

**FIG. 1A: The cDNA (SEQ ID NO:1) and amino acid sequence (SEQ ID NO:2) of 191P4D12. The start methionine is underlined. The open reading frame extends from nucleic acid 264-1796 including the stop codon.**

```

1  ggccgtcgttgttgccacagcgtgggaagcagctctgggggagctcggagctcccgatc
61  acggcttcttggggtagctacggctgggtgtgtagaacggggcggggctgggctggg
121  tcccctagtggagacccaagtgcgagaggcaagaactctgcagcttcctgccttctgggt
181  cagttccttattcaagtctgcagccggtcccaggagatctcgggtggaacttcagaaac
1      M P L S L G A E M W G P E
241  gctgggcagctctgcctttcaaccATGCCCCCTGTCCCTGGGAGCCGAGATGTGGGGCCCTG
14   A W L L L L L L L A S F T G R C P A G E
301  AGGCCTGGCTGCTGCTGCTGCTACTGCTGGCATCATTTACAGGCCGGTGCCCCGCGGGTG
34   L E T S D V V T V V L G Q D A K L P C F
361  AGCTGGAGACCTCAGACGTGGTAACTGTGGTGCTGGGCCAGGACGCAAACTGCCTGCT
54   Y R G D S G E Q V G Q V A W A R V D A G
421  TCTACCGAGGGGACTCCGGCGAGCAAGTGGGGCAAGTGGCATGGGCTCGGGTGGACGCGG
74   E G A Q E L A L L H S K Y G L H V S P A
481  GCGAAGGCGCCAGGAAGTAGCGCTACTGCACTCCAAATACGGGCTTCATGTGAGCCCCG
94   Y E G R V E Q P P P P R N P L D G S V L
541  CTTACGAGGGCCGCGTGGAGCAGCCCGCCCCACGCAACCCCTGGACGGCTCAGTGC
114  L R N A V Q A D E G E Y E C R V S T F P
601  TCCTGCGCAACGCAGTGCAGGCGGATGAGGGCGAGTACGAGTGCCGGGTCAGCACCTTCC
134  A G S F Q A R L R L R V L V P P L P S L
661  CCGCCGCGCAGCTTCCAGGCGCGGCTGCGGCTCCGAGTGCTGGTGCCCTCCCTGCCTCAC
154  N P G P A L E E G Q G L T L A A S C T A
721  TGAATCTGGTCCAGCACTAGAAGAGGGCCAGGGCCTGACCTGGCAGCCTCCTGCACAG
174  E G S P A P S V T W D T E V K G T T S S
781  CTGAGGGCAGCCAGCCCCAGCGTGACCTGGGACACGGAGGTCAAAGGCACAACGTCCA
194  R S F K H S R S A A V T S E F H L V P S
841  GCCGTTCTTCAAGCACTCCCGCTCTGCTGCCGTACCTCAGAGTTCCACTTGGTGCTTA
214  R S M N G Q P L T C V V S H P G L L Q D
901  GCCGCAGCATGAATGGGCAGCCACTGACTTGTGTGGTGTCCCATCCTGGCCTGCTCCAGG
234  Q R I T H I L H V S F L A E A S V R G L
961  ACCAAAGGATCACCCACATCCTCCACGTGTCCTTCCTTGCTGAGGCCTCTGTGAGGGGCC
254  E D Q N L W H I G R E G A M L K C L S E
1021  TTGAAGACCAAAATCTGTGGCACATTGGCAGAGAAGGAGCTATGCTCAAGTGCCTGAGTG
274  G Q P P P S Y N W T R L D G P L P S G V
1081  AAGGGCAGCCCCCTCCCTCATACAACTGGACACGGCTGGATGGGCCTCTGCCCAGTGGGG
294  R V D G D T L G F P P L T T E H S G I Y
1141  TACGAGTGGATGGGGACACTTTGGGCTTTCCCCACTGACCACTGAGCACAGCGGCATCT
314  V C H V S N E F S S R D S Q V T V D V L
1201  ACGTCTGCCATGTGAGCAATGAGTCTCCTCAAGGGATTCTCAGGTCACTGTGGATGTTT
334  D P Q E D S G K Q V D L V S A S V V V V

```

1261 TTGACCCCCAGGAAGACTCTGGGAAGCAGGTGGACCTAGTGTGACGCTCGGTGGTGGTGG  
354 G V I A A L L F C L L V V V V V L M S R  
1321 TGGGTGTGATCGCCGCAAGGCCAGCAGATGACCCAGAAATATGAGGAGGAGCTGACCCCTGA  
374 Y H R R K A Q Q M T Q K Y E E E L T L T  
1381 GATACCATCGGCGCAAGGCCAGCAGATGACCCAGAAATATGAGGAGGAGCTGACCCCTGA  
394 R E N S I R R L H S H H T D P R S Q P E  
1441 CCAGGGAGAACTCCATCCGGAGGCTGCATTCCCATCACACGGACCCCAGGAGCCAGCCGG  
414 E S V G L R A E G H P D S L K D N S S C  
1501 AGGAGAGTGTAGGGCTGAGAGCCGAGGGCCACCCTGATAGTCTCAAGGACAACAGTAGCT  
434 S V M S E E P E G R S Y S T L T T V R E  
1561 GCTCTGTGATGAGTGAAGAGCCCGAGGGCCGAGTTACTCCACGCTGACCACGGTGAGGG  
454 I E T Q T E L L S P G S G R A E E E E D  
1621 AGATAGAAACACAGACTGAACTGCTGTCTCCAGGCTCTGGGCGGGCCGAGGAGGAGGAAG  
474 Q D E G I K Q A M N H F V Q E N G T L R  
1681 ATCAGGATGAAGGCATCAAACAGGCCATGAACCATTTTGTTCAGGAGAATGGGACCCTAC  
494 A K P T G N G I Y I N G R G H L V \*  
1741 GGGCCAAGCCCACGGGCAATGGCATCTACATCAATGGGCGGGACACCTGGTCTGAcccc  
1801 ggccctgcctccctccctagggcctgcctccttctgttgacatgggagatttttagctcatc  
1861 ttgggggcctccttaaacacccccatttcttgcggaagatgctccccatcccactgactg  
1921 cttgacctttacctccaacccttctgttcacogggagggctccaccaattgagtcctctcc  
1981 caccatgcatgcaggctcactgtgtgtgtgcatgtgtgcctgtgtgagtggtgactgactg  
2041 tgtgtgtgtggaggggtgactgtccgtggaggggtgactgtgtccgtggtgtgtattatg  
2101 ctgtcatatcagagtcgaagtgaactgtggtgtatgtgccacgggatttgagtggttgctg  
2161 gggcaaacactgtcaggggttgccgtgtgtgtcatgtggctgtgtgtgacctctgcctgaa  
2221 aaagcaggatatttctcagaccccagagcagtgattaatgatgcagaggttgaggagagaga  
2281 ggtggagactgtggctcagacccagggtgtgcgggcatagctggagctggaatctgcctcc  
2341 ggtgtgagggaaacctgtctcctaccacttcggagccatgggggcaagtgtgaagcagcca  
2401 gtccctgggtcagccagaggcttgaaactgttacagaagccctctgcctctggtggcctc  
2461 tgggcctgctgcatgtacatatatttctgtaaatatacatgcgccgggagcttcttgcaag  
2521 aatactgctccgaatcacttttaattttttctttttttttcttgccctttccattagt  
2581 tgtattttttattttattttttatttttttttttagagatggagctctcactatgttgc  
2641 tcaggctggccttgaaactcctgggtcaagcaatcctcctgcctcagcctccctagtagc  
2701 tgggactttaagtgtacaccactgtgcctgctttgaatcctttacgaagagaaaaaaa  
2761 attaaagaaagccttttagatttatccaatgtttactactgggattgcttaaagtgaggcc  
2821 cctccaacaccaggggttaattcctgtgattgtgaaaggggctacttccaaggcatctt  
2881 catgcaggcagcccttgggagggcacctgagagctggtagagtctgaaattagggatgt  
2941 gagcctcgtggttactgagtaaggtaaaattgcatccaccattgtttgtgataccttagg  
3001 gaattgcttgacctggtgacaagggtcctgttcaatagtgggtgttggggagagagaga  
3061 gcagtgattatagaccgagagagtaggagttgaggtgaggtgaaggaggtgctgggggtg  
3121 agaatgtcgcctttccccctgggttttggatcactaattcaaggctcttctggtatgttc  
3181 tctgggttgggctggagttcaatgaggtttattttttagctggccaccagatacactc  
3241 agccagaatacctagatttagtacccaaactcttcttagtctgaaatctgctggatttct  
3301 ggcctaagggagaggtcccatccttcgttccccagccagcctaggacttcgaatgtgga  
3361 gcctgaagatctaagatcctaacatgtacattttatgtaaatatgtgcatatttgatcat  
3421 aaaatgatattctgtttttaataaacagacaaaacttgaaaaa

**FIG. 1A**  
**(Continued)**

**FIG. 1B: The cDNA (SEQ ID NO:3) and amino acid sequence (SEQ ID NO:4) of Ha22-2(2,4)6.1 heavy chain. Double-underlined is the leader sequence, underlined is the heavy chain variable region, and underlined with a dashed line is the human IgG1 constant region.**

M E L G L C W V F L V A I L E

```

1  GGTGATCAGCACTGAACACAGAGGACTCACCATGGAGTTGGGGCTGTGCTGGGTTTTCCTTGTGCTATTTTAGA
   · G V Q C E V Q L V E S G G G L V Q P G G S L R L S
76  AGGTGTCCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGAGACTCTC
   · C A A S G F T F S S Y N M N W V R Q A P G K G L E
151 CTGTGCAGCCTCTGGATTACCTTCAGTAGCTATAACATGAAGTGGGTCGCCAGGCTCCAGGGAAGGGCTGGA
   · W V S Y I S S S S S S T I Y Y A D S V K G R F T I S
226 GTGGGTTTCATACATTAGTAGTAGTAGTAGTACCATATACTACGCAGACTCTGTGAAGGCCGATTACCATCTC
   · R D N A K N S L S L Q M N S L R D E D T A V Y Y C
301 CAGAGACAATGCCAAGAAGTCACTGTCTCTGCAAAATGAACAGCCTGAGAGACGAGGACACGGCTGTGTATTACTG
   · A R A Y Y Y G M D V W G Q G T T V T V S S A S T K
376 TGGCAGAGCATACTACTACGGTATGGAGTCTGGGGCCAAGGGACACCGTCACCGTCTCCTCAGCCTCCACCAA
   · G P S V F P L A P S S K S T S G G T A A L G C L V
451 GGGCCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGGT
   · K D Y F P E P V T V S W N S G A L T S G V H T F P
526 CAAGGACTACTTCCCCGAACCGGTGACGGTGTGCTGGAAGTCAAGGCGCCCTGACGAGCGCGTGCACACCTTCCC
   · A V L Q S S G L Y S L S S V V T V P S S S L G T Q
601 GGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACGTCGCCCTCCAGCAGCTTGGGCACCCA
   · T Y I C N V N H K P S N T K V D K R V E P K S C D
676 GACCTACATCTGCAACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAATCTTGTGA
   · K T H T C P P C P A P E L L G G P S V F L F P P K
751 CAAAACTCACACATGCCACCGTGGCCAGCACCTGAAGTCTTGGGGGACCGTCAGTCTTCTCTTCCCCCAAA
   · P K D T L M I S R T P E V T C V V V D V S H E D P
826 ACCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTGACATGCGTGGTGGTGGACGTGAGCCACGAAGACCC
   · E V K F N W Y V D G V E V H N A K T K P R E E Q Y
901 TGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGAGTA
   · N S T Y R V S V L T V L H Q D W L N G K E Y K C
976 CAACAGCAGTACCGTGTGGTTCAGCTCTCACCGTCTGCACCAGGACTGGCTGAATGCCAAGGATACAGTG
   · K V S N K A L P A P I E K T I S K A K G Q P R E P
1051 CAAGGTCTCCAACAAAGCCCTCCAGCCCAATCGAGAAAACCATCTCCAAGGCCAAGGGCAGCCCCGAGAACC
   · Q V Y T L P P S R E E M T K N Q V S L T C L V K G
1126 ACAGGTGTACACCTGCCCCATCCCGGAGGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAGG
   · F Y P S D I A V E W E S N G Q P E N N Y K T T P P
1201 CTTCTATCCAGCGACATCGCCGTGGAGTGGAGACCAATGGGCGAGAGCAACTACAAGACCATCCCTCC
   · V L D S D G S F F L Y S K L T V D K S R W Q Q G N
1276 CGTGCTGACTCCGACGGCTCCTTCTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGSCAGAGGGGAA
   · V F S C S V M H E A L H N H Y T Q K S L S L S P G
1351 CGTCTTCTCATGCTCCGTGATGACGCTCTGCACAAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGG
   · K *
1426 TAAATGA

```

**FIG. 1C: The cDNA (SEQ ID NO:5) and amino acid sequence (SEQ ID NO:6) of Ha22-2(2,4)6.1 light chain. Double-underlined is the leader sequence, underlined is the light chain variable region, and underlined with a dashed line is the human kappa constant region.**

M D M R V P A Q L L G L L L L W F

```

1  AGTCAGACCCAGTCAGGACACAGCATGGACATGAGGGTCCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGTTC
   P G S R C D I Q M T Q S P S S V S A S V G D R V T
76  CCAGGTTCAGATGCGACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTTGGAGACAGTCAAC
   I T C R A S Q G I S G W L A W Y Q Q K P G K A P K
151 ATCACTTGTGCGGCGAGTCAGGGTATTAGCGGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAG
   F L I Y A A S T L Q S G V P S R F S G S G S G T D
226 TTCTGTATCTATGCTGCATCCACTTTGCAAAGTGGGTGCCATCAAGGTTACGCGCAGTGGATCTGGGACAT
   F T L T I S S L Q P E D F A T Y Y C Q Q A N S F P
301 TTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCT
   P T F G G G T K V E I K R T V A A P S V F I F P P
376 CCCACTTTCCGGCGAGGGACCAAGGTGGAGATCAAAACGAAGTGTGGCTGCACCATCTGTCTTCCCGCCA
   S D E Q L K S G T A S V V C L L N N F Y P R E A K
451 TCTGATGAGCAGTTGAAATCTGGAATCGCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCAGAGAGGCCAAA
   V Q W K V D N A L Q S G G N S Q E S V T E Q D S K D
526 GTACAGTGGAGGTGGATAACGCCCTCCAAATCGGGTAAGTCCAGGAGAGTGTACAGAGCAGCAGCAGCAAGGAC
   S T Y S L S S T L T L S K A D Y E K H K V Y A C E
601 AGCACCTCAGCCTCAGCAGCACCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCTGCCGAA
   V T H Q G L S S P V T K S F N R G E C *
676 GTACCCCATCAGGGCTTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTAG

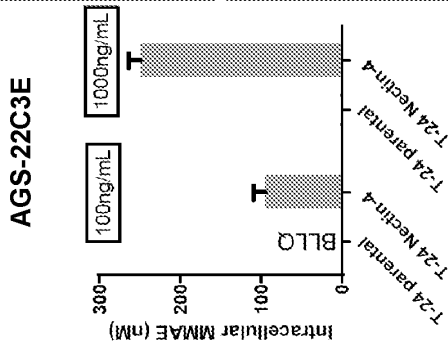
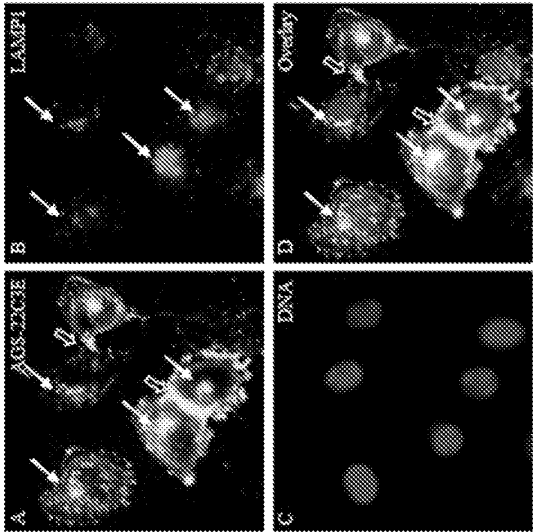
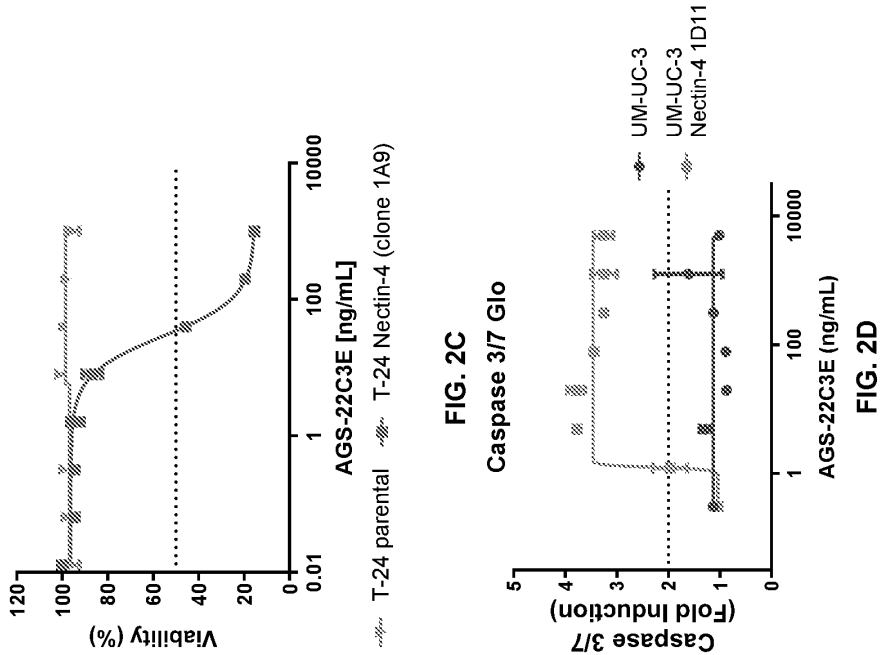
```

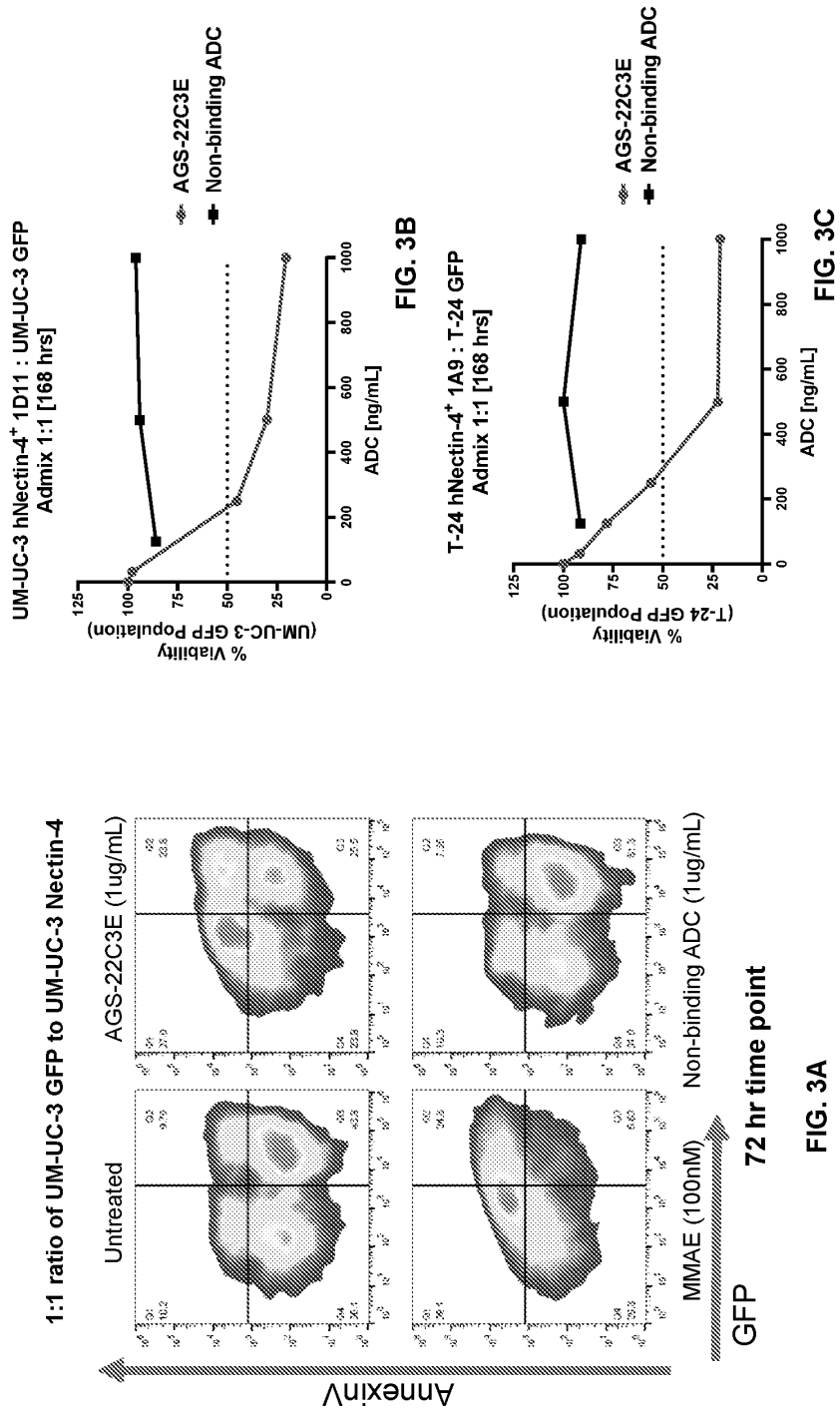
**FIG. 1D: The amino acid sequence (SEQ ID NO:7) of Ha22-2(2,4)6.1 heavy chain. Double-underlined is the leader sequence, underlined is the heavy chain variable region, (SEQ ID NO:22, which is the sequence ranging from the 20th to the 136th amino acid of SEQ ID NO:7) and underlined with a dashed line is the human IgG1 constant region.**

```
1  MELGLCWVFLVAILEGVOCEVOLVESGGGLVQPGGSLRLSCAASGFTFSS  
51 YNMNVWRQAPGKGLEWVSYISSSSSTIYYADSVKGRFTISRDNAKNSLSL  
101 QMNSLRDEDTAVYYCARAYYGMDVWGQGTTVTVSSASTKGPSVFPLAPS  
151 SKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYS  
201 LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPA  
251 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG  
301 VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP  
351 IEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW  
401 ESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEA  
451 LHNHYTQKSLSLSPGK
```

**FIG. 1E: The amino acid sequence (SEQ ID NO:8) of Ha22-2(2,4)6.1 light chain. Double-underlined is the leader sequence, underlined is the light chain variable region (SEQ ID NO:23, which is the sequence ranging from the 23rd to the 130th amino acid of SEQ ID NO:8), and underlined with a dashed line is the human kappa constant region.**

```
1  MDMRVPAQLLGLLLLWFPGSRCDIQMTQSPSSVSASVGDRVTITCRASQG  
51 ISGWLAWYQQKPGKAPKFLIYAASTLQSGVPSRFSGSGSGTDFTLTISL  
101 QPEDFATYYCQQANSFPPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSG  
151 TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSST  
201 LTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC
```





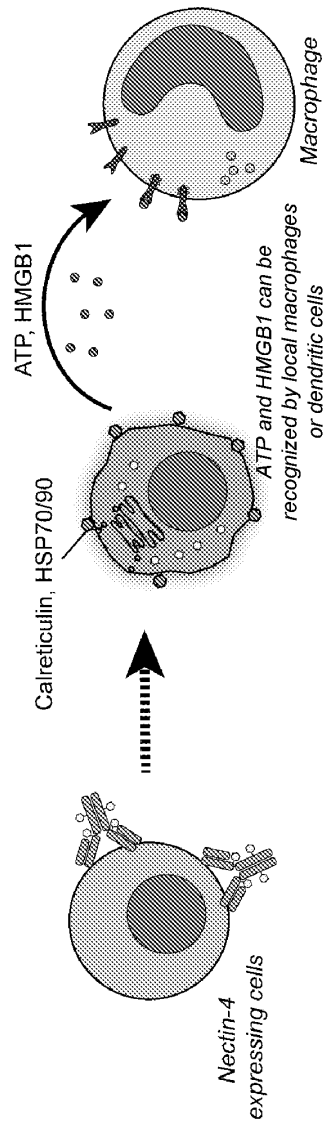


FIG. 4A

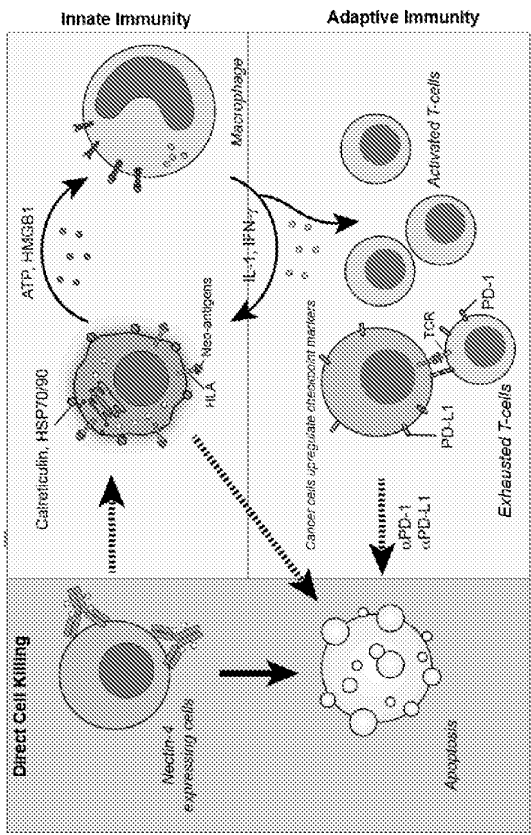
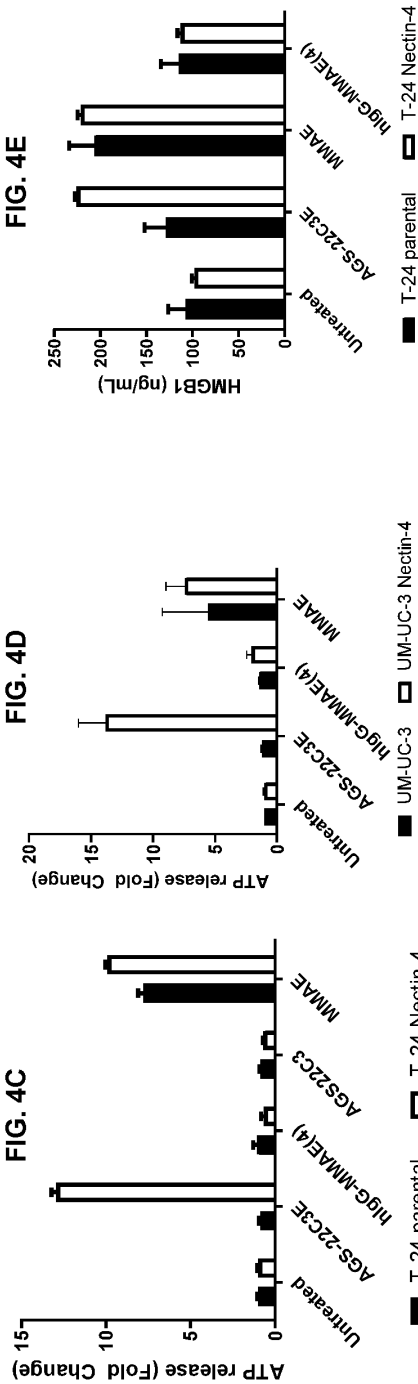
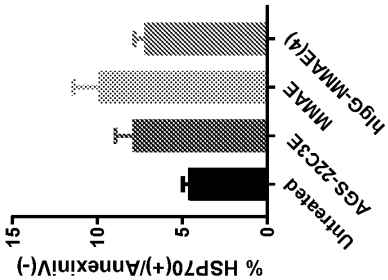


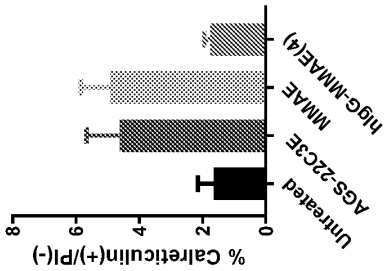
FIG. 4B



Cell Surface HSP70



Cell Surface Calreticulin



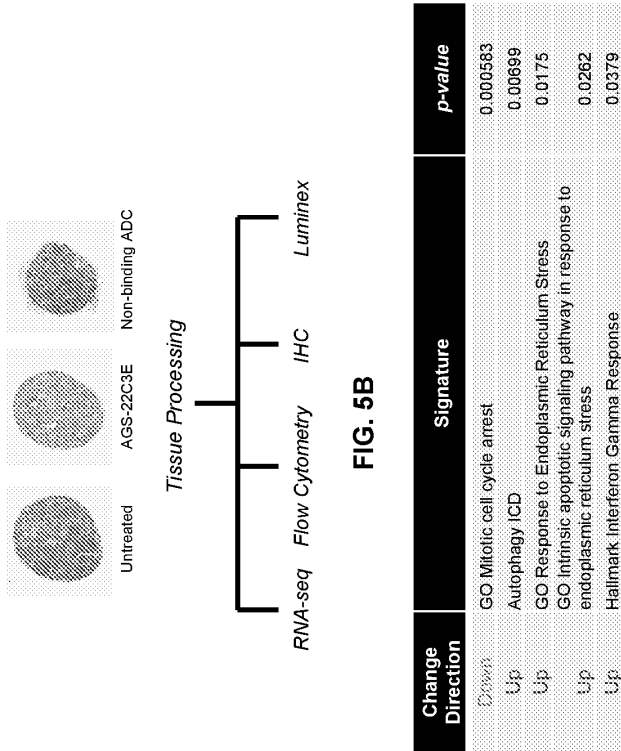


FIG. 5B

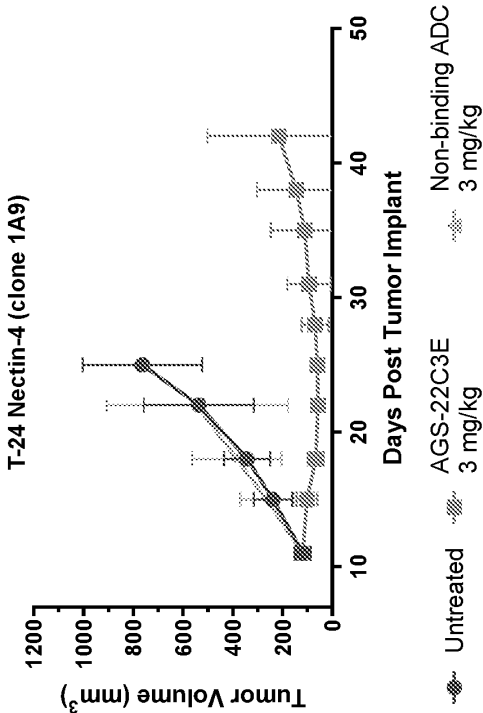


FIG. 5A

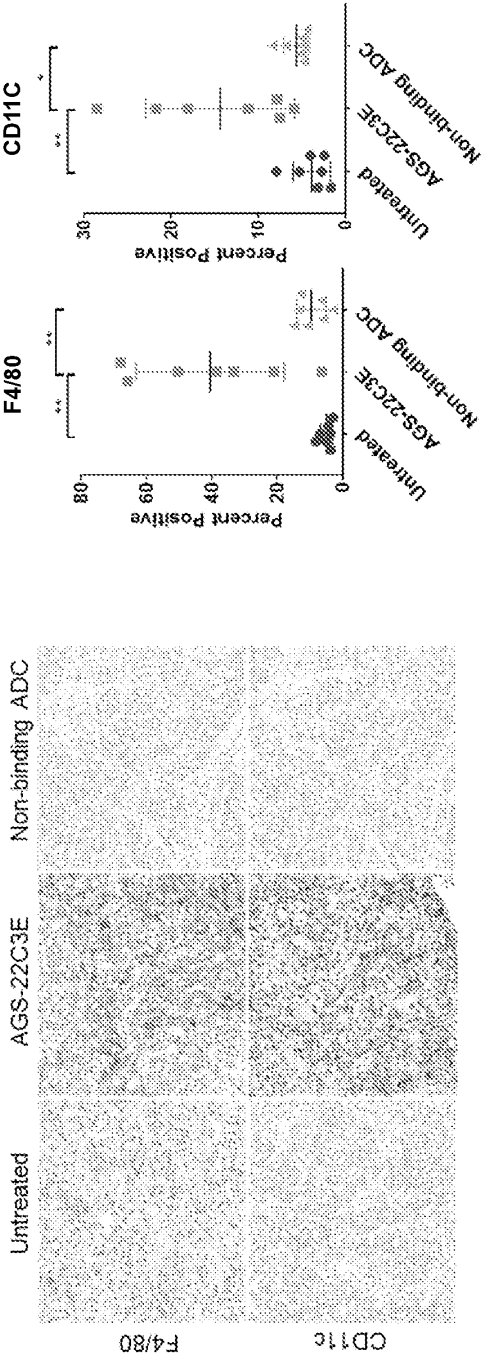
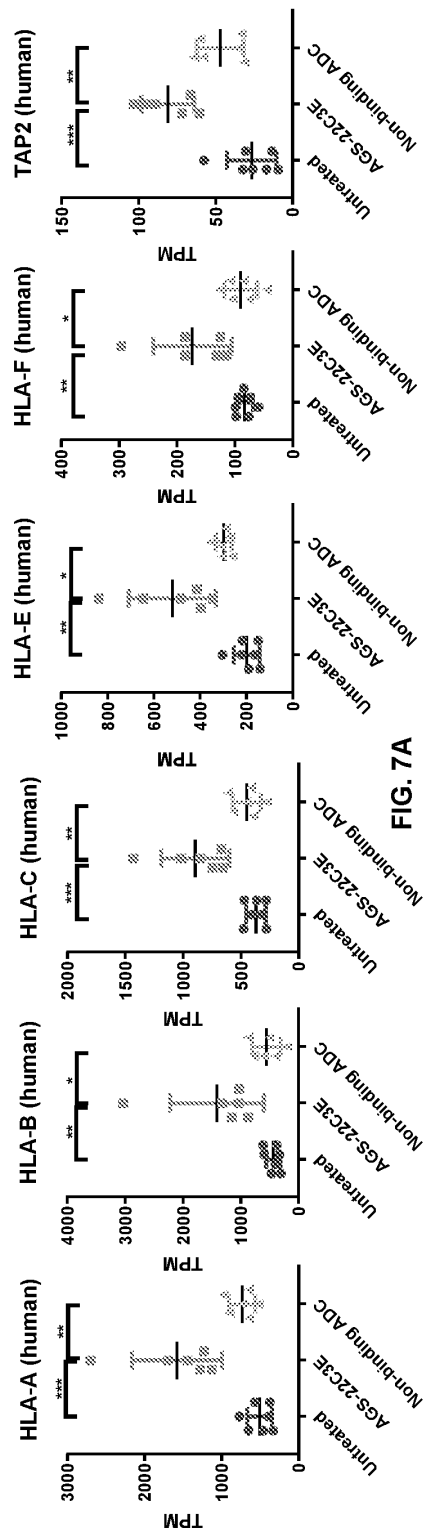


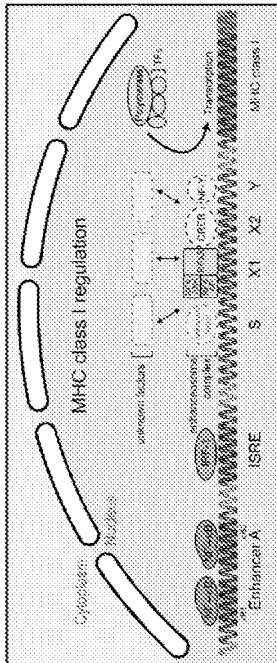
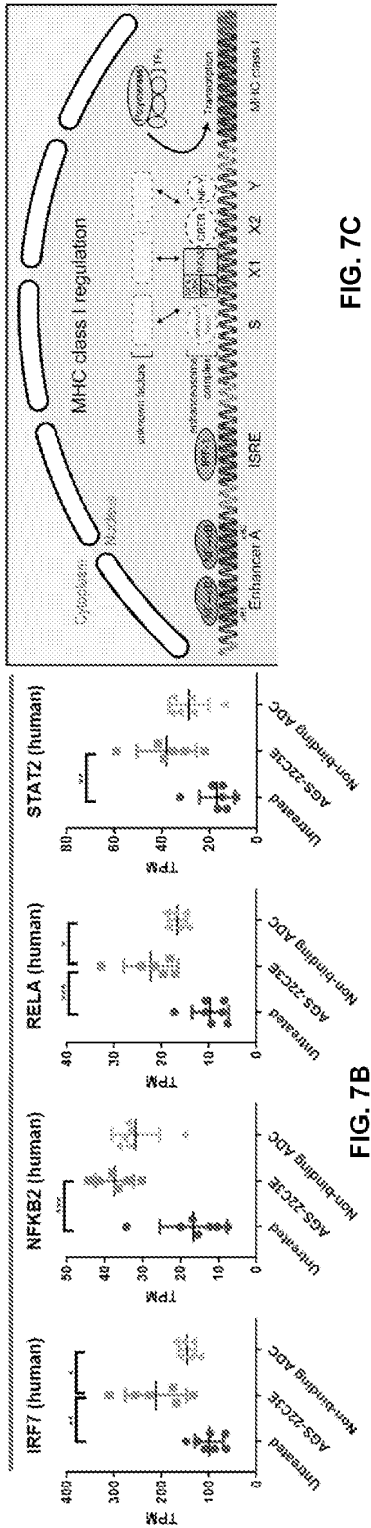
FIG. 6C

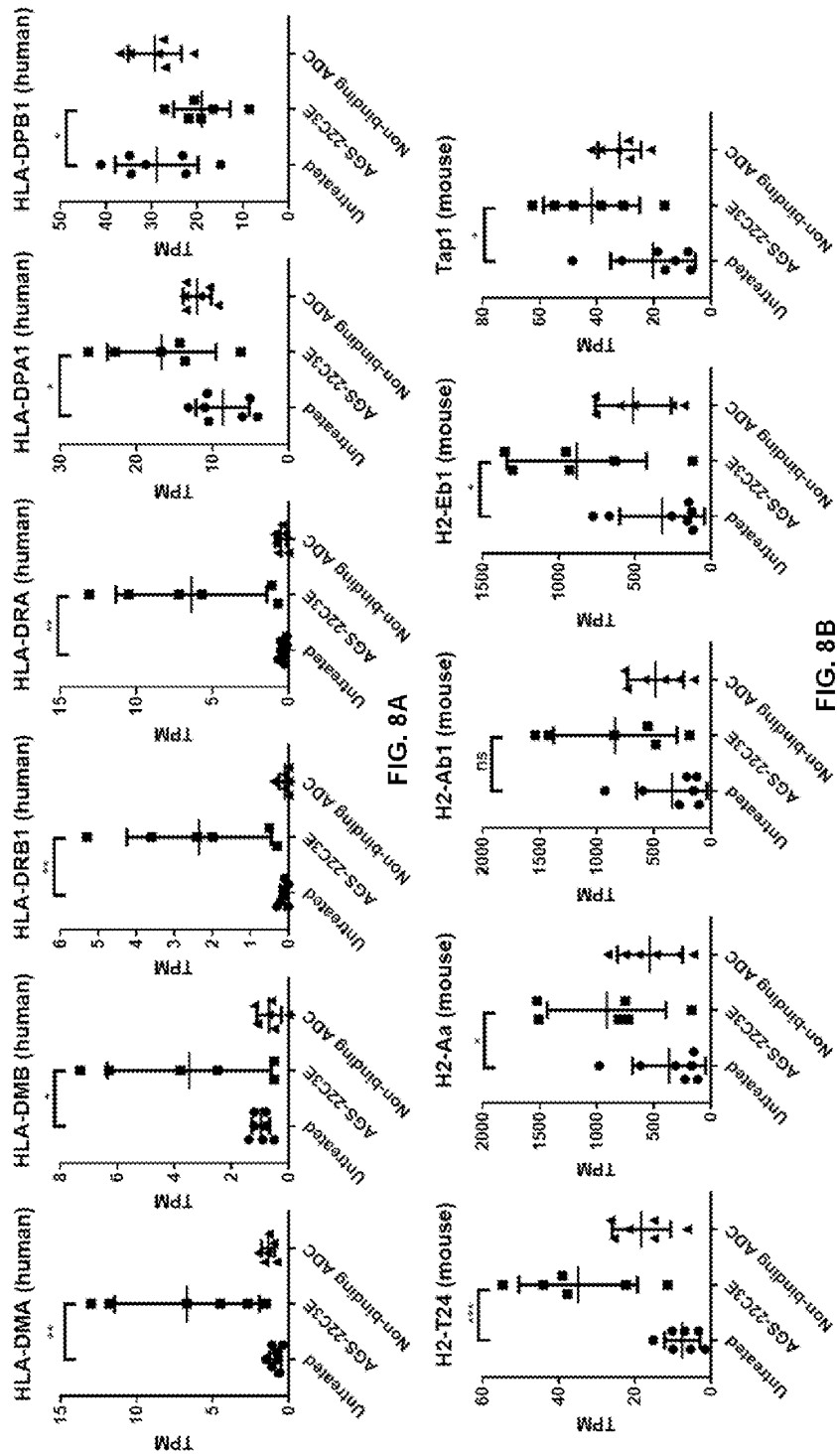
FIG. 6B

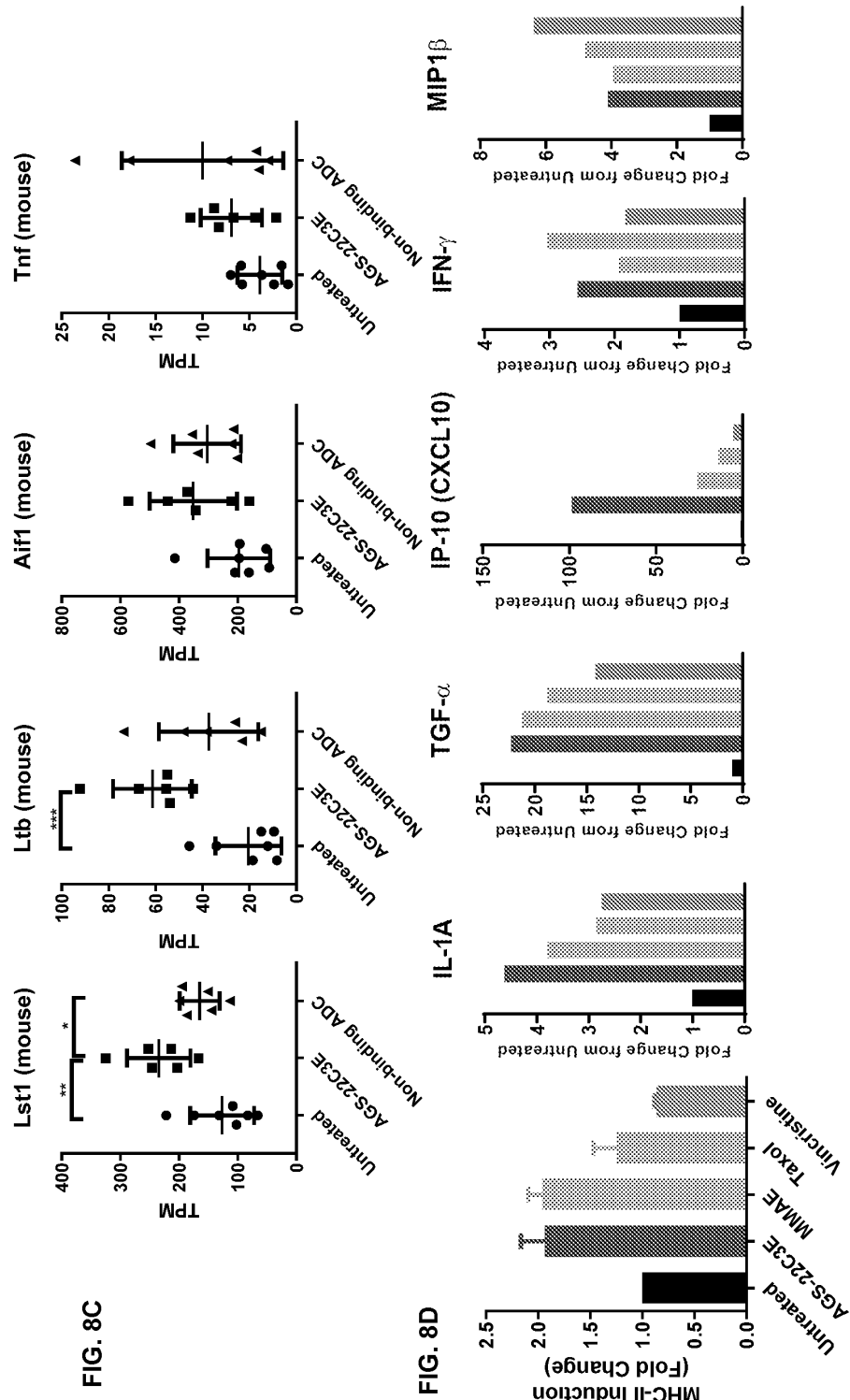
FIG. 6A



Interferon and Immune Activation Genes







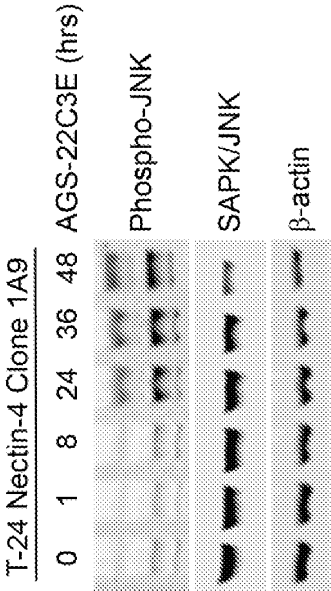


FIG. 9B

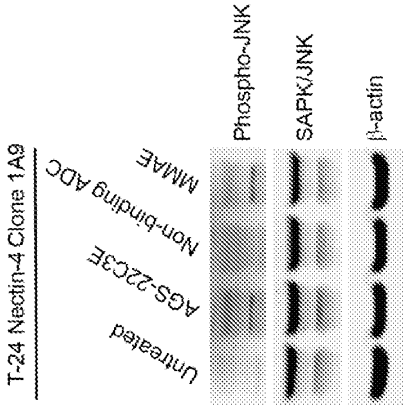


FIG. 9C

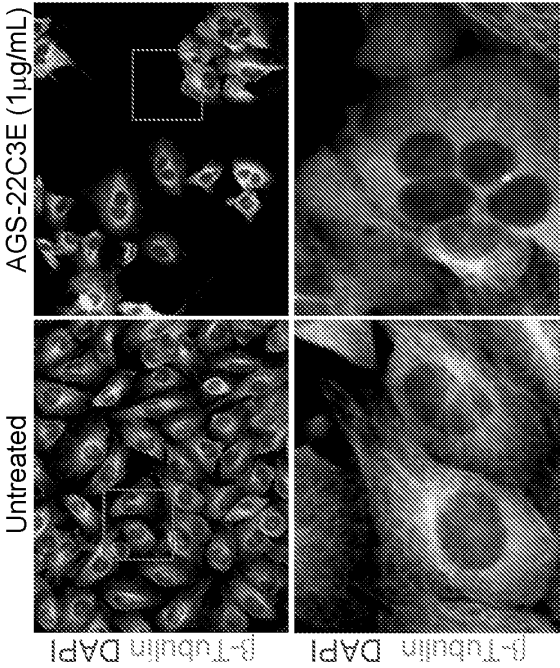


FIG. 9A

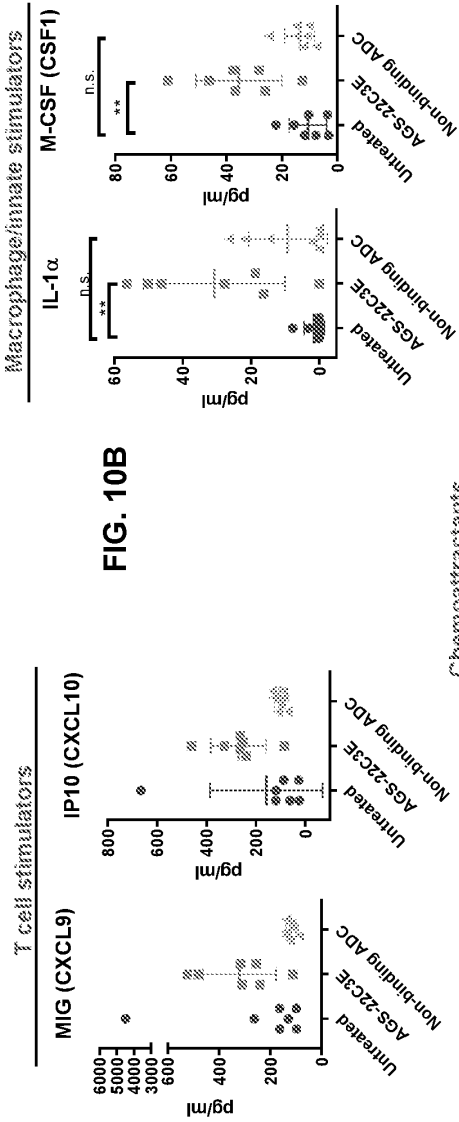
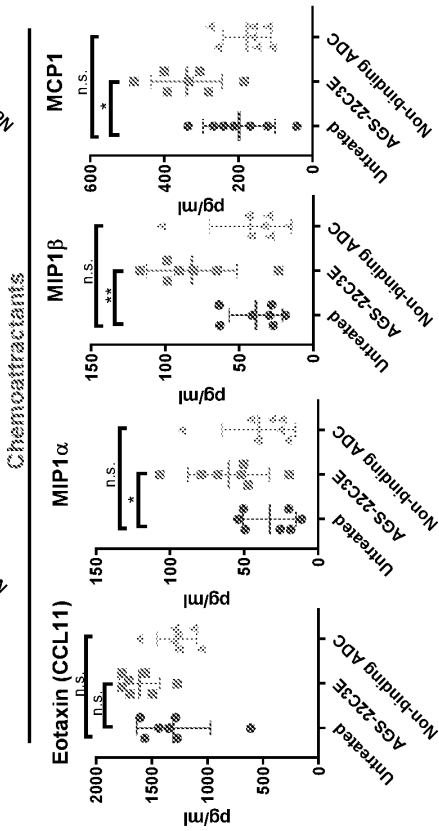


FIG. 10B



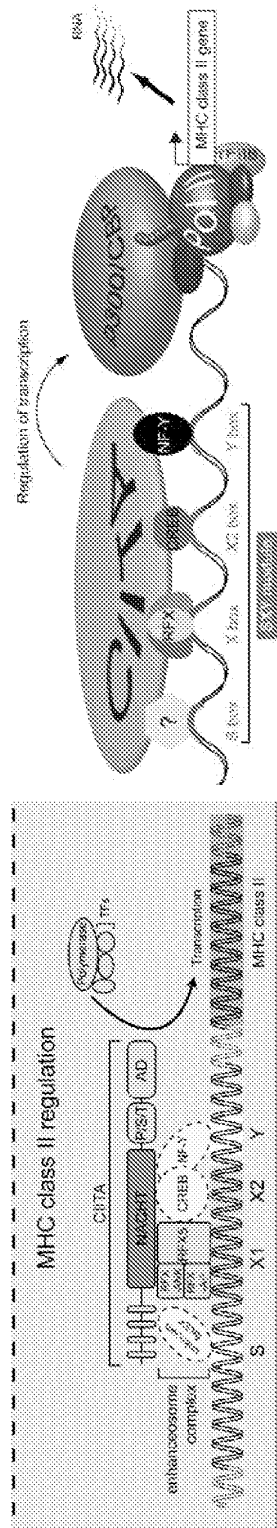
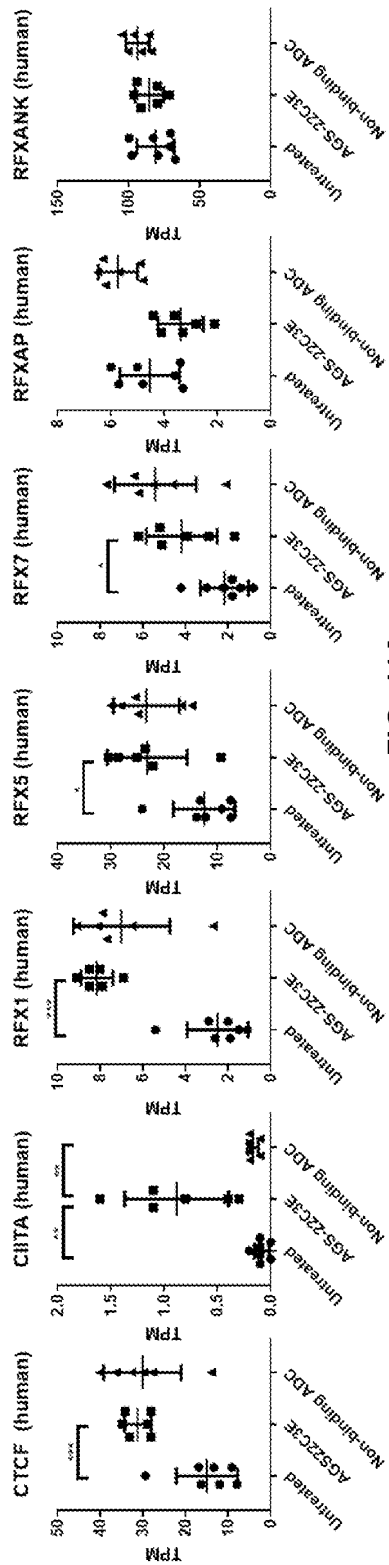
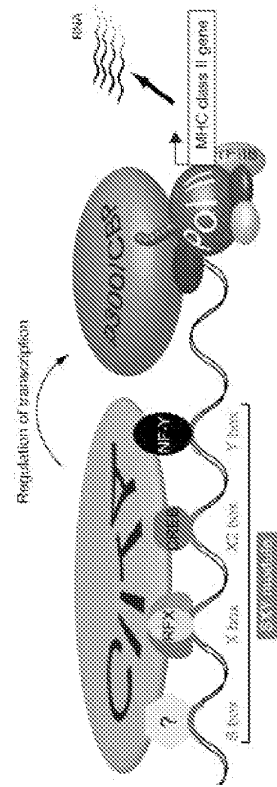


FIG. 11C



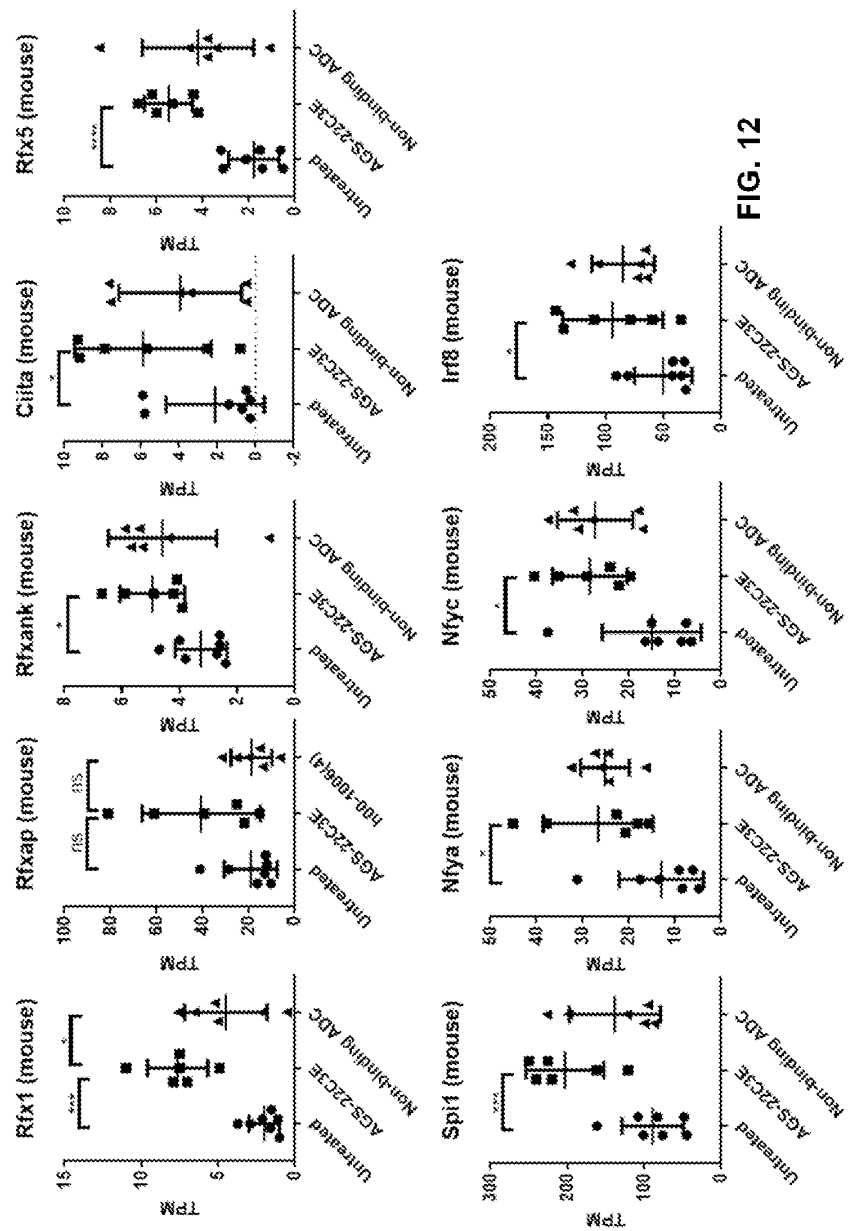


FIG. 12

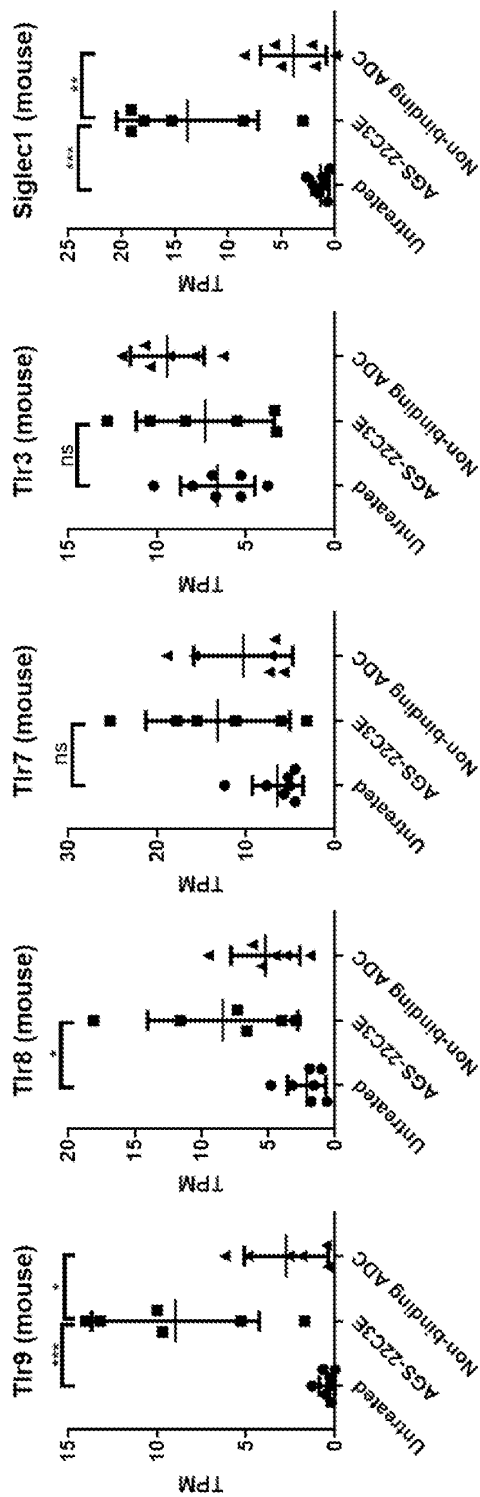


FIG. 13

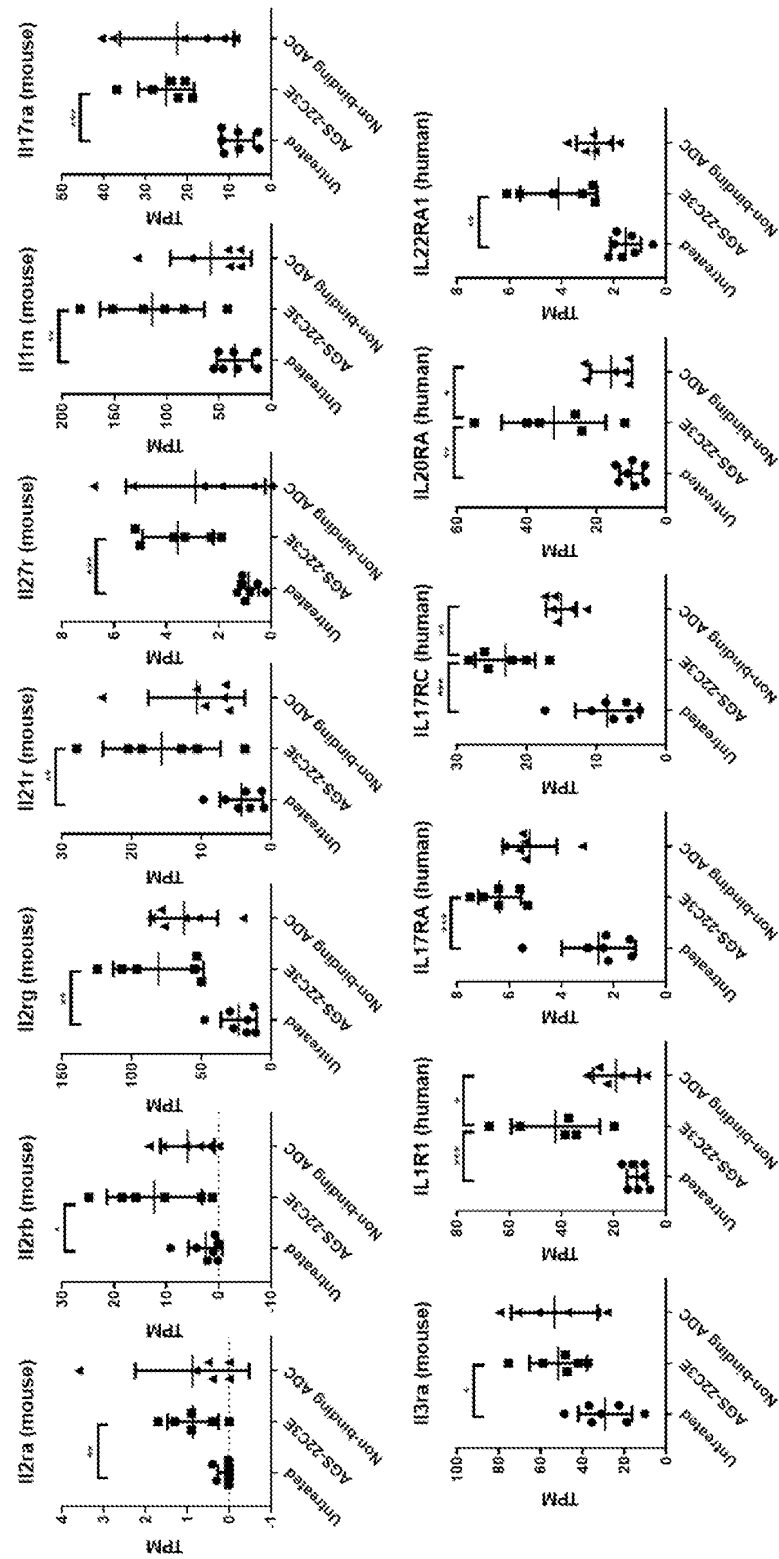


FIG. 14

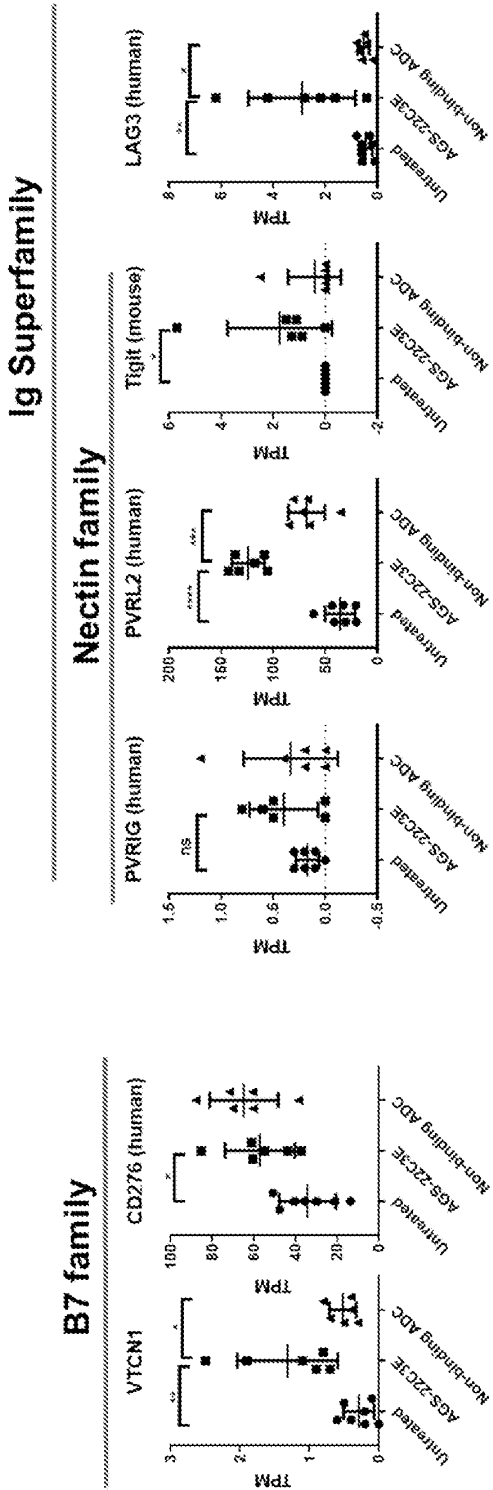
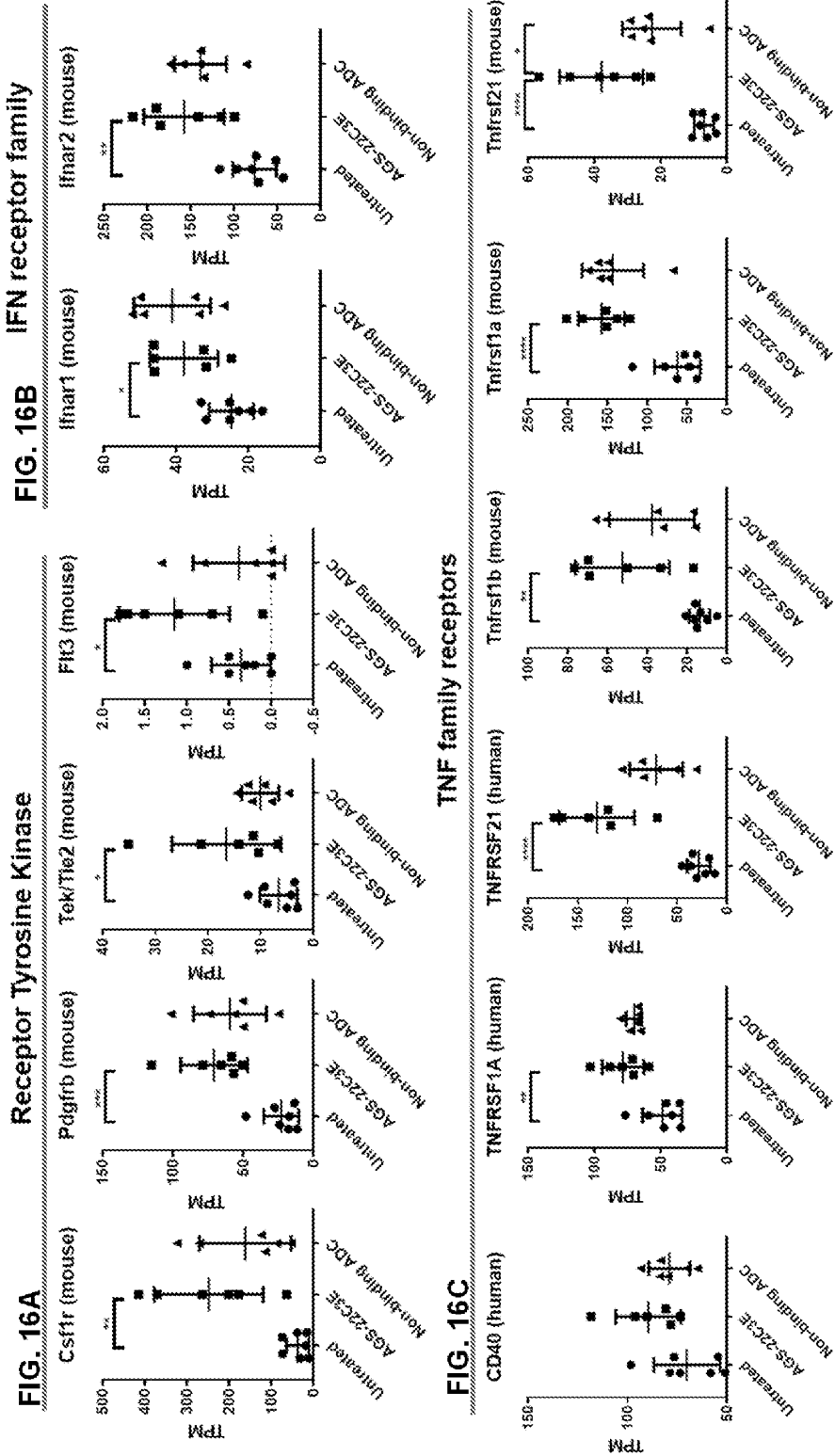


FIG. 15B

FIG. 15A



Inhibitory Immunoreceptors

FIG. 17A

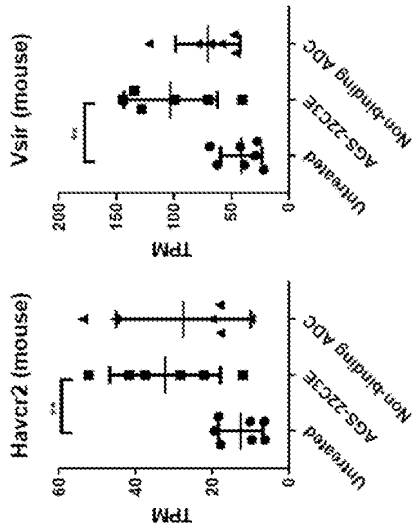
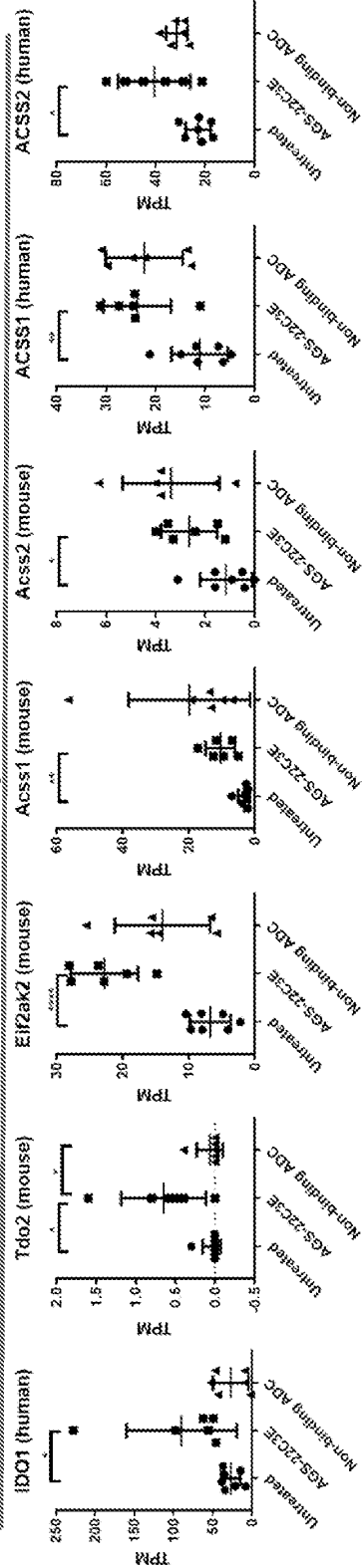


FIG. 17B

Metabolic Enzymes



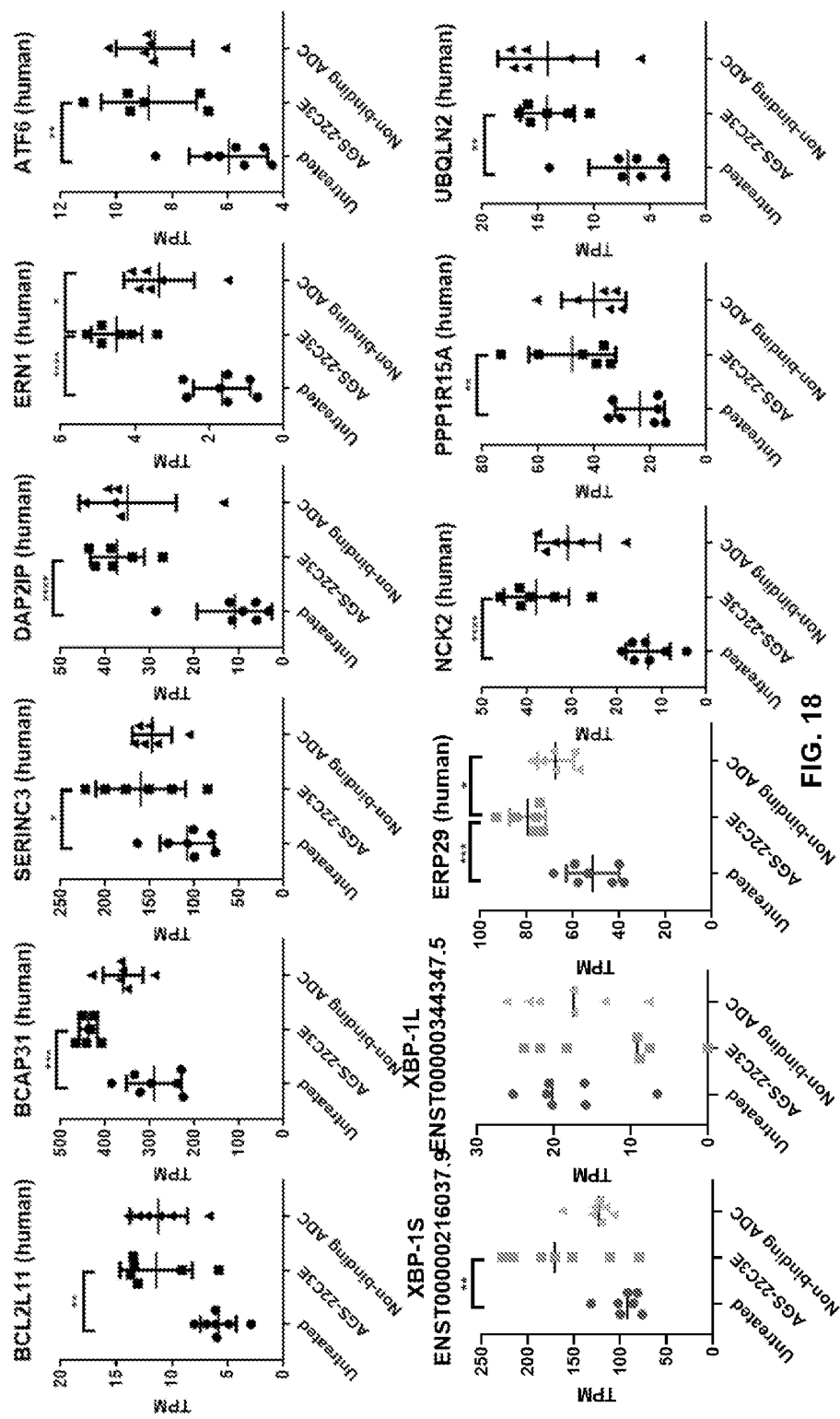


FIG. 18

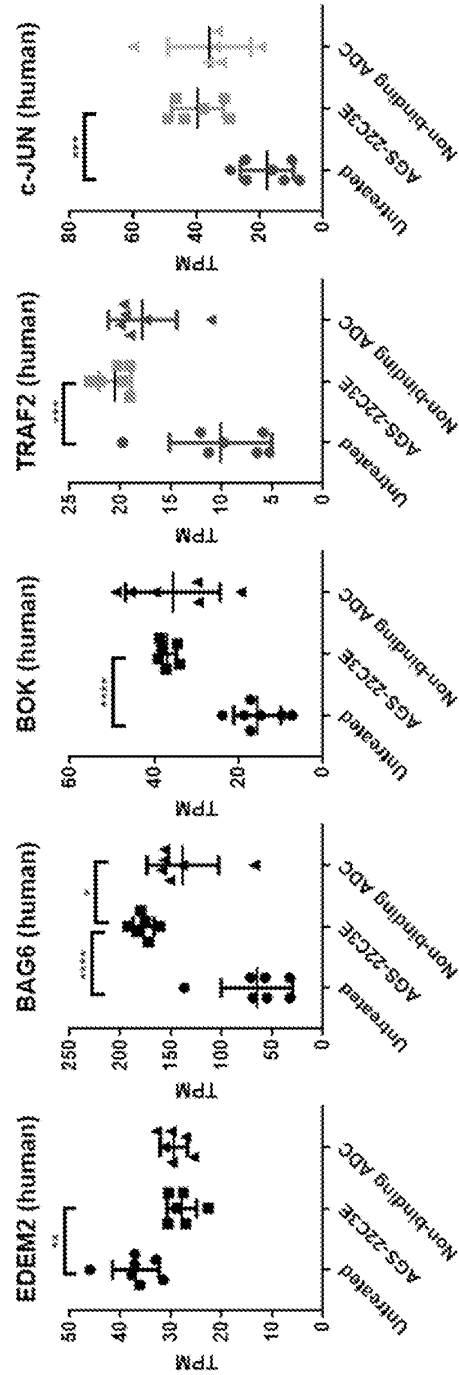
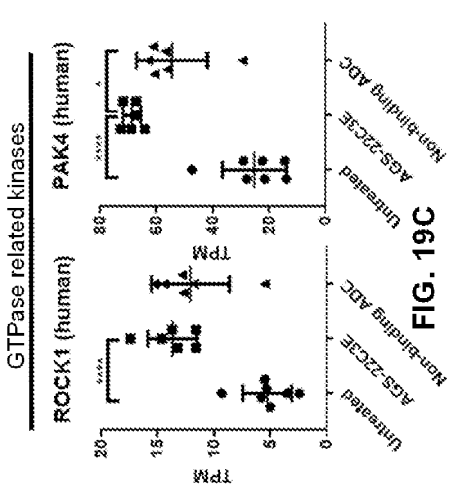
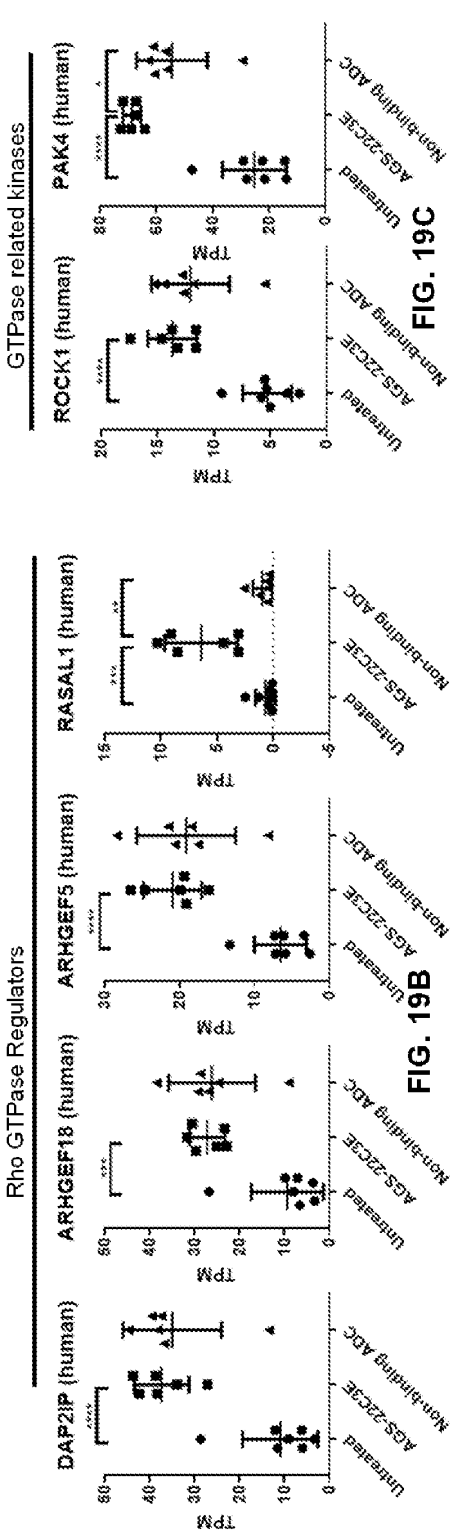
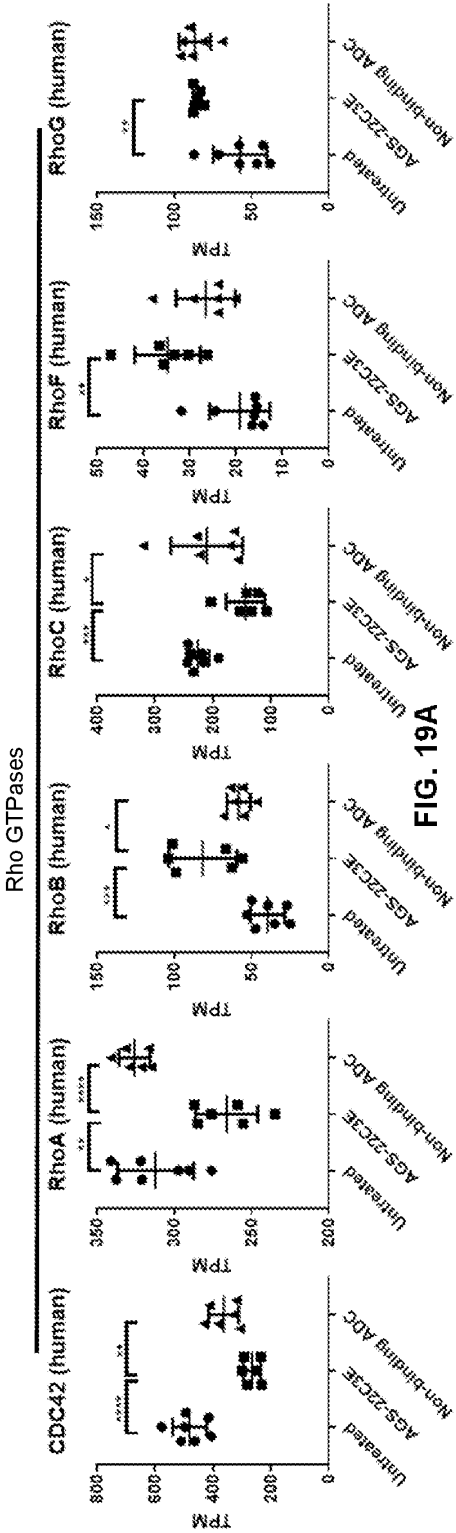


FIG. 18 (Continued)



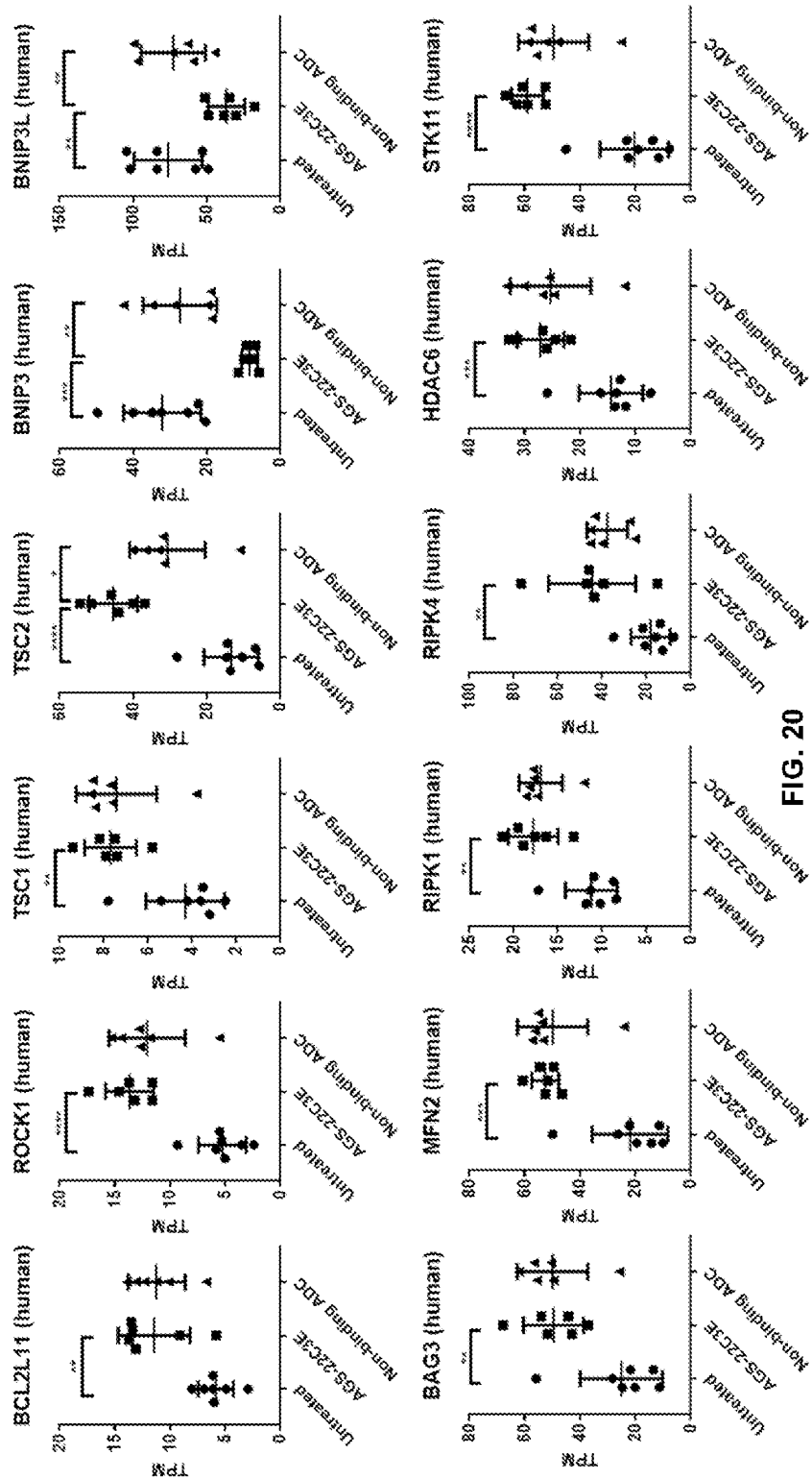


FIG. 20

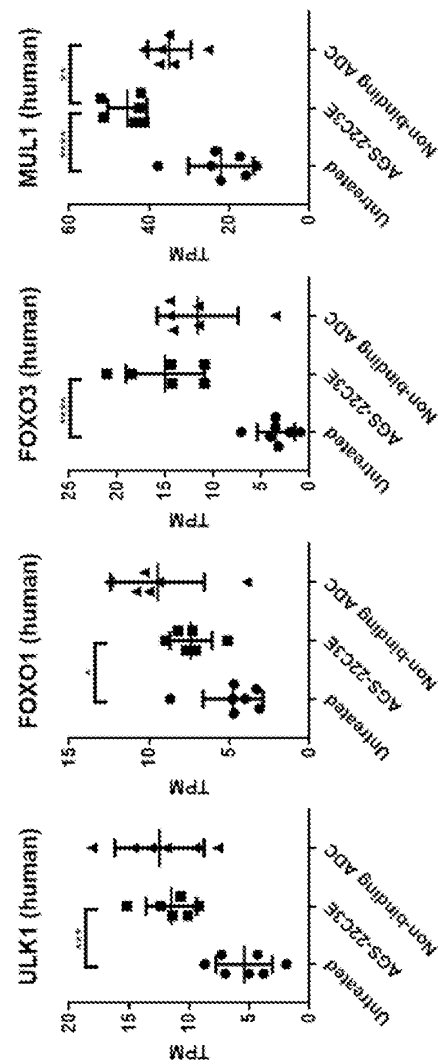
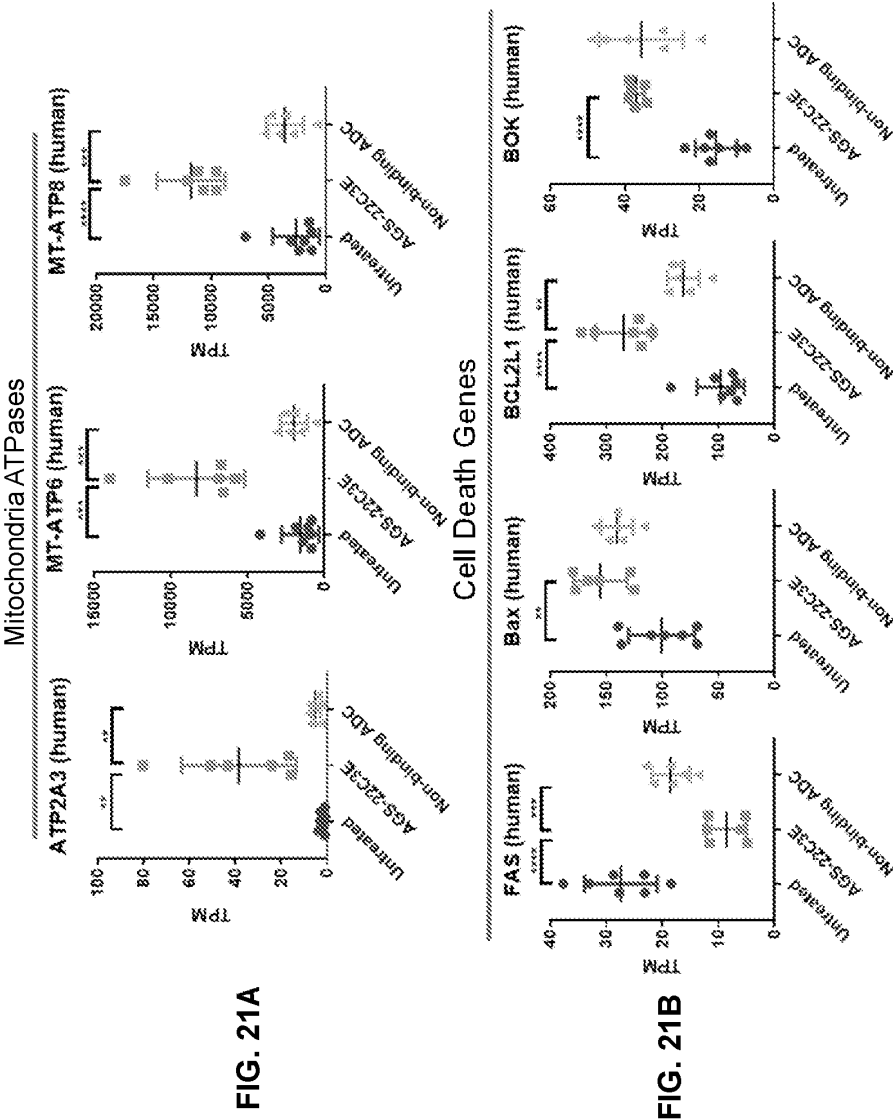


FIG. 20 (Continued)



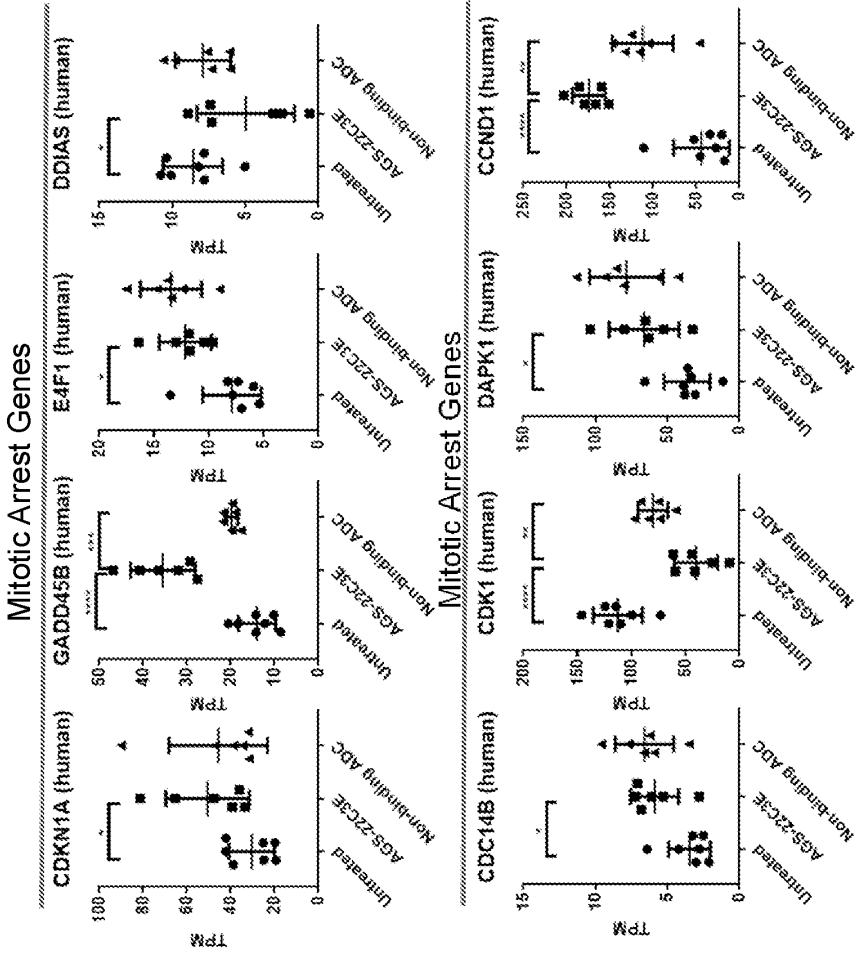
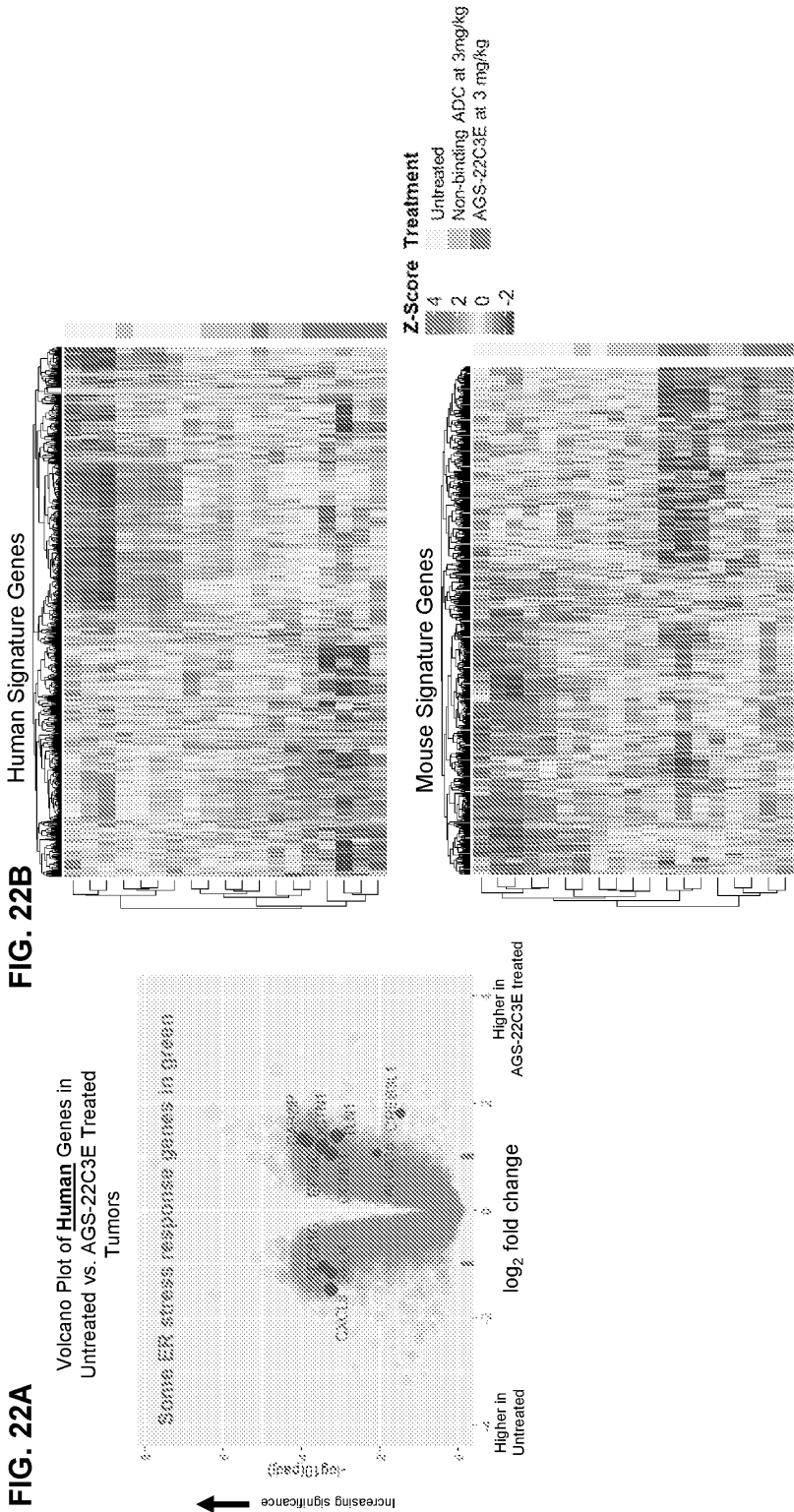


FIG. 21C



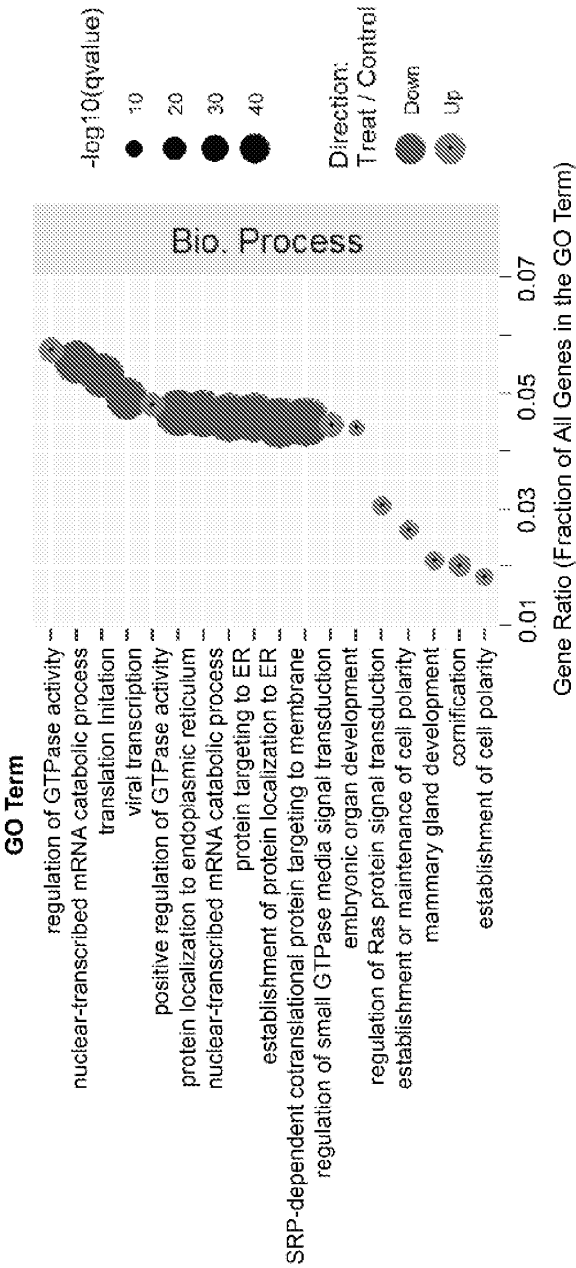


FIG. 22C