

FIG. 1

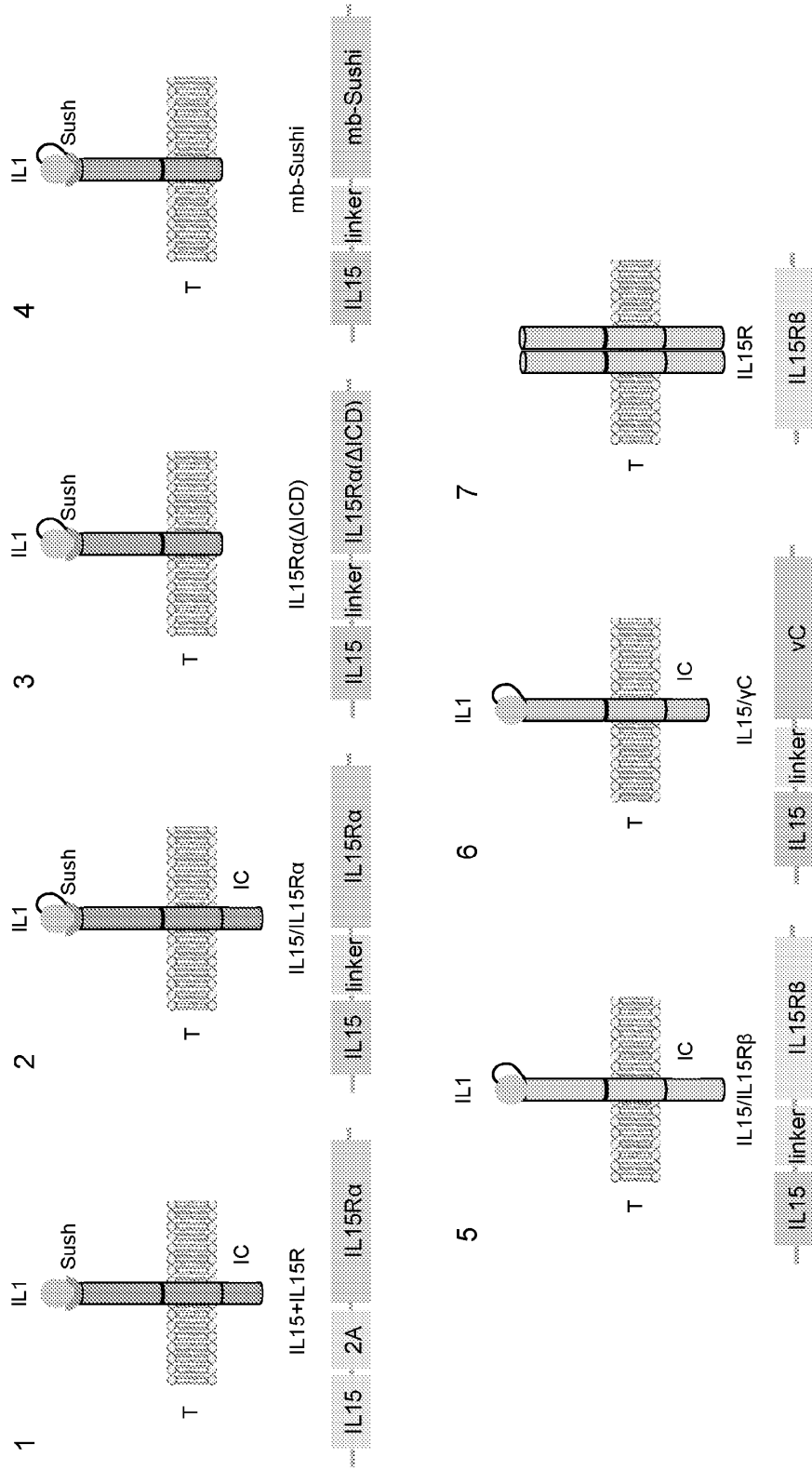


FIG. 2A

CD38	LHA		Transgene 1		RHA	CD38
------	-----	--	-------------	--	-----	------

FIG. 2B

CD38	LHA		Promoter	Transgene 1		RHA	CD38
------	-----	--	----------	-------------	--	-----	------

FIG. 2C

CD38	LHA		Transgene 1	2A	Transgene 2		RHA	CD38
------	-----	--	-------------	----	-------------	--	-----	------

FIG. 2D

CD38	LHA		Promoter		Transgene 1	2A	Transgene 2		RHA	CD38
------	-----	--	----------	--	-------------	----	-------------	--	-----	------

LHA/CD38-insol-CAG-IL15RF(tr)-P2A-hnCD16-TKpA-insol-RHA/CD38:

CAGAGGGCATTGTGTGCACACACGTATAGAAGCAGGCAGCCACCCCTCATGCTTTCCAGG SEQ ID NO: 22

AAGCAAATGTGGCTCAGGTGTAAAGTGCCCGGTTGATGAAGGGAGTTAGCGGAGGGAGTA

TAAGGATGTACTGTCTGCCCCCTTAGGACACCTGCAGAGGATTAAGGTGGCTGTTTCTCC

CTGGAGGTGGAGTGGGTGGGTCACTGCACAGGAGCCTATAGTTGTTGGTCTTTTAACTC

TTATTGGTGTAACCAGCCACGGAACCTCTGAGGCAAGGGGTTGGGGGTGGGAAGGGAAACA

GAGAAAAGGCAAGTGAACAGAAGGGGAGGTGCAGTTTCAGAACCAGCCAGCCTCTCTC

TTGCTGCCTAGCCTCCTGCCGGCCTCATCTTCGCCAGCCAACCCCGCCTGGAGCCCTAT

GGCCAACTGCAGTTTCAGCCCGGTGTCCGGGGACAAACCCTGCTGCCGGCTCTCTAGGAG

AGCCCAACTCTGTCTTGCGCTCAGTATCCTGGTCTGATCCTCGTCGTGGTGCTCGCGGT

GGTCGTCCCGAGGTGGCGCCAGCAGTGGAGCGGTCCGGGCACCAAGCGCTTTCCCGA

GTCAGCCTAAAGCTTTTTCCCGTATCCCCCAGGTGTCTGCAGGCTCAAAGAGCAGCGA SEQ ID NO: 23GAAGCGTTCAGAGGAAAGCGATCCCGTGCCACCTTCCCGTGCCCGGGCTGTCCCGCACGCTGCCGGCTCGGGGATGCGGGGGGAGCGCCGGACCGGAGCGGAGCCCCGGGCGGCTCGCTGCTGCCCCCTAGCGGGGAGGGACGTAATTACATCCCTGGGGGCTTTGGGGGGGGCTGTCCCGTGAGCTCATCGATACTAGTGACAGTTAATGATGTTGACATTGATTATTGACT SEQ ID NO: 24

AGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCGCG

GTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTG

ACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAA

TGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCA

AGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCAGTAC

ATGACCTTATGGGACTTTCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACC

ATGGTCGAGGTGAGCCCCACGTTCTGCTTCACTCTCCCCATCTCCCCCCCCTCCCCACCC

CCAATTTTGTATTTATTTATTTTAAATTATTTTGTGCAGCGATGGGGGCGGGGGGGGG

GGGGGGCGCGGCCAGGCGGGGCGGGGCGGGGCGAGGGGCGGGGCGGGGCGAGGCGGAGA

GGTGCGGCGGCAGCCAATCAGAGCGGCGCGCTCCGAAAGTTTCCTTTATGGCGAGGCGG

CGGCGGCGGCGGCCCTATAAAAGCGAAGCGCGCGGGGCGGGGAGTCGCTGCGACGCT

GCCTTCGCCCCGTGCCCGCTCCGCCCGCCTCGCGCGCCCGCCCCGGCTCTGACTGA

FIG. 3

4/25

CCGCGTTACTCCACAGGTGAGCGGGCGGGACGGCCCTTCTCCTCCGGGCTGAATTAGC
GCTTGGTTTAATGACGGCTTGTTCTTTCTGTGGCTGCGTGAAAGCCTTGAGGGGCTCC
GGGAGGGCCCTTTGTGCGGGGGAGCGGCTCGGGGGTGCGTGCGTGTGTGTGCGTGG
GGAGCGCCGCGTGCGGCTCCGCGCTGCCGCGGCTGTGAGCGCTGCGGGCGCGGCGCGG
GGCTTTGTGCGCTCCGAGTGTGCGCGAGGGGAGCGCGGCCGGGGCGGTGCCCCGCGGT
GCGGGGGGGGCTGCGAGGGGAACAAAGGCTGCGTGCGGGGTGTGTGCGTGGGGGGGTGAG
CAGGGGGTGTGGGCGCGTCGGTCGGGCTGCAACCCCCCTGCACCCCCCTCCCCGAGTTG
CTGAGCACGGCCCCGGCTTCGGGTGCGGGGCTCCGTACGGGGCGTGCGCGGGGCTCGCCG
TGCCGGGCGGGGGGTGGCGGCAGGTGGGGGTGCCGGGCGGGGCGGGGCCCTCGGGCCG
GGGAGGGCTCGGGGGAGGGGCGCGCGGCCCGGAGCGCCGGCGGCTGTGAGGCGCGG
CGAGCCGAGCCATTGCCTTTTATGGTAATCGTGCGAGAGGGCGCAGGGACTTCCTTTGT
CCCAAATCTGTGCGGAGCCGAAATCTGGGAGGCGCCGCGCACCCCCCTAGCGGGCGCG
GGGCGAAGCGGTGCGGCGCGGCGAGGAAGGAAATGGGCGGGGAGGGCCTTCGTGCGTCGC
CGCGCCGCGTCCCCTTCTCCCTCTCCAGCCTCGGGGCTGTCCGCGGGGGGACGGTGCC
TTCGGGGGGGACGGGGCAGGGCGGGGTTGCGCTTCTGGCGTGTGACCGGCGGCTCTAGAG
CCTCTGCTAACCATGTTTCATGCCTTCTTCTTTTCTACAGCTCCTGGGCAACGTGCTGG
TTATTGTGCTGTCTCATCATTTTGGCAAAGAATTGCTAGCGCCACCATGGACTGGACCTG SEQ ID NO: 25
GATTCTGTTCTGCTGCGGCTGCAACGCGAGTCCATAGCGGTATCCATGTTTTATTCT
TGGGTGTTTTTCTGCTGGGCTGCCTAAGACCGAGGCCAACTGGGTAAATGTCATCAGTGA
CCTCAAGAAAAATAGAAGACCTTATACAAAGCATGCACATTGATGCTACTCTCTACACTGA
GTCAGATGTACATCCCTCATGCAAAGTGACGGCCATGAAATGTTTCTCCTCGAACTTCA
AGTCATATCTCTGAAAAGTGCGGACGCGTCCATCCACGACACGGTCGAAAACCTGATAAT
ACTCGCTAATAATAGTCTCTTTCAAATGGTAACGTAACCGAGTCAGGTTGCAAAGAGTG
CGAAGAGTTGGAAGAAAAAACATAAAGGAGTTCCTGCAAAGTTTCGTGCACATTGTGCA
GATGTTCATTAATACCTCTAGCGGCGGAGGATCAGGTGGCGGTGGAAGCGGAGGTGGAGG
CTCCGGTGGAGGAGGTAGTGGCGGAGGTTCTTTCAAATAACTTGTCTCCACCGATGTC
CGTAGAACATGCGGATATTTGGGTAAATCCTATAGCTTGTACAGCCGAGAGCGGTATAT

FIG. 3 con't.

5/25

CTGCAACAGCGGCTTCAAGCGGAAGGCCGGCACAAAGCAGCCTGACCGAGTGCGTGCTGAA
CAAGGCCACCAACGTGGCCCACTGGACCACCCCTAGCCTGAAGTGCATCAGAGATCCCGC
CCTGGTGCATCAGCGGCTGCCCTCCAAGCACAGTGACAACAGCTGGCGTGACCCCCA
GCCTGAGAGCCTGAGCCCTTCTGGAAAAGAGCCTGCCGCCAGCAGCCCCAGCAGCAACAA
TACTGCCGCCACCACAGCGCCATCGTGCTGGATCTCAGCTGATGCCCAGCAAGAGCCC
TAGCACCGGCACCACCGAGATCAGCAGCCACGAGTCTAGCCACGGCACCCCATCTCAGAC
CACCGCCAAGAACTGGGAGCTGACAGCCAGCGCCTCTACCAGCCTCCAGGCGTGATCCC
TCAGGGCCACAGCGATACCACAGTGCCCATCAGCACCTCCACCGTGCTGCTGTGTGGACT
GAGCGCCGTGTCACTGCTGGCCTGCTACCTGAAGTCCAGACAGGGATCCGGAGCTACTAA SEQ ID NO: 26
CTTCAGCCTGCTGAAGCAGGCTGGAGACGTGGAGGAGAACCCTGGACCTATGTGGCAGCT SEQ ID NO: 27
GCTGCTGCCTACAGCTCTCCTGCTGCTGGTGTCCGCCGGCATGAGAACCGAGGATCTGCC
TAAGGCCGTGGTGTTCTTGGAACCCAGTGGTACAGAGTGCTGGAAAAGGACAGCGTGAC
CCTGAAGTGCCAGGGCGCCTACAGCCCTGAGGACAATTCCACACAGTGTTTTCACAATGA
GAGCCTCATCTCAAGCCAGGCCTCGAGCTACTTCATCGACGCCGCCACCGTGGACGACAG
CGGCGAGTATAGATGCCAGACCAACCTGAGCACCTGAGCGACCCCGTGACGCTGGAAGT
GCACATCGGATGGCTGCTGCTGTCAGGCCCCAGATGGGTGTTCAAAGAAGAGGACCCCAT
CCACCTGAGATGCCACTCTTGGAAGAACACCGCCTGCACAAAGTGACCTACCTGCAGAA
CGGCAAGGGCAGAAAGTACTTCCACCACAACAGCGACTTCTACATCCCCAAGGCCACCCCT
GAAGGACTCCGGCTCCTACTTCTGCAGAGGCCTCGTGGGCAGCAAGAACGTGTCCAGCGA
GACAGTGAACATCACCATCACCCAGGGCCTGGCCGTGCCTACCATCAGCAGCTTTTTCCC
ACCCGGCTACCAGGTGTCCTTCTGCCTCGTGATGGTGCTGCTGTTCCCGTGGACACCGG
CCTGTACTTCAGCGTGAAAACAAACATCAGAAGCAGCACCCGGGACTGGAAGGACCACAA
GTTCAAGTGGCGGAAGGACCCCAAGGACAAGTGAACGCGTGGGGGAGGCTAACTGAAACA SEQ ID NO: 28
CGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAA
ACGCACGGGTGTTGGGTGCTTTGTTTCATAAACGCGGGTTTCGGTCCCAGGGCTGGCACTC
TGTCGATACCCACCGAGACCCCATTTGGGGCAATACGCCCCGCTTTCTTCCTTTTCCCC

FIG. 3 con't.

6/25

ACCCCACCCCCAAGTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGG
 CCCTGCCATAGCAGGTACCTCAGCCTAAAGCTTTTTCCCCGTATCCCCCAGGTGTCTGC SEQ ID NO: 23
 AGGCTCAAAGAGCAGCGAGAAGCGTTCAGAGGAAAGCGATCCCGTGCCACCTTCCCCGTG
 CCCGGGCTGTCCCGCACGCTGCCGGCTCGGGGATGCGGGGGAGCGCCGGACCGGAGCG
 GAGCCCCGGGCGGCTCGCTGCTGCCCCCTAGCGGGGAGGGACGTAATTACATCCCTGGG
 GGCTTTGGGGGGGGCTGTCCCCGTGAGCTCGATGCGTCAAGTAACTGAAATTCATCCT SEQ ID NO: 29
 GAGATGAGGTGGGTTGGCGACTAAGGCGCACCGGTGGGCACTGCGGGGACAGCAGGGCCC
 CGCGCGCAGGGAAGCCGCCCGGATCGCCGGAACCGGGCATCTTCCGTGGCGGGTCAGCC
 GAGAGCCCGCCGGTGGTGTGCTAGTAGGGAGTCCCGGGCTCGGGGCTCCGCGGGCCGCTT
 TCAGGAGCAGCTGGCCTTGGCACCGAGCGTGCCCGCGGGAGGCGGGGGGGGCGCTGCTC
 GGTGGCTCTGCTGCGTAGCCGGTGAACACTTGGCACCGATGCCCGCTTCTGGGCAAGGT
 GCCCTGAGCCAGCCCCTCGCCGGGCTGCAGCCACCCTCGGCGCGCTCAGCCCGCTTCA
 CCGCTTCAGGACGGAATAGAAGTGCAGATGCAGGGTGTGCTGACATTTTCAACTTTT
 TCTGCGGTTTCCGCCGCTGTCTCTGACCCGAAAGTGCCCCGGGACGGTTACAGAGGACA
 CTTAAGTGGTTTGCAAAGCCTGTGGTAGGGGAGGAGGGGTAGAAAGGGCCAAACACGGA
 ACTTAGTTTTATTCAATTTATATAAAGCAGCA

- **LHA/CD38**: can have variable length and sequence depending on the targeting site; exemplary sequence--SEQ ID NO: 22
- **insol**: not required, sequence can vary; exemplary sequence-- SEQ ID NO: 23
- **CAG**: can be any exogenous promoters; exemplary sequence-- SEQ ID NO: 24
- **IL15RF(tr)-P2A-hnCD16**: can be any transgenes
- **IL15RF(tr)**: can be any versions of IL15/R fusion protein; exemplary sequence--SEQ ID NO: 25
- **P2A**: can be any 2A variants; exemplary sequence-- SEQ ID NO: 26
- **hnCD16**: can be any Fc receptors; exemplary sequence-- SEQ ID NO: 27
- **TKpA**: can be any poly A signals; exemplary sequence-- SEQ ID NO: 28
- **insol**: not required, sequence can vary; exemplary sequence-- SEQ ID NO: 23
- **RHA/CD38**: can have variable length and sequence depending on the targeting site exemplary sequence-- SEQ ID NO: 29

FIG. 3 con't.

LHA/CD38-T2A-IL15RF(tr)-P2A-hnCD16-TKpA-RHA/CD38:

AGAGGGCATTGTGTGCACACACGTATAGAAGCAGGCAGCCACCCCTCATGCTTTCCAGGA SEQ ID NO: 30

AGCAAATGTGGCTCAGGTGTAAAGTGCCCGTTGATGAAGGGAGTTAGCGGAGGGAGTAT

AAGGATGTACTGTCTGCCCCCTTAGGACACCTGCAGAGGATTAAGGTGGCTGTTTCTCCC

TGGAGGTGGAGTGGGTGGGTCACTGCACAGGAGCCTATAGTTGTTGGTCTTTTAACTCT

TATTGGTGTAACCAGCCACGGAACCTCTGAGGCAAGGGGTTGGGGTGGGAAGGGAACAG

AGAAAAGGCAAGTGAAACAGAAGGGGAGGTGCAGTTTCAGAACCCAGCCAGCCTCTCTCT

TGCTGCCTAGCCTCCTGCCGCTCATCTTCGCCAGCCAACCCGCTGGAGCCCTATG

GCCAACTGCGAGTTCAGCCCGGTGTCGGGGACAAACCCTGCTGCCGGCTCTCTAGGAGA

GCCAACTCTGTCTTGGCGTCAGTATCCTGGTCCTGATCCTCGTCGTGGTGCTCGCGGTG

GTCGTCCCGAGGTGGCGCCAGCAGTGGAGCGGTCCGGGCACCACCAAGCGCTTCCCGAG

GGCAGCGGAGAGGGCAGAGGAAGTCTTCTAACATGCGGTGACGTGGAGGAGAATCCCGGC SEQ ID NO: 31CCTATGGACTGGACCTGGATTCTGTTCTCTGGTCGCGGTGCAACGCGAGTCCATAGCGGT SEQ ID NO: 25

ATCCATGTTTTATTCTTGGGTGTTTTCTGCTGGGCTGCCTAAGACCGAGGCCAACTGG

GTAAATGTCATCAGTGACCTCAAGAAAATAGAAGACCTTATACAAAGCATGCACATTGAT

GCTACTCTCTACACTGAGTCAGATGTACATCCCTCATGCAAAGTGACGGCCATGAAATGT

TTCCTCCTCGAACTTCAAGTCATATCTCTGGAAGTGCGGACGCGTCCATCCACGACACG

GTCGAAAACCTGATAATACTCGCTAATAATAGTCTCTCTTCAAATGGTAACGTAACCGAG

TCAGGTTGCAAAGAGTGCGAAGAGTTGGAAGAAAAAACATAAAGGAGTTCCTGCAAAGT

TTCGTGCACATTGTGCAGATGTTCAATTAATACCTCTAGCGGCGGAGGATCAGGTGGCGGT

GGAAGCGGAGGTGGAGGCTCCGGTGGAGGAGGTAGTGGCGGAGGTTCTCTTCAAATAACT

TGTCCTCCACCGATGTCCGTAGAACATGCGGATATTTGGGTAAAATCCTATAGCTTGTAC

AGCCGAGAGCGGTATATCTGCAACAGCGGCTTCAAGCGGAAGGCCGGCACAAAGCAGCCTG

ACCGAGTGCGTGCTGAACAAGGCCACCAACGTGGCCCACTGGACCACCCCTAGCCTGAAG

TGCATCAGAGATCCCGCCCTGGTGATCAGCGGCTGCCCTCCAAGCACAGTGACAACA

GCTGGCGTGACCCCCAGCCTGAGAGCCTGAGCCCTTCTGGAAAAGAGCCTGCCGCCAGC

AGCCCCAGCAGCAACAATACTGCCGCCACCACAGCCGCATCGTGCCTGGATCTCAGCTG

FIG. 4

8/25

ATGCCCAGCAAGAGCCCTAGCACCGGCACCACCGAGATCAGCAGCCACGAGTCTAGCCAC
GGCACCCCATCTCAGACCACCGCCAAGAAGTGGGAGCTGACAGCCAGCGCCTCTCACCAG
CCTCCAGGCGTGTACCTCAGGGCCACAGCGATACCACAGTGGCCATCAGCACCTCCACC
GTGCTGCTGTGTGGACTGAGCGCCGTGTCACTGCTGGCCTGCTACCTGAAGTCCAGACAG
GGATCCGGAGCTACTAAGTTCAGCCTGCTGAAGCAGGCTGGAGACGTGGAGGAGAACCCT SEQ ID NO: 26
GGACCTATGTGGCAGCTGCTGCTGCCTACAGCTCTCCTGCTGCTGGTGTCCGCCGGCATG SEQ ID NO: 27
AGAACCAGGAGTCTGCCTAAGGCCGTGGTGTTCCTGGAACCCAGTGGTACAGAGTGTG
GAAAAGGACAGCGTGACCCTGAAGTCCAGGGCGCCTACAGCCCTGAGGACAATTCCACA
CAGTGGTTTTACAATGAGAGCCTCATCTCAAGCCAGGCCTCGAGCTACTTCATCGACGCC
GCCACCGTGGACGACAGCGGCGAGTATAGATGCCAGACCAACCTGAGCACCTGAGCGAC
CCCGTGCAGCTGGAAGTGCACATCGGATGGCTGCTGCTGCAGGCCCCAGATGGGTGTTC
AAAGAAGAGGACCCCATCCACCTGAGATGCCACTCTTGAAGAACACCGCCCTGCACAAA
GTGACCTACCTGCAGAACGGCAAGGGCAGAAAGTACTTCCACCACAACAGCGACTTCTAC
ATCCCCAAGGCCACCTGAAGGACTCCGGCTCCTACTTCTGCAGAGGCCTCGTGGGCAGC
AAGACGTGTCCAGCGAGACAGTGAACATCACCATACCCAGGGCCTGGCCGTGCCTACC
ATCAGCAGCTTTTTCCACCCGGCTACCAGGTGTCCTTCTGCCTCGTGATGGTGTGCTG
TTCGCCGTGGACACCGCCTGTACTTCAGCGTGAACAAACATCAGAAGCAGCACCCGG
GACTGGAAGGACCACAAGTTCAAGTGGCGGAAGGACCCCCAGGACAAGTGAACGCGTGGG SEQ ID NO: 28
GGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAA
TAAAAAGACAGAATAAAACGCACGGGTGTTGGGTCGTTTGTTCATAAACGCGGGTTCCG
TCCCAGGGCTGGCACTCTGTGATACCCACCGAGACCCATTGGGGCCAATACGCCCGC
GTTTCTTCTTTTCCCCACCCACCCCAAGTTTCGGGTGAAGGCCAGGGCTCGCAGCC
AACGTCGGGGCGGCAGGCCCTGCCATAGCAGGTACCGATGCGTCAAGTACACTGAAATTC SEQ ID NO: 32
ATCCTGAGATGAGGTGGTTGGCGACTAAGGCGCACCGGTGGGCACTGCGGGGACAGCAG
GGCCCCGCGCGAGGGAAGCCGCCCGGATCGCCGGAACCGGGCATCTTCCGTGGCGGGT
CAGCCGAGAGCCCGCGGGTGGTGTGAGTAGGGAGTCCCGGGCTCGGGGCTCCGCGGGC
CGCTTTCAGGAGCAGCTGGCCTTGGCACCGAGCGTGCCCGGGAGGCGGGGGGGGGCGC

FIG. 4 con't.

9/25

TGCTCGGTGGCTCTGCTGCGTAGCCGGTGAACACTTGGCACCGATGCCCGCCTTCTGGGC
AAGGTGCCCTGAGCCCAGCCCCTCGCCGGGCTGCAGCCCACCCTCGGCGCGCTCAGCCCG
CTTACCGCTTCAGGGACGGAATAGAACTCGCAGATGCAGGGTGTGCTGACATTTTCAA
CTTTTCTGCGGTTTCCGCCCCTGTCTCTGACCCGAAAGTGCCCCGGACGGTTACAGA
GGACACTTAAGTGGTTTGCAAAGCCTGTGGTAGGGGAGGAGGGGTAGAAGGGCCAAACC
ACGGAACTTAGTTTTATTCAATTATATAAAGCAGCA

- **LHA/CD38**: can have variable length and sequence depending on the targeting site; exemplary sequence--SEQ ID NO: 30
- **I2A**: can be any 2A variants; exemplary sequence-- SEQ ID NO: 31
- **IL15RF(tr)-P2A-hnCD16**: can be any transgenes
- **IL15RF(tr)**: can be any versions of IL15/R fusion protein; exemplary sequence-- SEQ ID NO: 25
- **P2A**: can be any 2A variants; exemplary sequence-- SEQ ID NO: 26
- **hnCD16**: can be any Fc receptors; exemplary sequence-- SEQ ID NO: 27
- **TKpA**: can be any poly A signals; exemplary sequence-- SEQ ID NO: 28
- **RHA/CD38**: can have variable length and sequence depending on the targeting site; exemplary sequence-- SEQ ID NO: 32

FIG. 4 con't.

FIG. 5

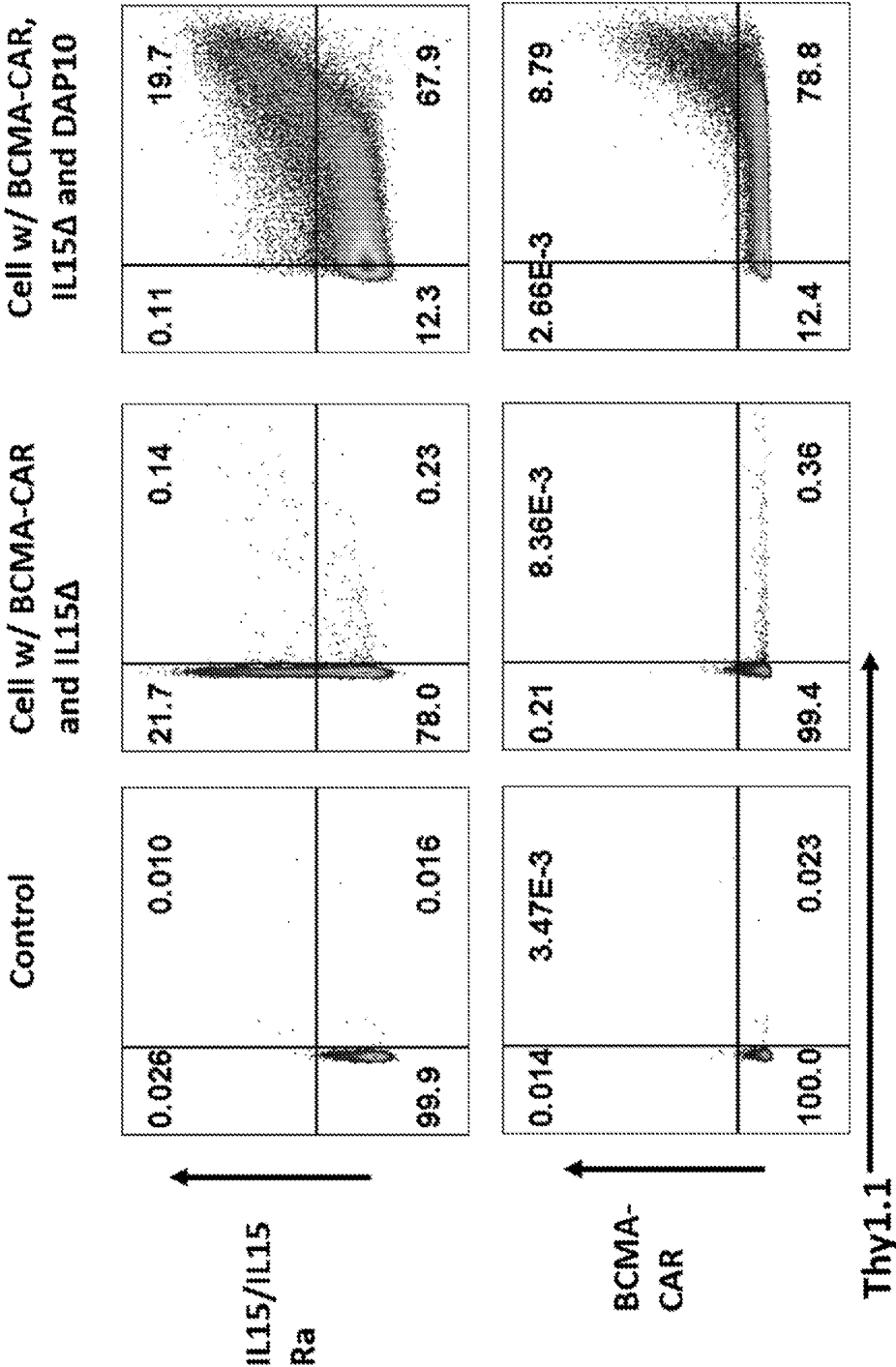
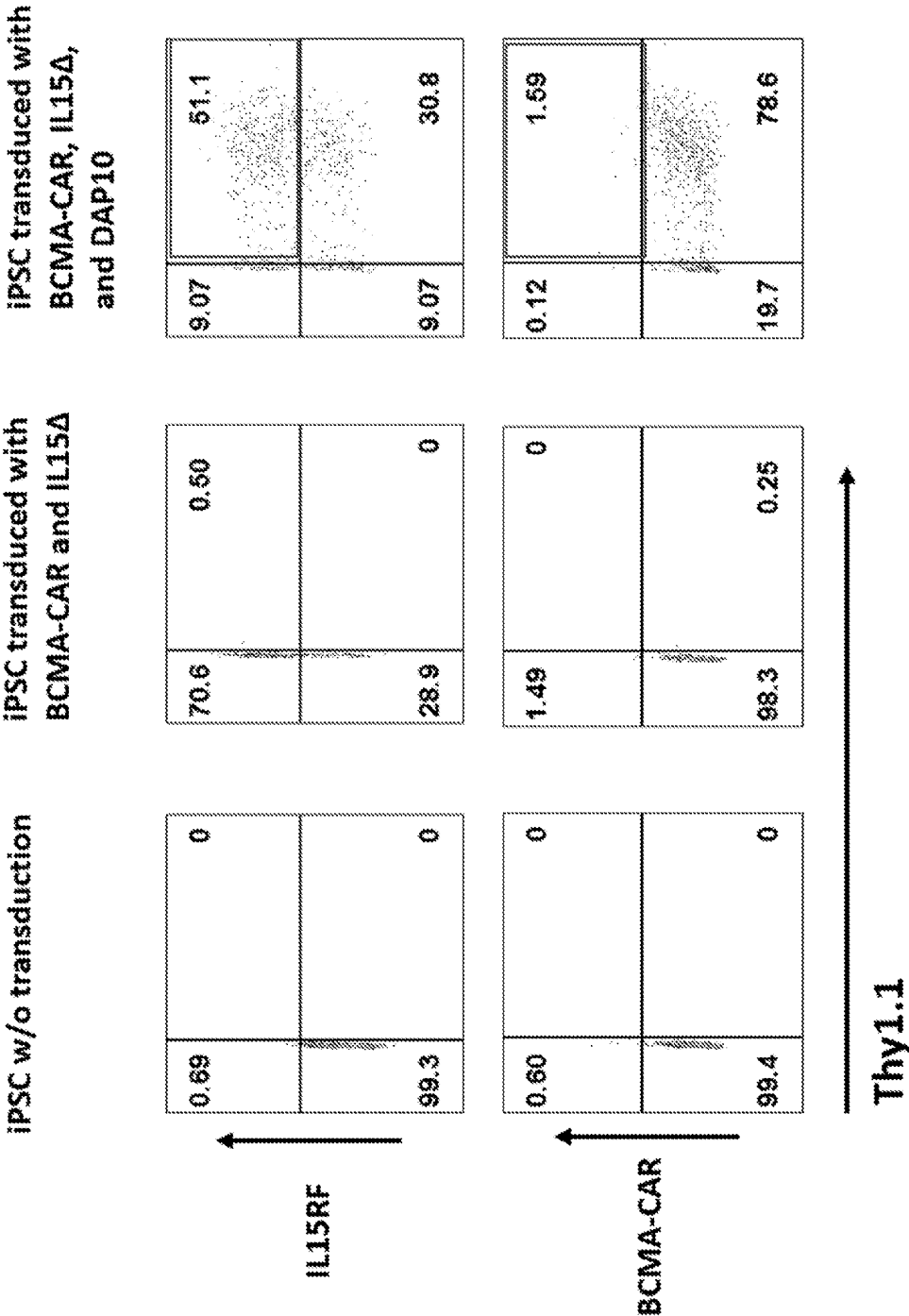


FIG. 6



12/25

FIG. 7A

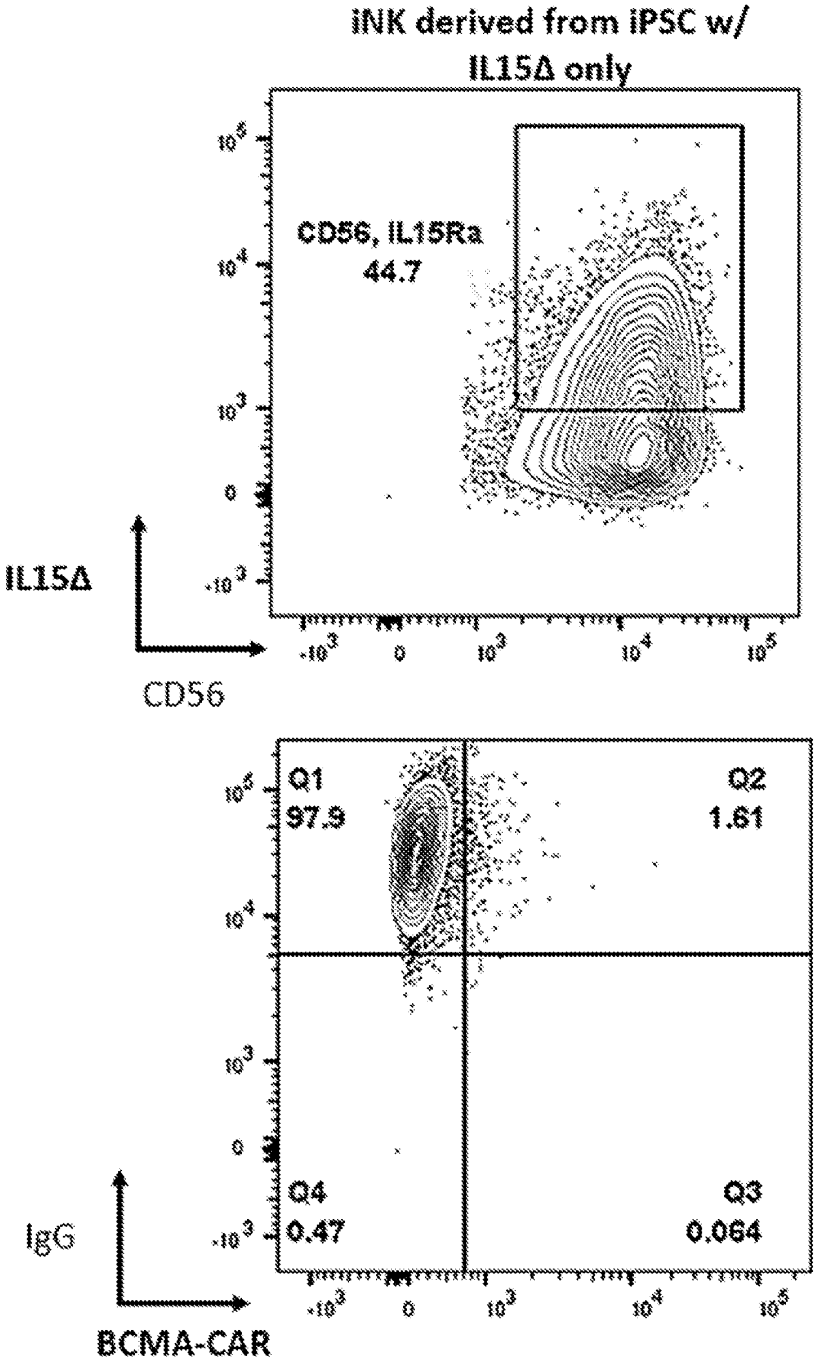


FIG. 7B

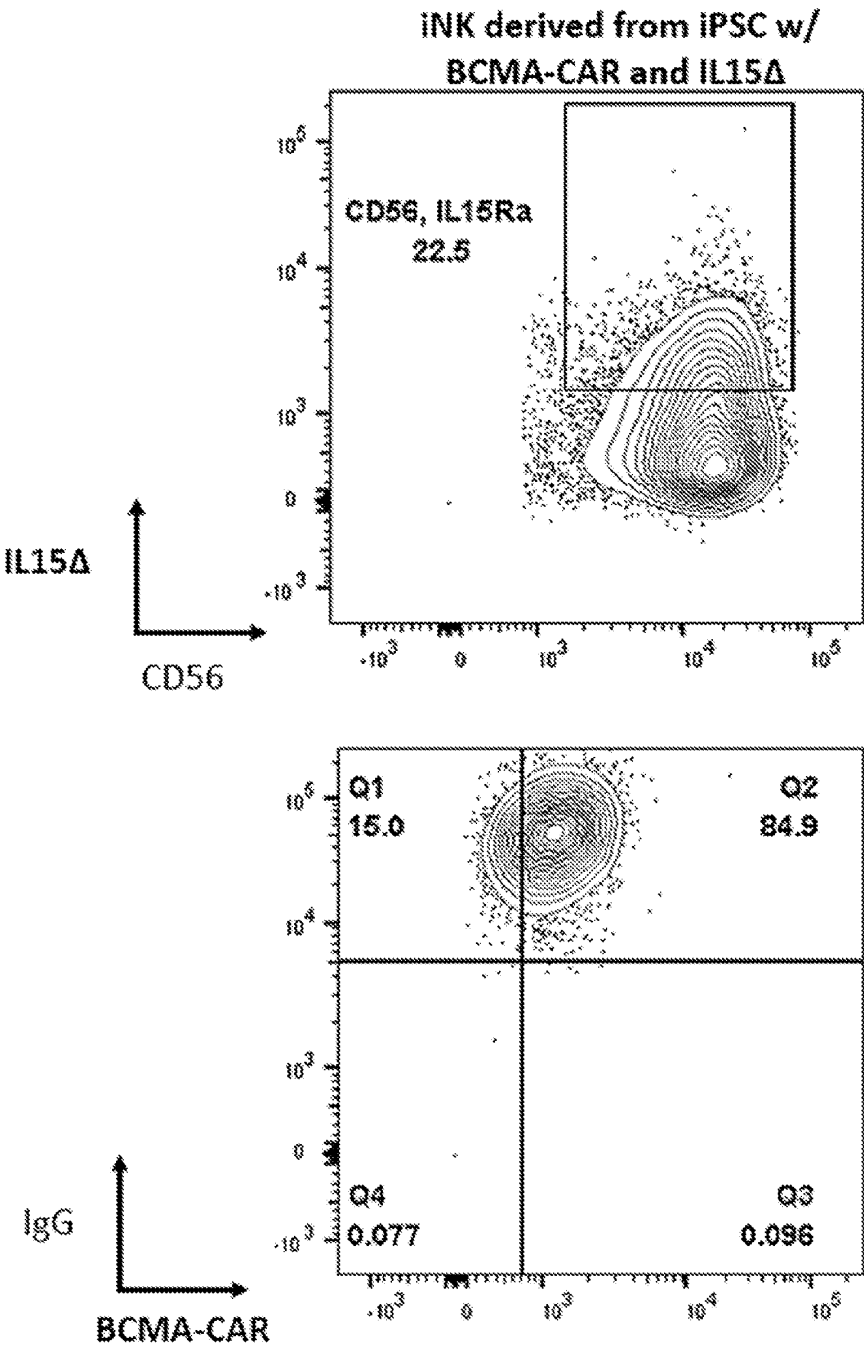


FIG. 7C

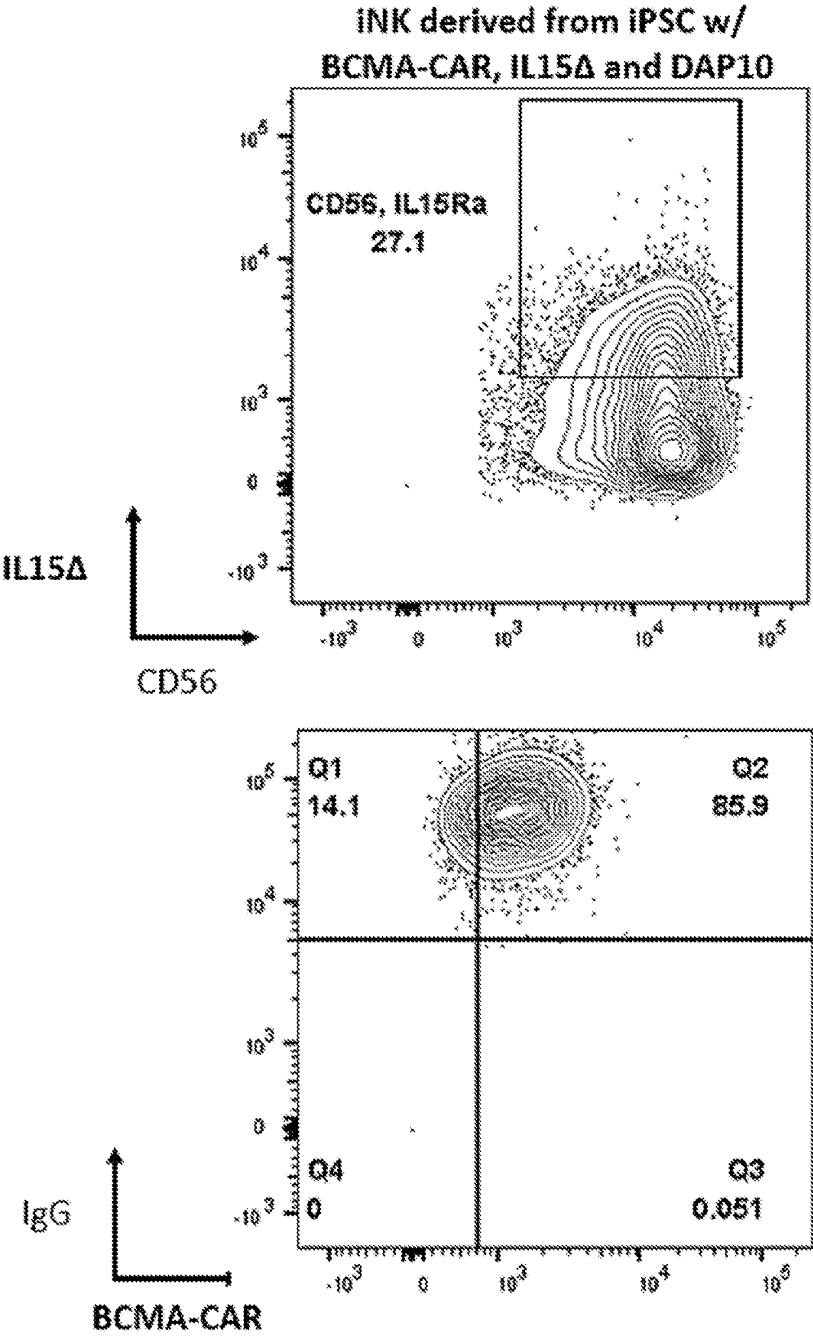


FIG. 8

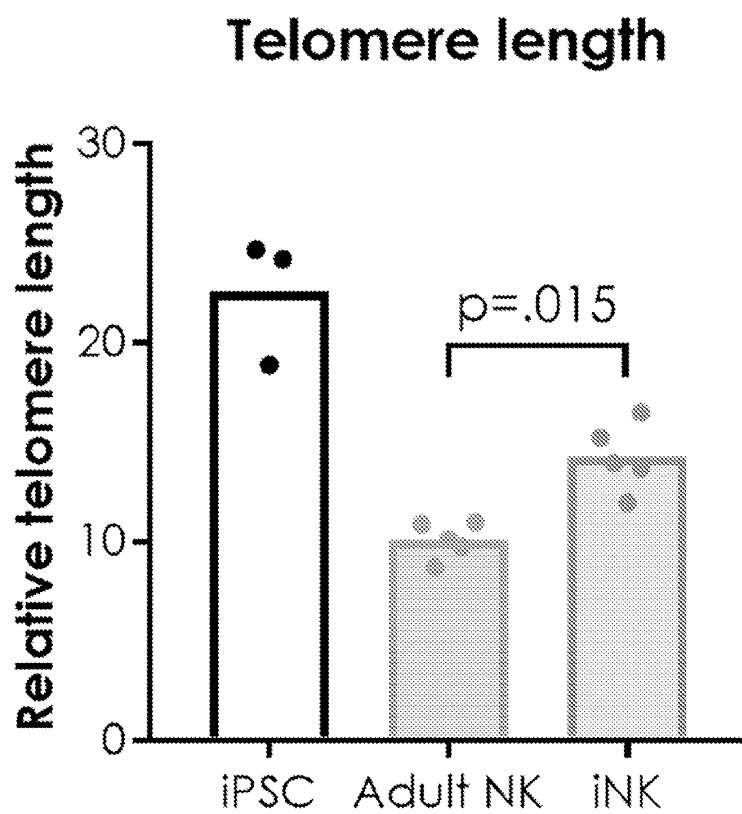
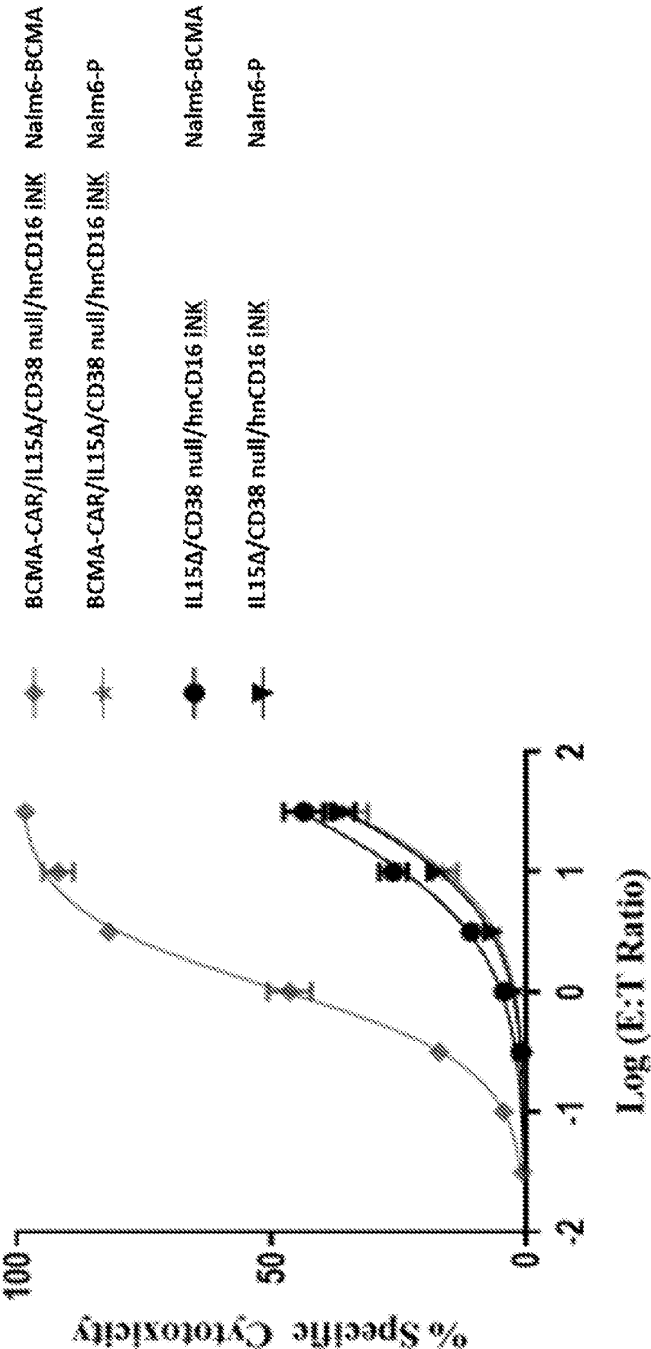
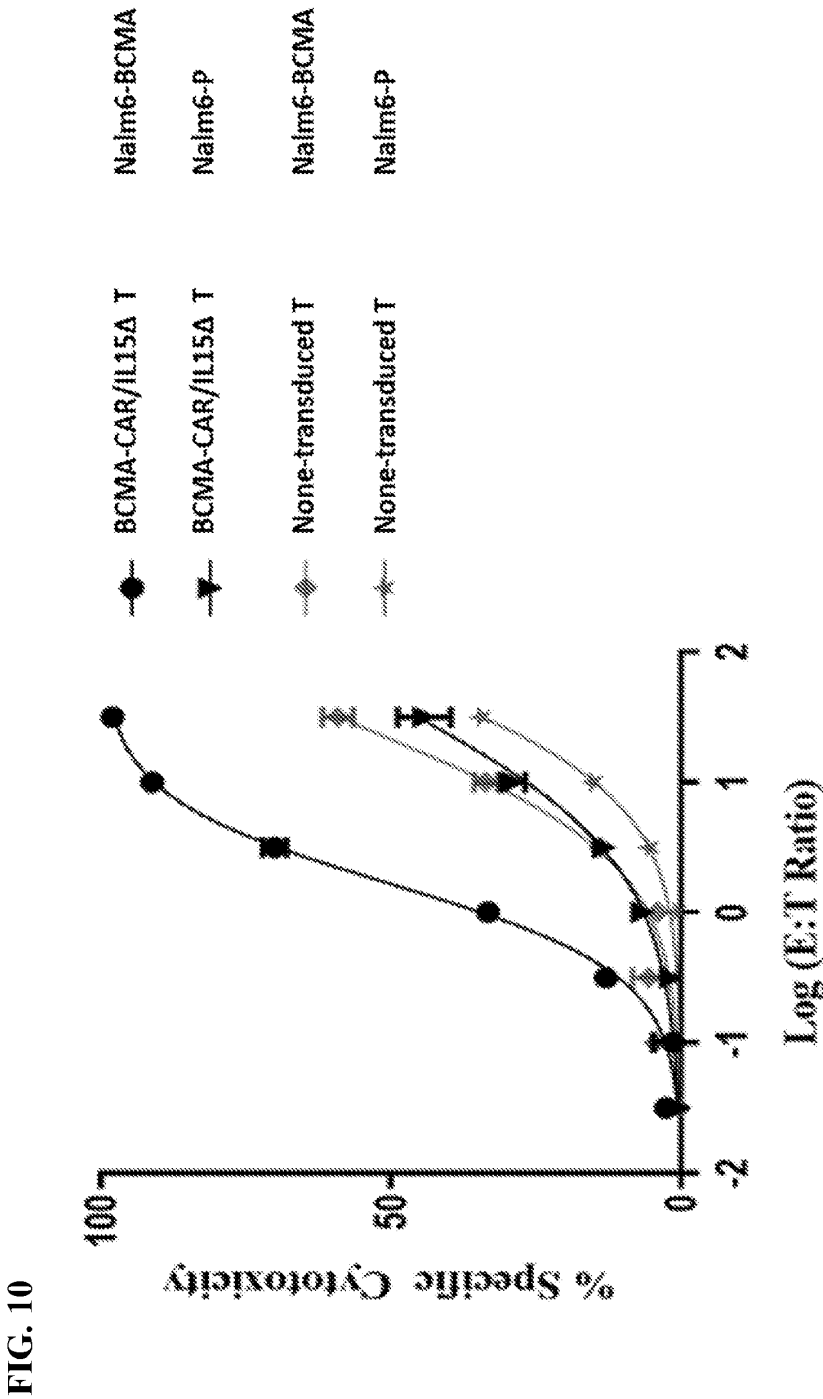
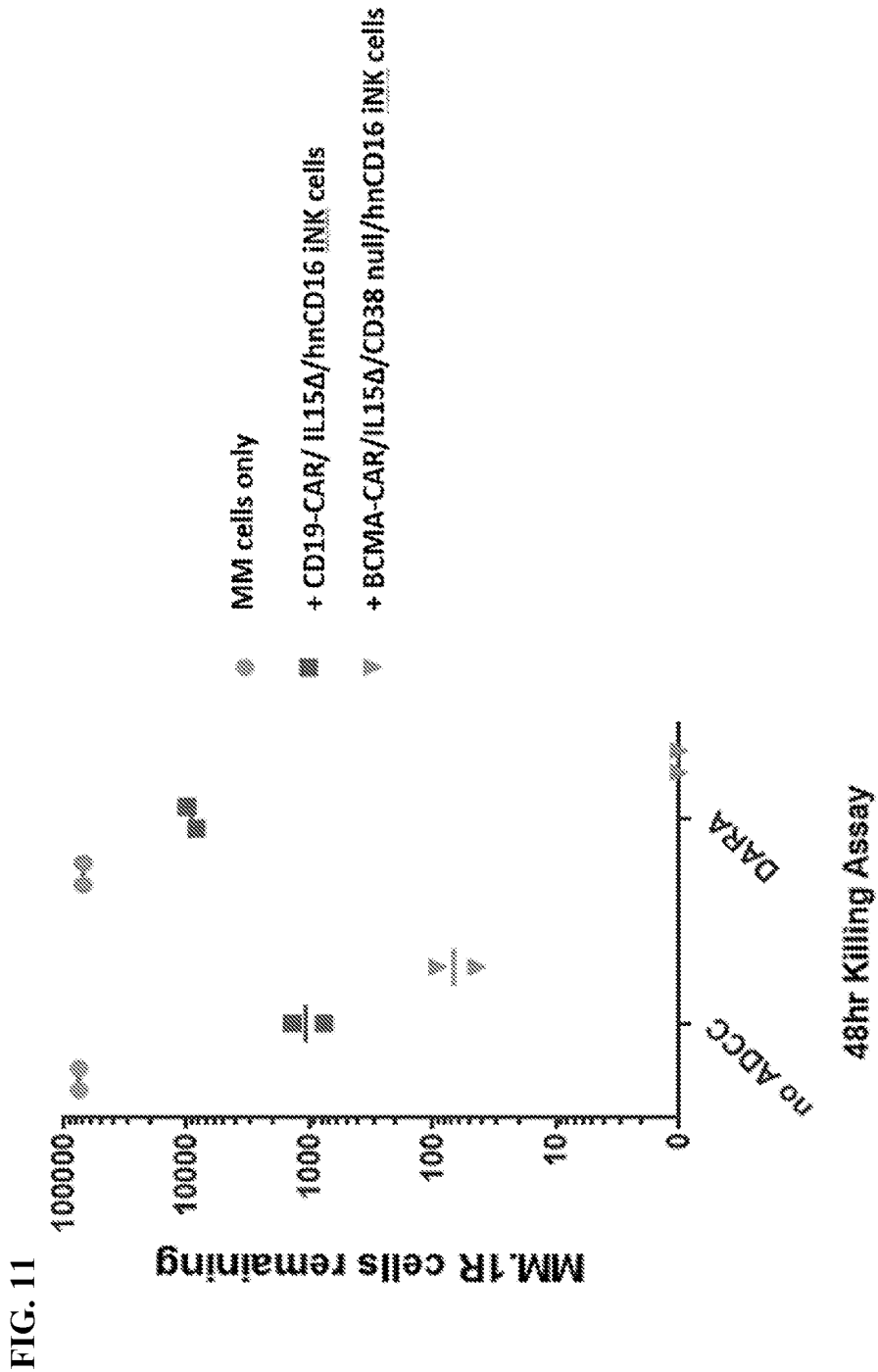


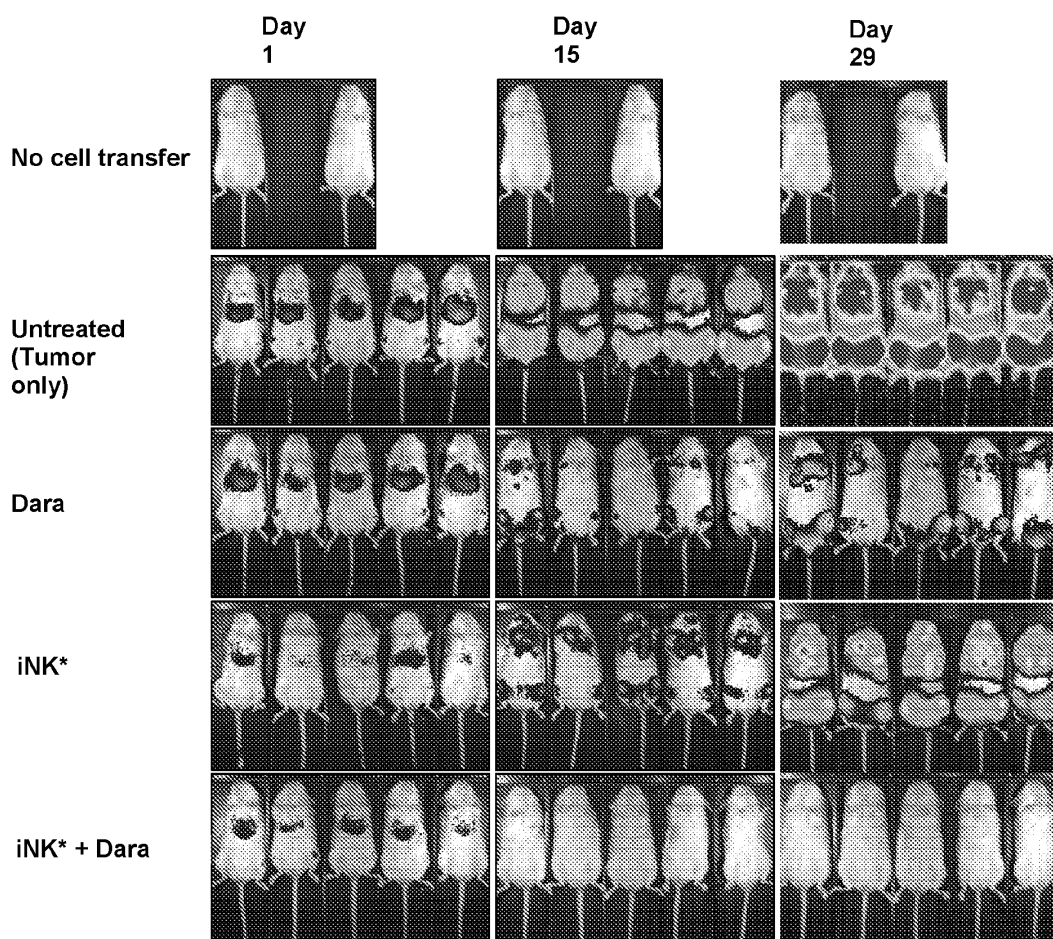
FIG. 9







19/25

FIG. 12A

iNK*: BCMA-CAR/IL15 Δ /CD38 null/hnCD16 iNK cells

20/25

FIG. 12B

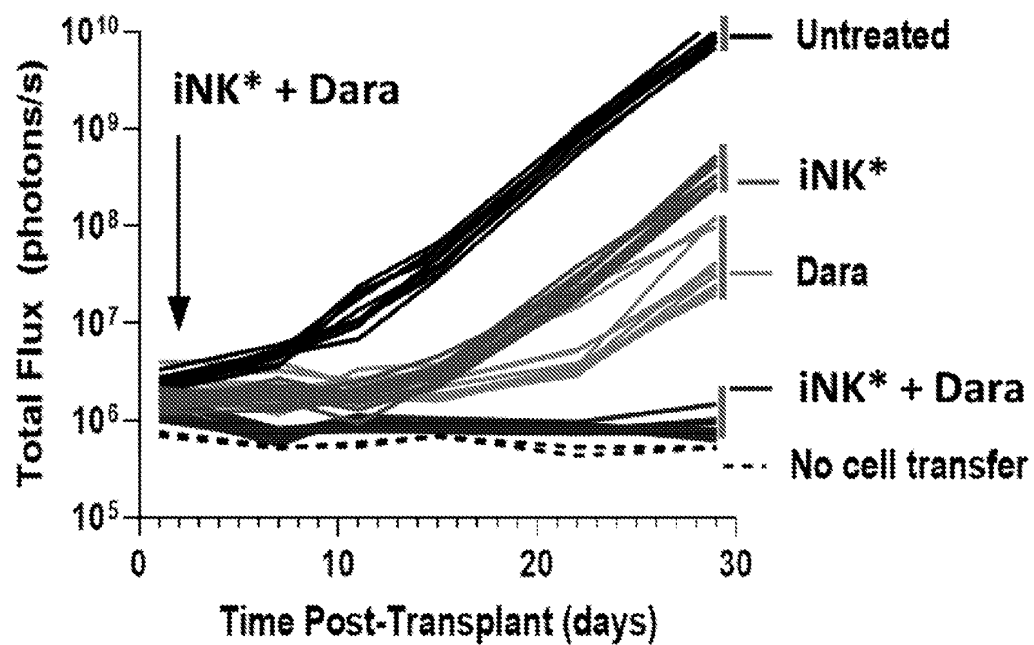


FIG. 13

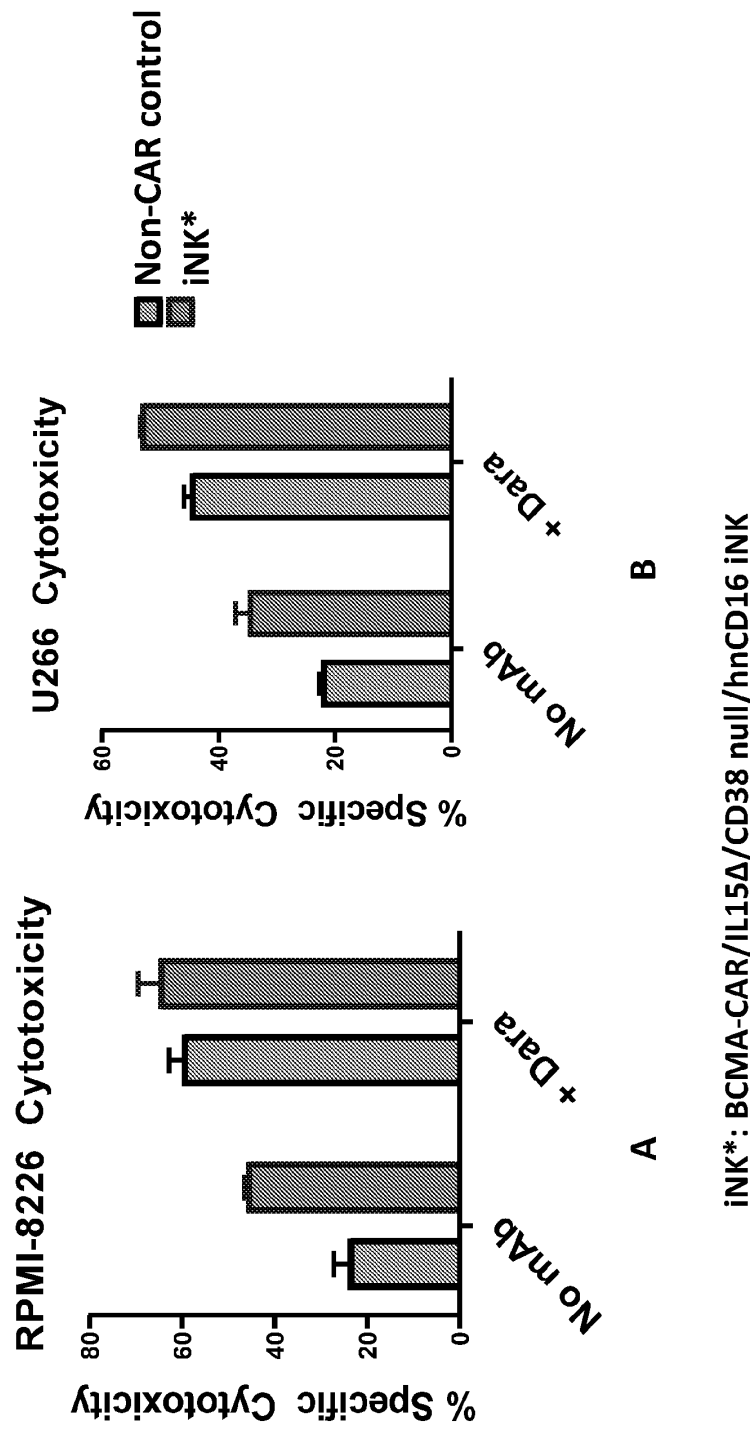
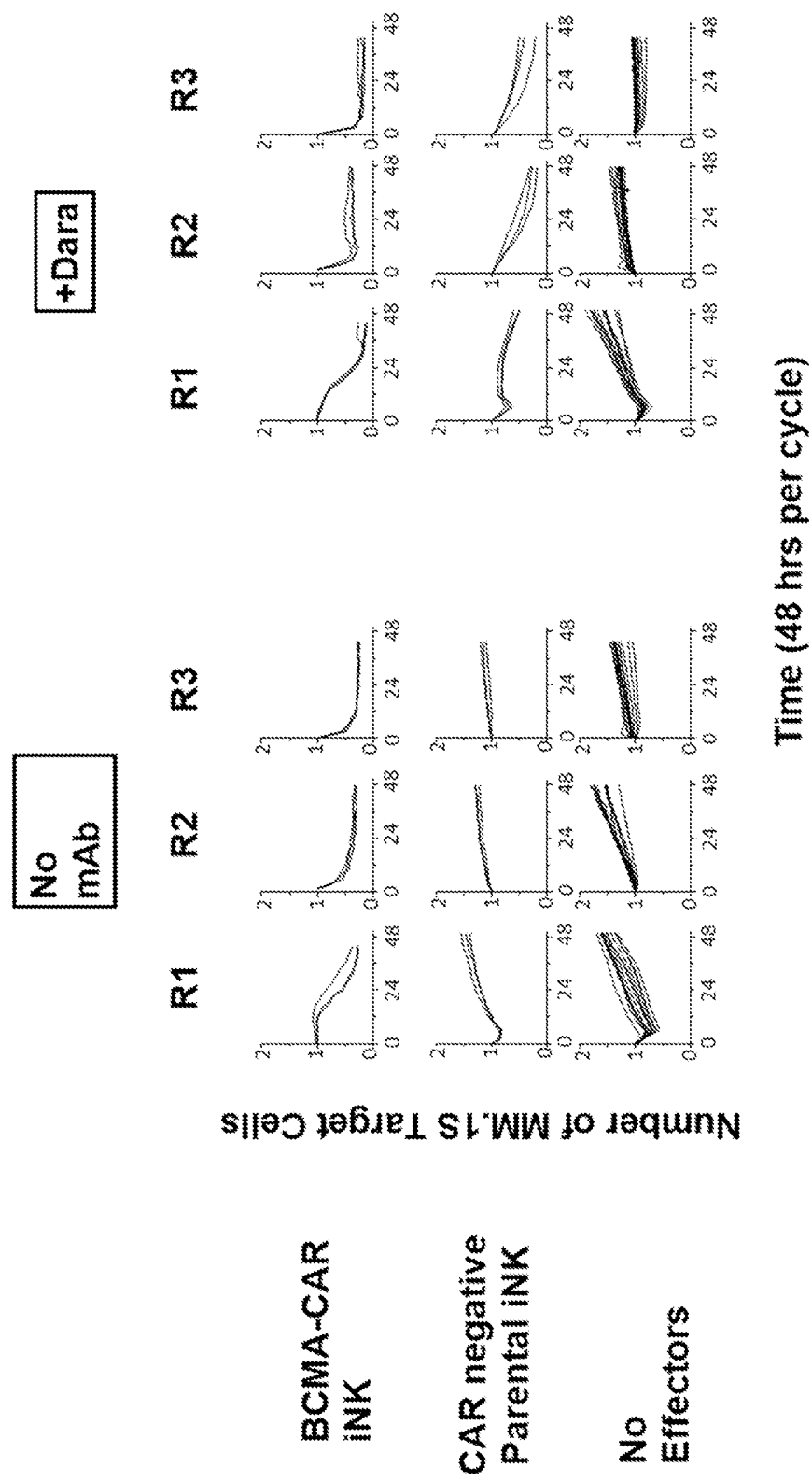


FIG. 14



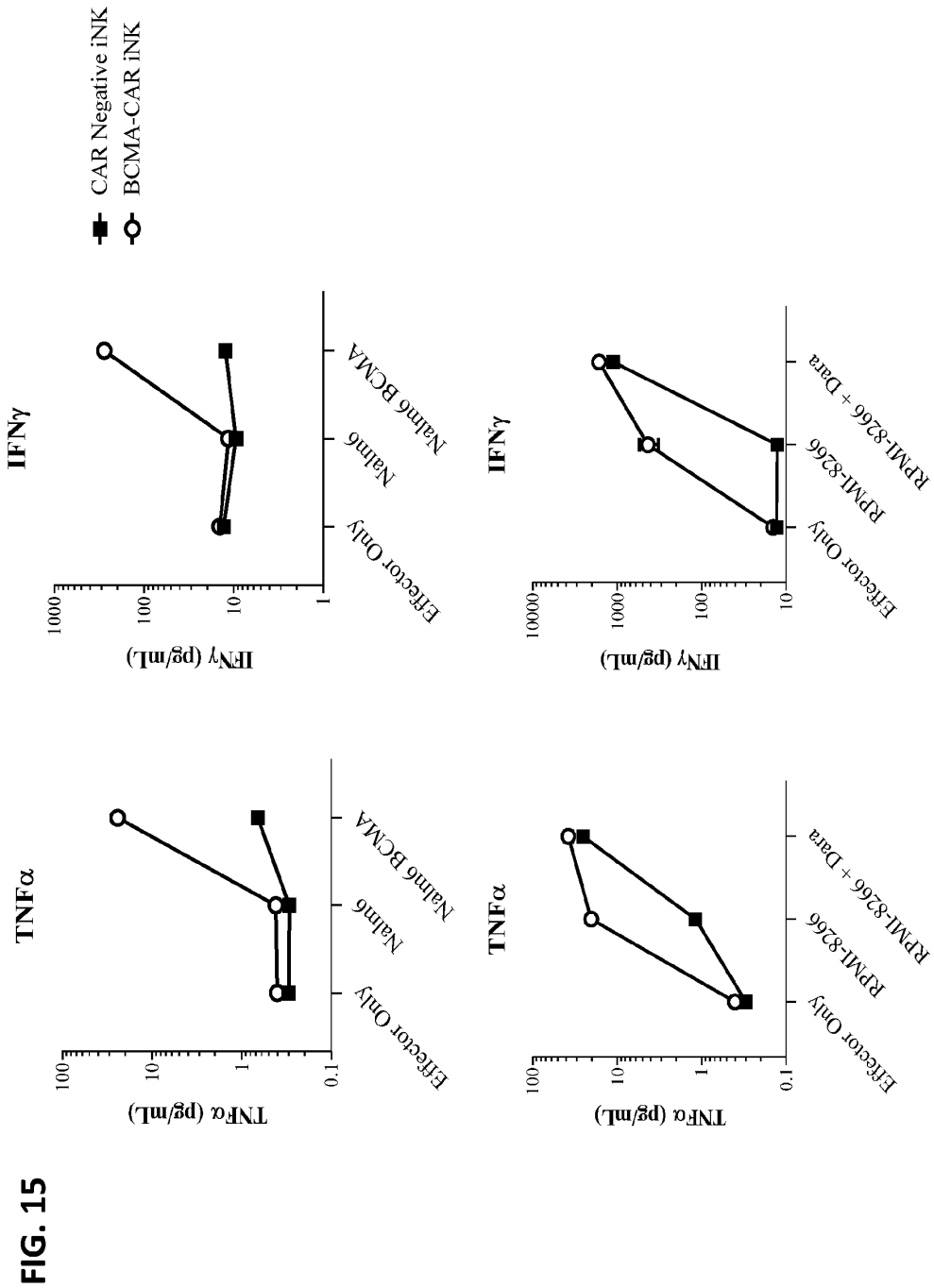


FIG. 16

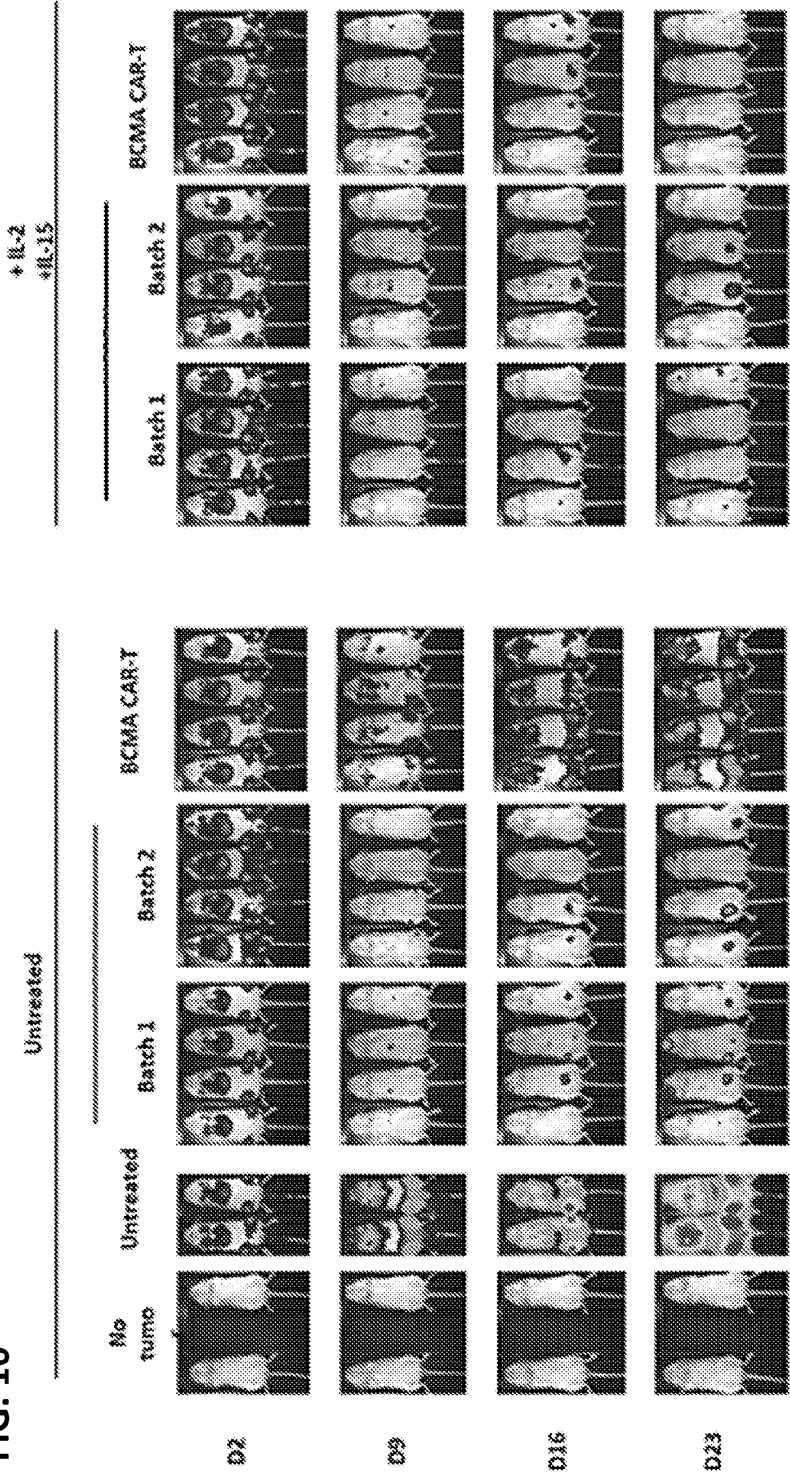


FIG. 17

