPYT  |
| SEQ ID:314 | SEQ ID:315 | SEQ ID:316 |

FIG. 2 cont.

**Hu-17\_VH** SEQ ID NO: 217

QVQLVQSGAEVKRPGASVKVSCRVSGYTLTALSSMYWVRQAPGKGLEWMGGFDPEDGETIY  
 AQKFQGRVTMTEDTSTGTAYMELSSLKSEDTAVYYCATRLRYFDWNYWGQGTPVTVSS

|            |            |             |
|------------|------------|-------------|
| GYTLTALS   | FDPEDGET   | ATRLRYFDWNY |
| SEQ ID:317 | SEQ ID:318 | SEQ ID:319  |

**Hu-17\_VL** SEQ ID NO: 218

DIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQORPGQPPRLIYKYSKRFSGVDPDRFSGS  
 GAGTDFTLKISRVEAEDVGVIYCTQGTQFPRTFGQGTKVEIK

|             |            |            |
|-------------|------------|------------|
| QSLVHSDGNTY | KVS        | TQGTQFPRT  |
| SEQ ID:320  | SEQ ID:321 | SEQ ID:322 |

**Hu-18** 17001.C8.2F9.1E1\_VH SEQ ID NO: 219

QVQLVQSGAEVKKPGASVKVSCRVSGYTLSALSSMYWVRQAPGKGLEWMGGFDPEDGKTIY  
 AQKFQGRVTMTEDTSTGTAYMELSSLRSEDTAIYYCATTLRYFDWNYWGQGTPVTVSS

|            |            |             |
|------------|------------|-------------|
| GYTLSALS   | FDPEDGKT   | ATTLRYFDWNY |
| SEQ ID:323 | SEQ ID:324 | SEQ ID:325  |

**Hu-18\_VL** SEQ ID NO: 220

DIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQORPGQPPRLIYKYSKRFSGVDPDRFSGS  
 GAGTDFTLKISRVEAEDVGVIYCTQGTQFPRTFGQGTKVEIK

|             |            |            |
|-------------|------------|------------|
| QSLVHSDGNTY | KVS        | TQGTQFPRT  |
| SEQ ID:326  | SEQ ID:327 | SEQ ID:328 |

FIG. 2 cont.

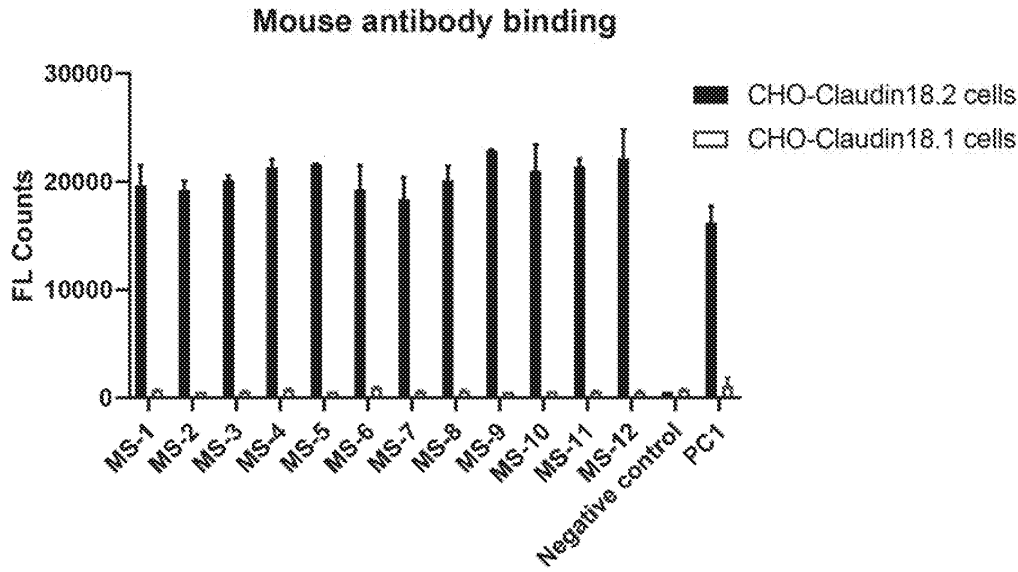
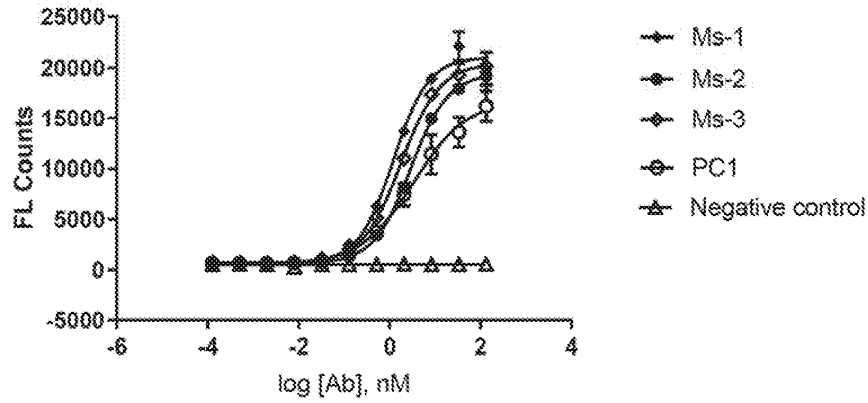
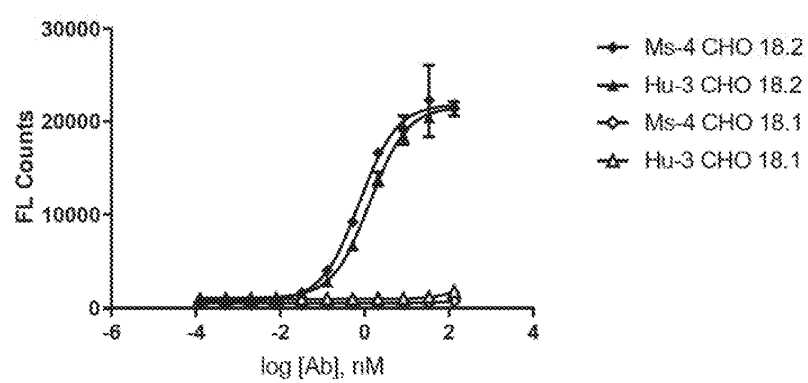


FIG. 3A



|          |      |      |      |     |                  |
|----------|------|------|------|-----|------------------|
|          | Ms-1 | Ms-2 | Ms-3 | PC1 | Negative control |
| EC50, nM | 1.2  | 2.8  | 1.8  | 3.2 | Inactive         |

FIG. 3B



|          | Ms-4 CHO<br>CLDN18.2 | Hu-3 CHO<br>CLDN18.2 | Ms-4 CHO<br>CLDN18.1 | Hu-3 CHO<br>CLDN18.1 |
|----------|----------------------|----------------------|----------------------|----------------------|
| EC50, nM | 0.75                 | 1.34                 | Inactive             | Inactive             |

FIG. 3C

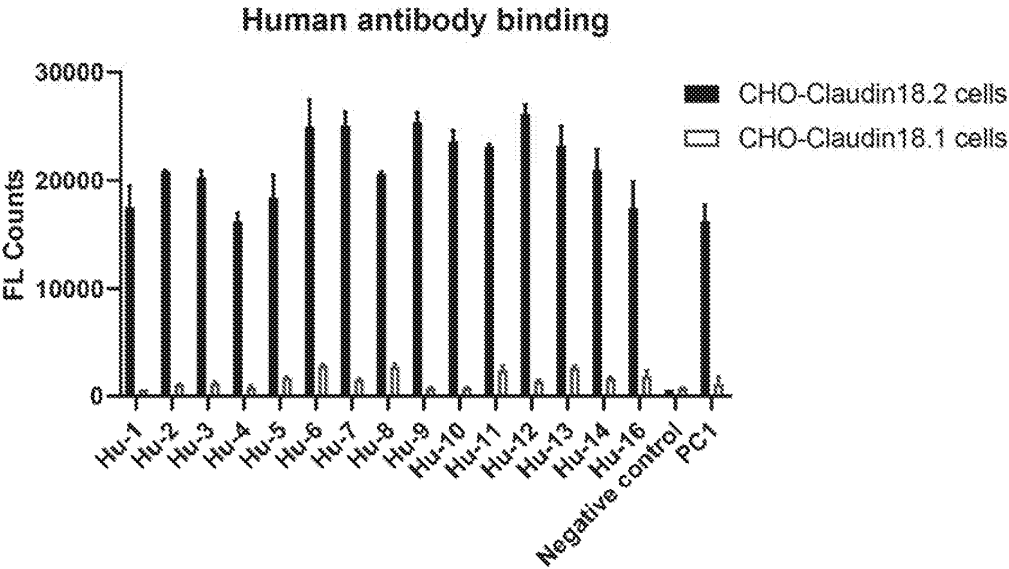
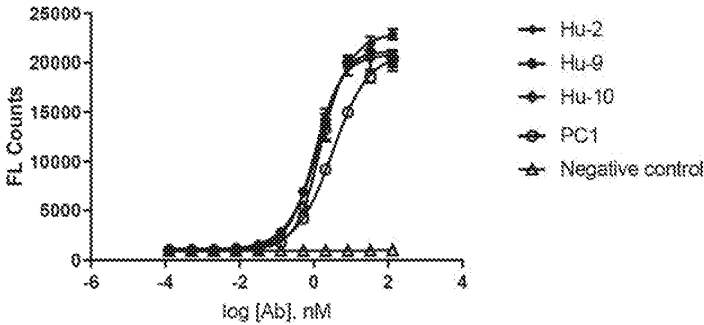


FIG. 4A



|          | Hu-2 | Hu-9 | Hu-10 | PC1 | Negative control |
|----------|------|------|-------|-----|------------------|
| EC50, nM | 1.5  | 1.1  | 1.5   | 3.2 | Inactive         |

FIG. 4B

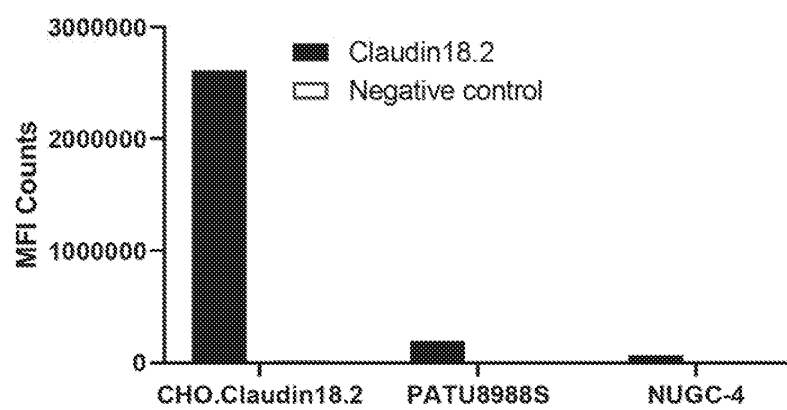


FIG. 5

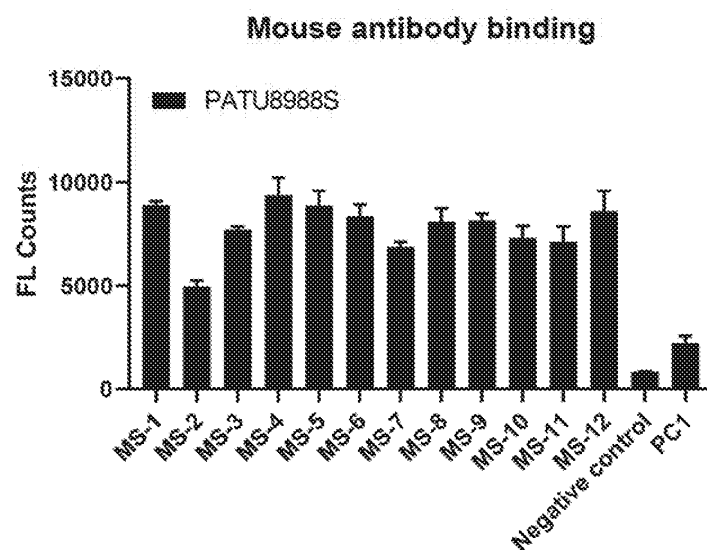


FIG. 6A

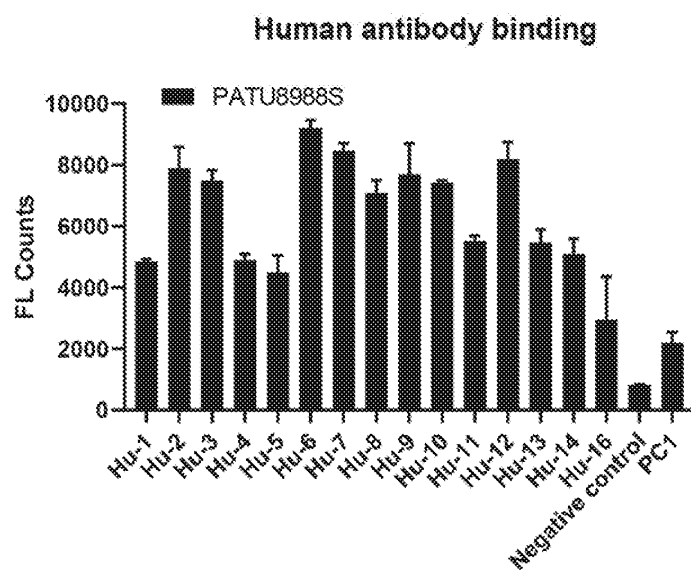


FIG. 6B

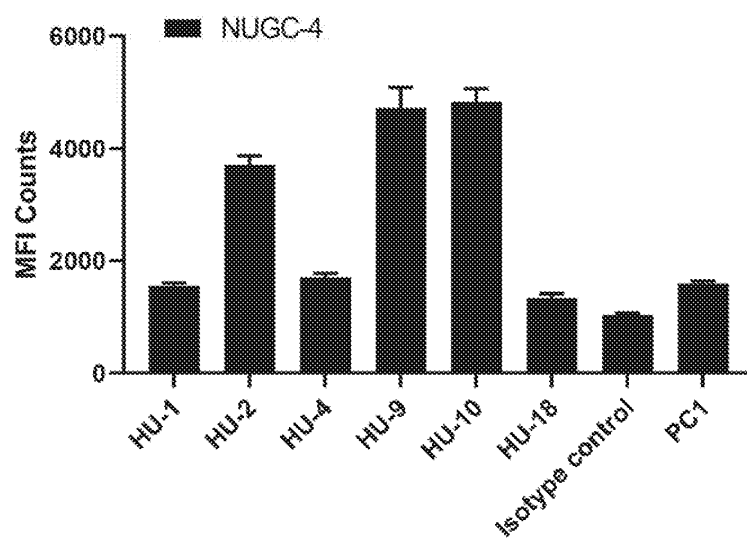


FIG. 7

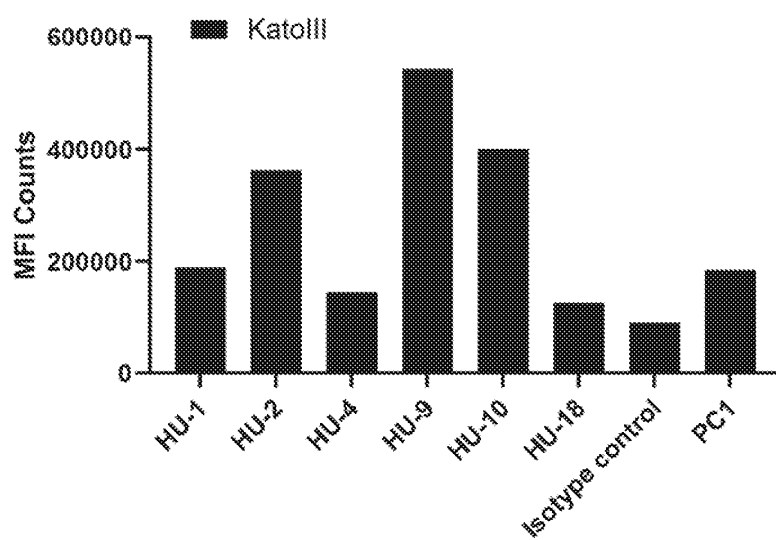
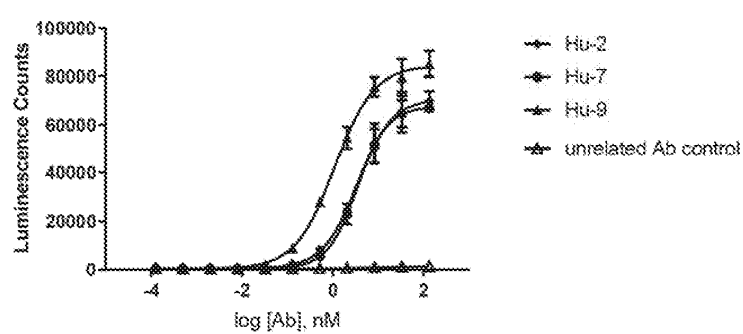


FIG. 8

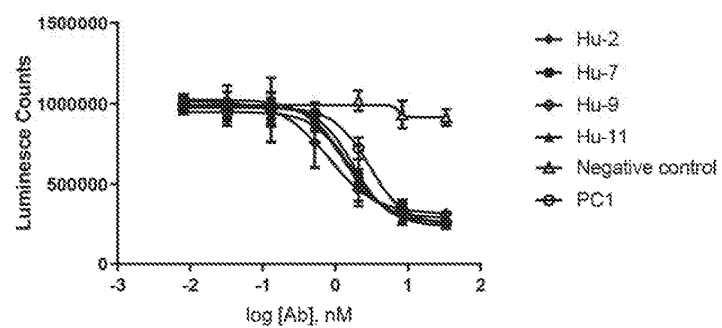
## ADCC Activity of Anti-Claudin18.2 antibodies



|          |      |      |      |                      |
|----------|------|------|------|----------------------|
|          | Hu-2 | Hu-7 | Hu-9 | Unrelated Ab control |
| EC50, nM | 3.51 | 3.52 | 1.10 | Inactive             |

FIG. 9

## Claudin-18.2 Antibody Endocytosis



|             | Hu-2  | Hu-7  | Hu-9  | Hu-11 | Unrelated<br>Ab control | PC1   |
|-------------|-------|-------|-------|-------|-------------------------|-------|
| EC50,<br>nM | 1.428 | 1.718 | 0.791 | 1.478 | >133.4                  | 2.927 |

FIG. 10

|                |                                                                                                                                                                                                                                                                                                                                                                                                                 |
|----------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| SEQ IDENTIFIER | HUMAN IgG1 HEAVY CHAIN                                                                                                                                                                                                                                                                                                                                                                                          |
| SEQ ID NO: 331 | ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS<br>WNSGALTSGV<br>HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT YICNVNHKPS<br>NTKVDKRVEP<br>KSCDKTHTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTF<br>EVTCVVVDVS<br>HEDPEVKFNW YVDGVEVHNA KTKPREEQYN STYRVVSVLT<br>VLHQDWLNGK<br>EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSREE<br>MTKNQVSLTCL<br>LVKGFYPSDI AVEWESNGQP ENNYKTTTPV LDSDGSFFLY<br>SKLTVDKSRW<br>QQGNVFSCSV MHEALHNHYT QKSLSLSPGK |
| SEQ ID NO: 332 | ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS<br>WNSGALTSGV<br>HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT YICNVNHKPS<br>NTKVDKRVEP<br>KSCDKTHTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTF<br>EVTCVVVDVS<br>HEDPEVKFNW YVDGVEVHNA KTKPREEQYN STYRVVSVLT<br>VLHQDWLNGK<br>EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE<br>LTKNQVSLTCL<br>LVKGFYPSDI AVEWESNGQP ENNYKTTTPV LDSDGSFFLY<br>SKLTVDKSRW<br>QQGNVFSCSV MHEALHNHYT QKSLSLSPGK |
| SEQ ID NO: 333 | ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS<br>WNSGALTSGV<br>HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT YICNVNHKPS<br>NTKVDKKVEP<br>KSCDKTHTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTF<br>EVTCVVVDVS<br>HEDPEVKFNW YVDGVEVHNA KTKPREEQYN STYRVVSVLT<br>VLHQDWLNGK<br>EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSREE<br>MTKNQVSLTCL<br>LVKGFYPSDI AVEWESNGQP ENNYKTTTPV LDSDGSFFLY<br>SKLTVDKSRW<br>QQGNVFSCSV MHEALHNHYT QKSLSLSPGK |
| SEQ ID NO: 334 | ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS<br>WNSGALTSGV<br>HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT YICNVNHKPS<br>NTKVDKKVEP<br>KSCDKTHTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTF<br>EVTCVVVDVS<br>HEDPEVKFNW YVDGVEVHNA KTKPREEQYN STYRVVSVLT<br>VLHQDWLNGK<br>EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE<br>LTKNQVSLTCL<br>LVKGFYPSDI AVEWESNGQP ENNYKTTTPV LDSDGSFFLY<br>SKLTVDKSRW<br>QQGNVFSCSV MHEALHNHYT QKSLSLSPGK |

FIG. 11A

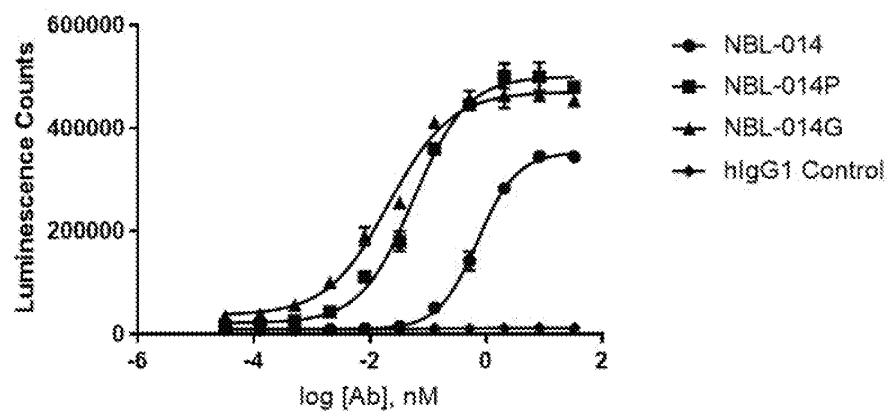
|                |                                                                                                                      |
|----------------|----------------------------------------------------------------------------------------------------------------------|
| SEQ IDENTIFIER | HUMAN KAPPA LIGHT CHAIN                                                                                              |
| SEQ ID NO: 335 | KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL<br>QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS<br>SPVTKSFNRGEC |

FIG. 11B

|                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
|----------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| SEQ IDENTIFIER | NBL-014 HEAVY CHAINS AND LIGHT CHAIN                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| SEQ ID NO: 336 | EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFAMTWVRQAPGKGLEW<br>VSSLSGSGRSTYYAASMKGRTISRDN SKNTLYLQMNSLRAEDTAIYY<br>CAKSLSYHYHYFDYWGGQTLVTVTSASTKGPSVFPLAPSSKSTSGGTA<br>ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTV<br>PSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELVG<br>GPSVFLLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV<br>HNAKTKPPEEQYNSTLRVVS VLTVLHQDWLNGKEYKCKVSNKALPAP<br>IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE<br>WESNGQPENNYKTTPLVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV<br>MHEALHNHYTQKSLSLSPGK |
| SEQ ID NO: 338 | EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFAMTWVRQAPGKGLEW<br>VSSLSGSGRSTYYAASMKGRTISRDN SKNTLYLQMNSLRAEDTAIYY<br>CAKSLSYHYHYFDYWGGQTLVTVTSASTKGPSVFPLAPSSKSTSGGTA<br>ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTV<br>PSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELVG<br>GPSVFLLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV<br>HNAKTKPPEEQYNSTLRVVS VLTVLHQDWLNGKEYKCKVSNKALPAP<br>IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE<br>WESNGQPENNYKTTPLVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV<br>MHEALHNHYTQKSLSLSPGK |
| SEQ ID NO: 337 | DIQLTQSPSFLSASVGD RVPITCRASQGISN FLAWYQQKPGKAPELLIHS<br>ASTLQSGVPSRFSGSGSGTEFTLTISNLQPQDFATYYCQQVNSYPLTFG<br>GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ<br>WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC<br>EVTHQGLSSPVTKSFNRGEC                                                                                                                                                                                                                                                               |

FIG. 12

## CHO-Claudin18.2 Cell ADCC



|          | NBL-014 | NBL-014P | NBL-014G | hlgG1 Control |
|----------|---------|----------|----------|---------------|
| EC50, nM | 0.73    | 0.06     | 0.02     | Inactive      |

FIG. 13A

## ADCC on CHO claudin18.2

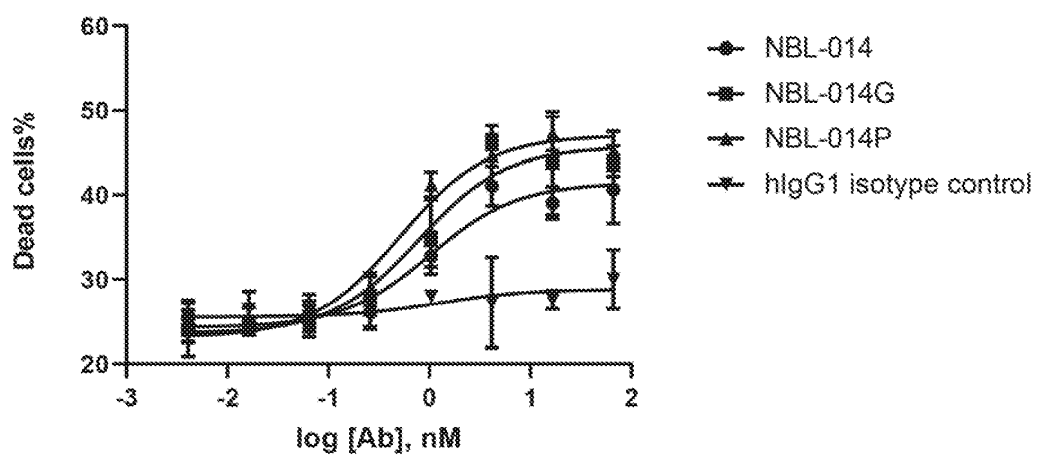
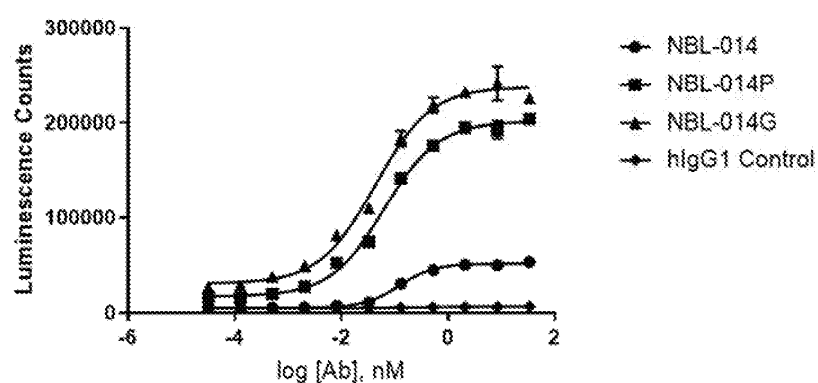


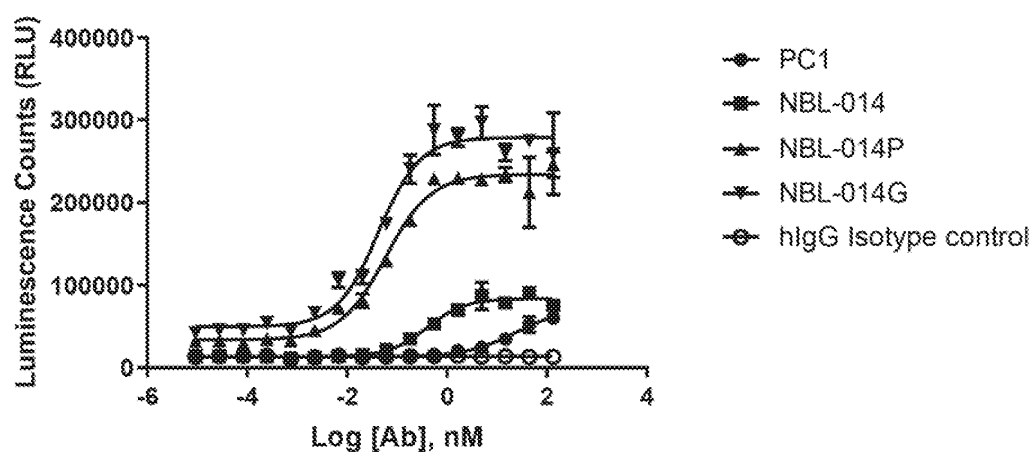
FIG. 13B



|          | NBL-014 | NBL-014P | NBL-014G | hlgG1 Control |
|----------|---------|----------|----------|---------------|
| EC50, nM | 0.12    | 0.06     | 0.04     | Inactive      |

NUGC-4 cell ADCC

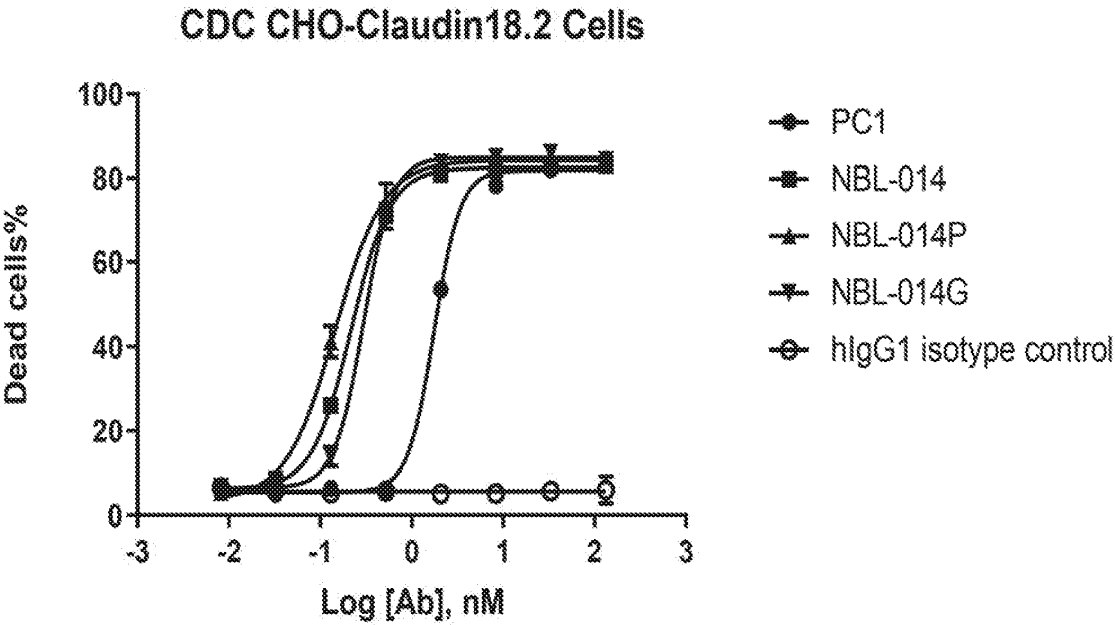
FIG. 14A



|          | PC1  | NBL-014 | NBL-014P | NBL-014G | Isotype Ctl |
|----------|------|---------|----------|----------|-------------|
| EC50, nM | >133 | 0.4     | 0.06     | 0.04     | Inactive    |

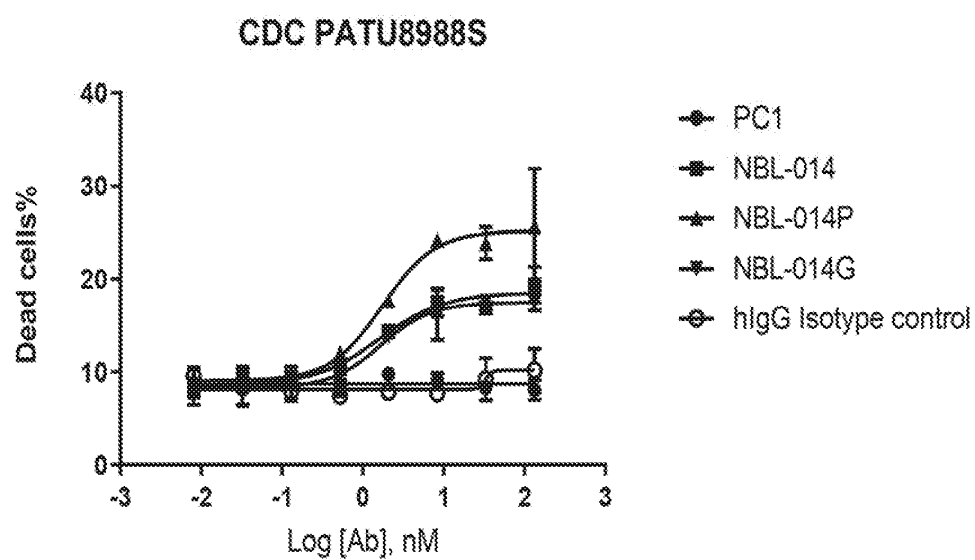
PATU8988S cell ADCC

FIG. 14B



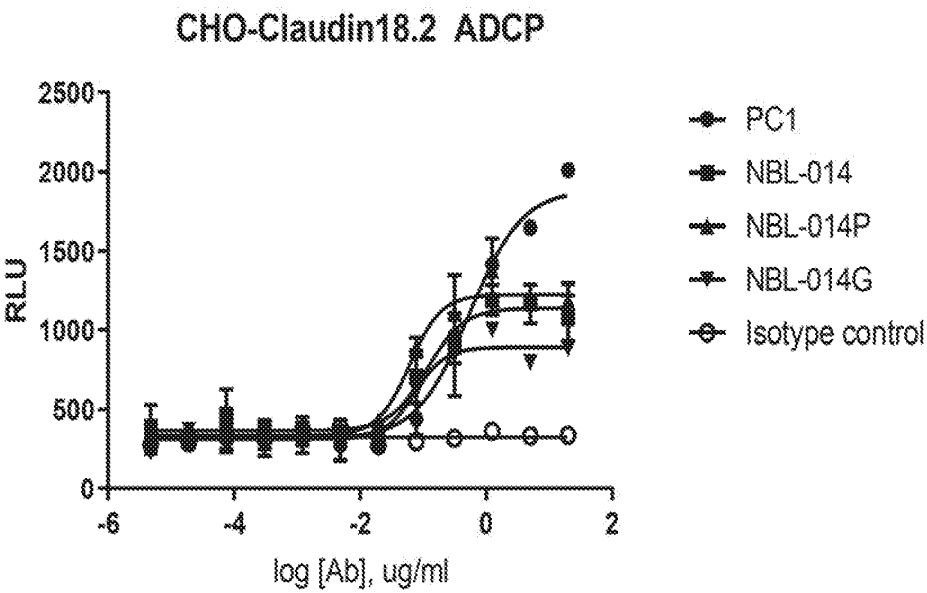
|          |      |         |          |          |             |
|----------|------|---------|----------|----------|-------------|
|          | PC1  | NBL-014 | NBL-014G | NBL-014P | Isotype Ctl |
| EC50, nM | 1.76 | 0.22    | 0.15     | 0.30     | Inactive    |

FIG. 15



|          | PC1       | NBL-014 | NBL-014G | NBL-014P | Isotype Ctl |
|----------|-----------|---------|----------|----------|-------------|
| EC50, nM | In active | 1.62    | 1.76     | 1.67     | Inactive    |

FIG. 16



|          | PC1  | NBL-014 | NBL-014P | NBL-014G | Isotype Ctl |
|----------|------|---------|----------|----------|-------------|
| EC50, nM | 0.54 | 0.11    | 0.06     | 0.07     | Inactive    |

FIG. 17A

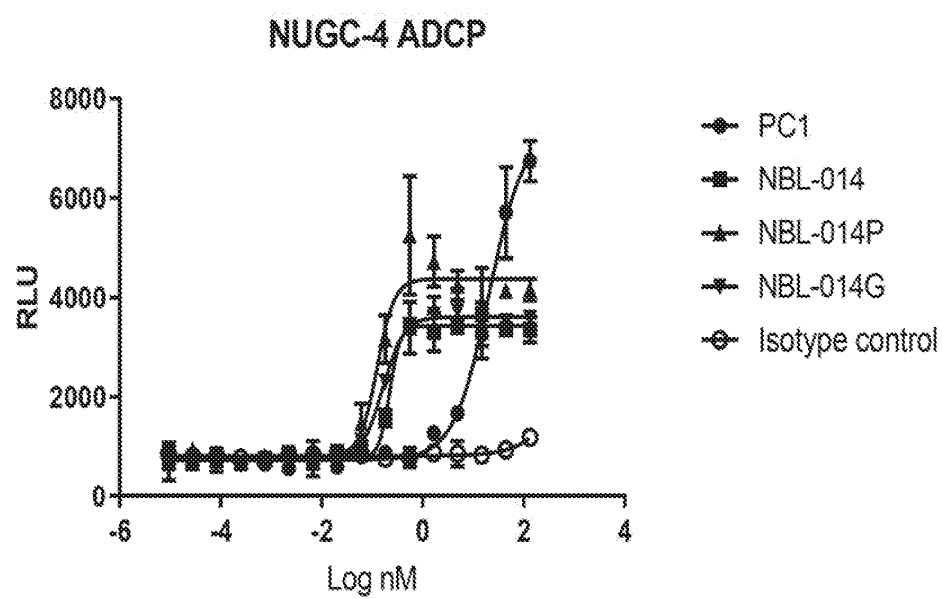


FIG. 17B

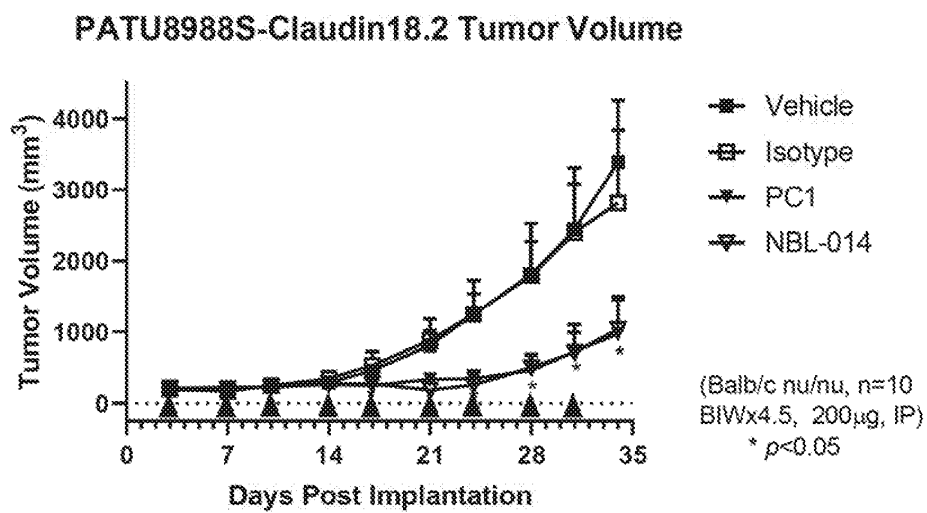


FIG. 18A

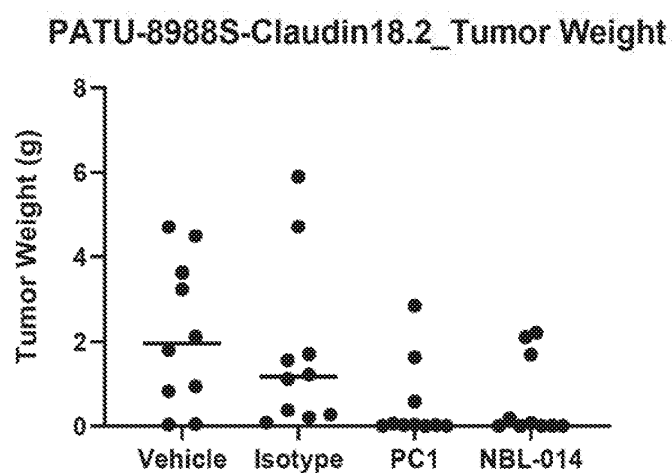


FIG. 18B

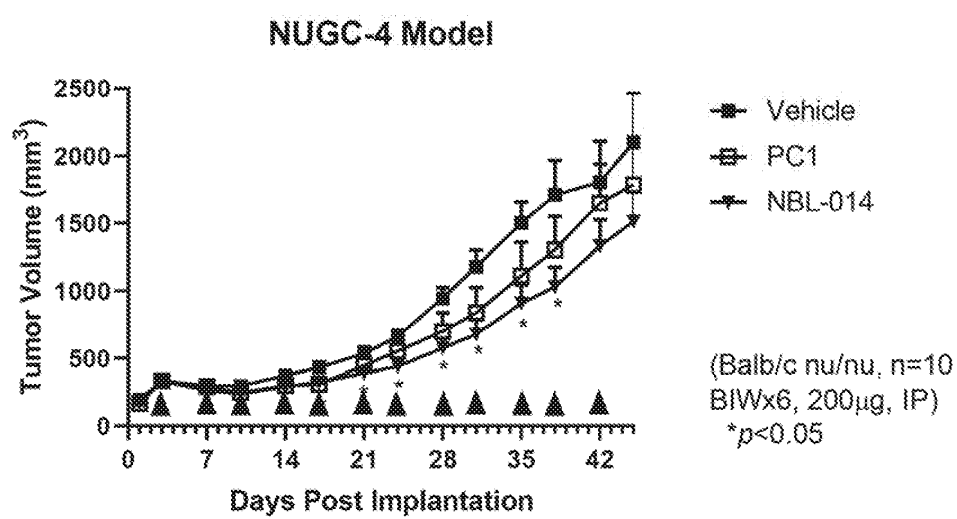


FIG. 19

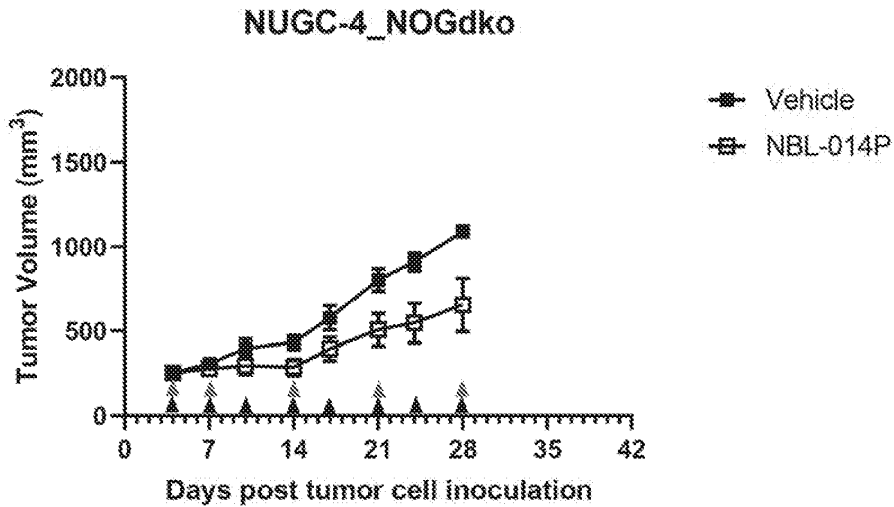


FIG. 20A

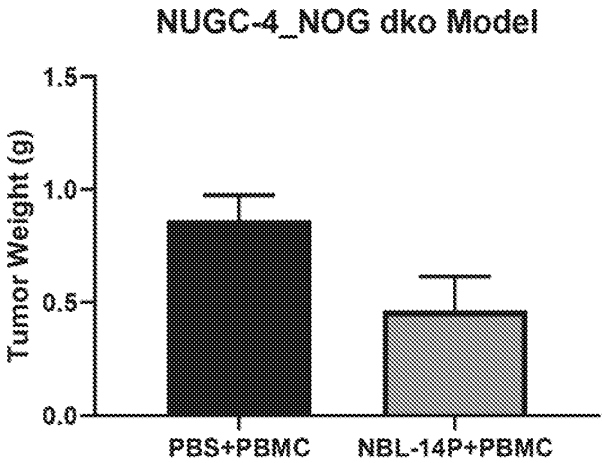


FIG. 20B

Human claudin 18 isoform 2, Uni-Prot entry P56856 (CLD18\_human) identified as P56856-2

MAVTACQGLGFVVSLIGIAGHIAATCMDQWSTQDLYNNPVTAVFNYQGLWRSCVRE  
SSGFTECRGYFTLLGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKA  
NMTLTSGIMFIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYT  
FGAALFVGWVAGGLTLIGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGF  
KASTGFGSNTKNKKIYDGGARTEDEVQSYPSKHDYV (SEQ ID NO: 329)

Human claudin 18 isoform 1, Uni-Prot entry P56856 (CLD18\_human) identified as P56856

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGGLWRSCVRQ  
SSGFTECRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKA  
NMTLTSGIMFIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYT  
FGAALFVGWVAGGLTLIGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGF  
KASTGFGSNTKNKKIYDGGARTEDEVQSYPSKHDYV (SEQ ID NO: 330)

FIG. 21