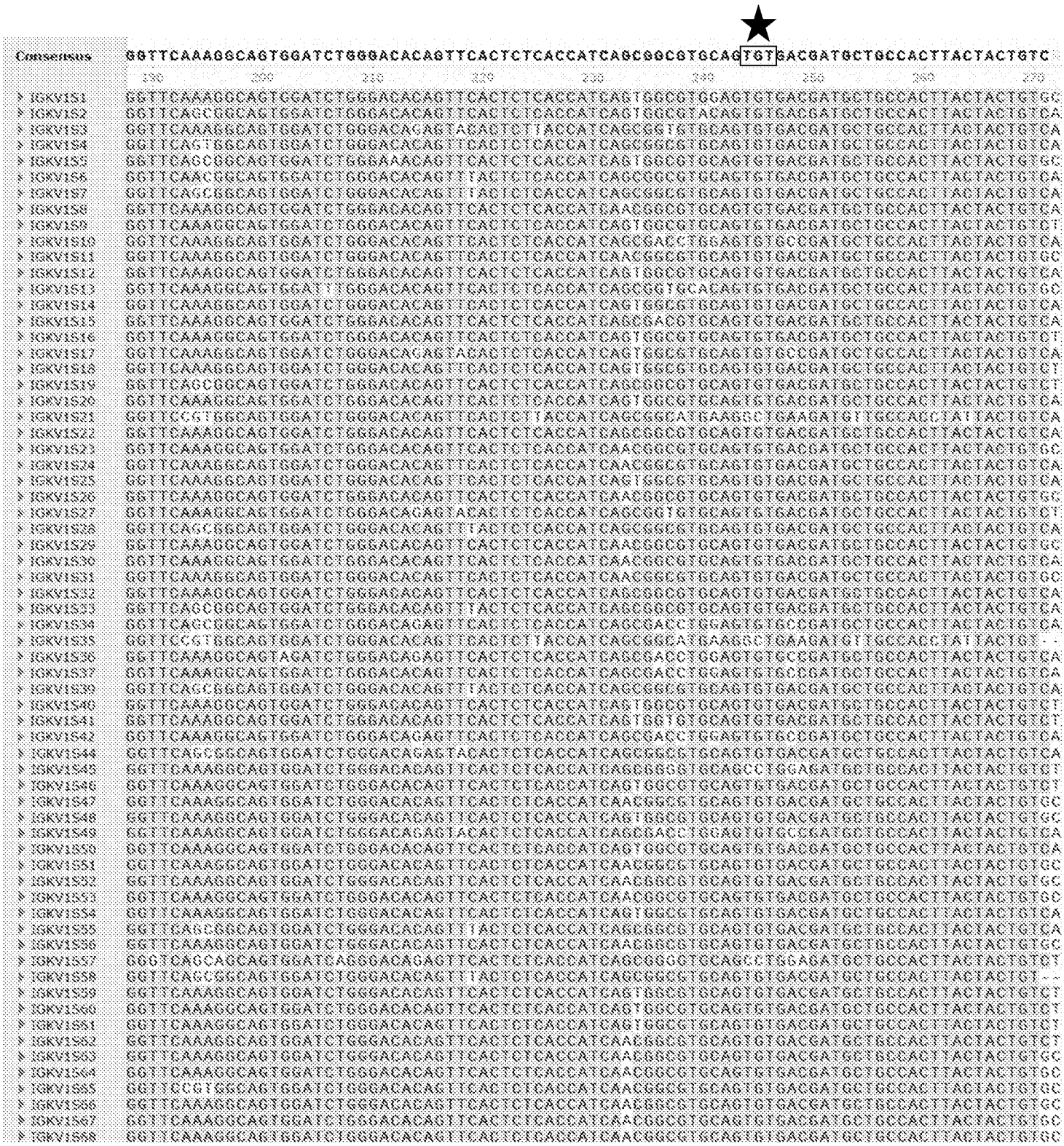

Consensus
GGTTCAAAGGCAGTGGATCTGGGACACAGTTCACTCTCACCATCAGCGGCGTGCAGTGTGACGATGCTGCCACTTACTACTGTC
190
200
210
220
230
240
250
260
270
IGKV1S1
IGKV1S2
IGKV1S3
IGKV1S4
IGKV1S5
IGKV1S6
IGKV1S7
IGKV1S8
IGKV1S9
IGKV1S10
IGKV1S11
IGKV1S12
IGKV1S13
IGKV1S14
IGKV1S15
IGKV1S16
IGKV1S17
IGKV1S18
IGKV1S19
IGKV1S20
IGKV1S21
IGKV1S22
IGKV1S23
IGKV1S24
IGKV1S25
IGKV1S26
IGKV1S27
IGKV1S28
IGKV1S29
IGKV1S30
IGKV1S31
IGKV1S32
IGKV1S33
IGKV1S34
IGKV1S35
IGKV1S36
IGKV1S37
IGKV1S39
IGKV1S40
IGKV1S41
IGKV1S42
IGKV1S44
IGKV1S45
IGKV1S46
IGKV1S47
IGKV1S48
IGKV1S49
IGKV1S50
IGKV1S51
IGKV1S52
IGKV1S53
IGKV1S54
IGKV1S55
IGKV1S56
IGKV1S57
IGKV1S58
IGKV1S59
IGKV1S60
IGKV1S61
IGKV1S62
IGKV1S63
IGKV1S64
IGKV1S65
IGKV1S66
IGKV1S67
IGKV1S68

FIG. 1

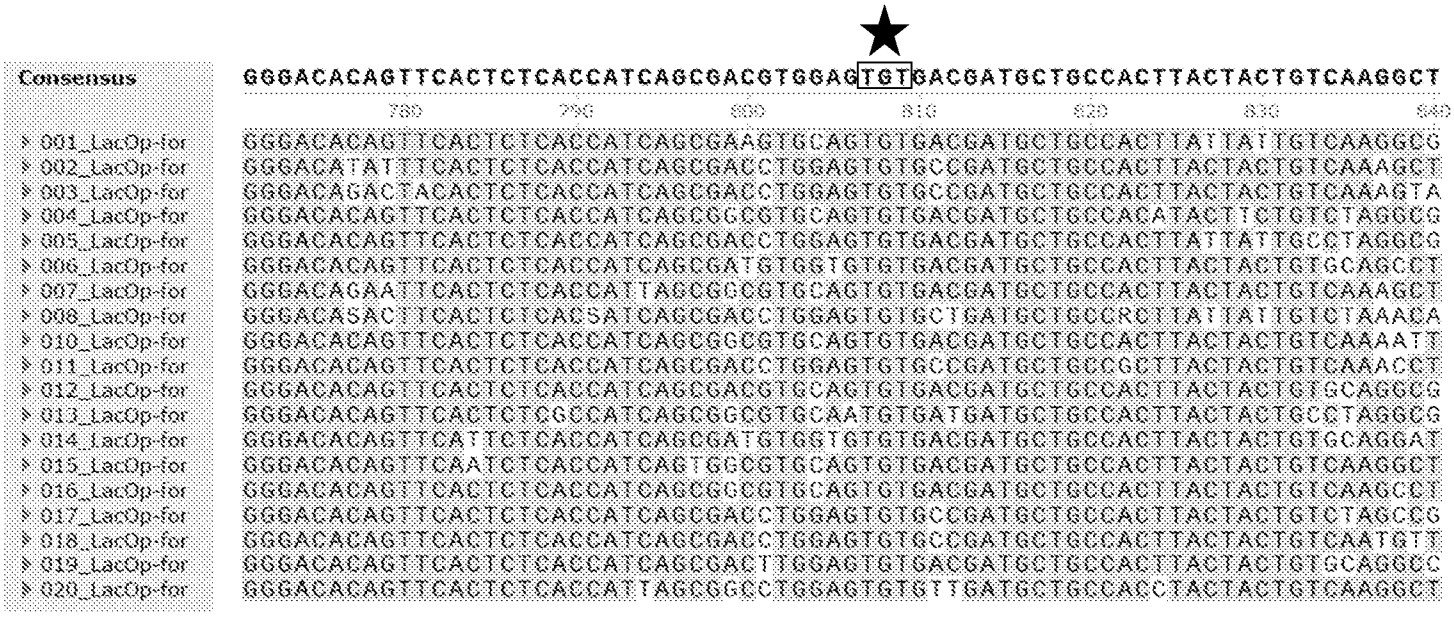

Consensus
GGGACACAGTTCACTCTCACCATCAGCGACGTGGAGTGTGACGATGCTGCCACTTACTACTGTCAAGGCT
780
790
800
810
820
830
840
001_LacOp-for GGGACACAGTTCACTCTCACCATCAGCGAAGTGCAGTGTGACGATGCTGCCACTTATTATTGTCAAGGCG
002_LacOp-for GGGACATATTTCACTCTCACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCAAAGCT
003_LacOp-for GGGACAGACTACACTCTCACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCAAAGTA
004_LacOp-for GGGACACAGTTCACTCTCACCATCAGCGGCGTGCAGTGTGACGATGCTGCCACATACTTCTGTCTAGGCG
005_LacOp-for GGGACACAGTTCACTCTCACCATCAGCGACCTGGAGTGTGACGATGCTGCCACTTATTATTGCCTAGGCG
006_LacOp-for GGGACACAGTTCACTCTCACCATCAGCGATGTGGTGTGTGACGATGCTGCCACTTACTACTGTGCAGCCT
007_LacOp-for GGGACAGAATTCACTCTCACCATTAGCGGCGTGCAGTGTGACGATGCTGCCACTTACTACTGTCAAAGCT
008_LacOp-for GGGACASACTTCACTCTCACSATCAGCGACCTGGAGTGTGCTGATGCTGCCRCTTATTATTGTCTAAACA
010_LacOp-for GGGACACAGTTCACTCTCACCATCAGCGGCGTGCAGTGTGACGATGCTGCCACTTACTACTGTCAAAATT
011_LacOp-for GGGACACAGTTCACTCTCACCATCAGCGACCTGGAGTGTGCCGATGCTGCCGCTTACTACTGTCAAACCT
012_LacOp-for GGGACACAGTTCACTCTCACCATCAGCGACGTGCAGTGTGACGATGCTGCCACTTACTACTGTGCAGGCG
013_LacOp-for GGGACACAGTTCACTCTCGCCATCAGCGGCGTGCAATGTGATGATGCTGCCACTTACTACTGCCTAGGCG
014_LacOp-for GGGACACAGTTCATTCTCACCATCAGCGATGTGGTGTGTGACGATGCTGCCACTTACTACTGTGCAGGAT
015_LacOp-for GGGACACAGTTCAATCTCACCATCAGTGGCGTGCAGTGTGACGATGCTGCCACTTACTACTGTCAAGGCT
016_LacOp-for GGGACACAGTTCACTCTCACCATCAGCGGCGTGCAGTGTGACGATGCTGCCACTTACTACTGTCAAGCCT
017_LacOp-for GGGACACAGTTCACTCTCACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCTAGCCG
018_LacOp-for GGGACACAGTTCACTCTCACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCAATGTT
019_LacOp-for GGGACACAGTTCACTCTCACCATCAGCGACTTGGAGTGTGACGATGCTGCCACTTACTACTGTGCAGGCC
020_LacOp-for GGGACACAGTTCACTCTCACCATTAGCGGCCTGGAGTGTGTTGATGCTGCCACCTACTACTGTCAAGGCT

FIG. 2


0.050
Sequence 5 (245 aa)
Sequence 48 (247 aa)
Sequence 36 (254 aa)
Sequence 41 (247 aa)
Sequence 1 (247 aa)
Sequence 61 (242 aa)
Sequence 18 (249 aa)
Sequence 52 (248 aa)
Sequence 53 (248 aa)
Sequence 47 (246 aa)
Sequence 38 (252 aa)
Sequence 54 (247 aa)
Sequence 55 (248 aa)
Sequence 30 (250 aa)
Sequence 11 (246 aa)
Sequence 3 (248 aa)
Sequence 13 (244 aa)
Sequence 14 (250 aa)
Sequence 19 (244 aa)
Sequence 8 (253 aa)
Sequence 51 (249 aa)
Sequence 56 (245 aa)
Sequence 31 (244 aa)
Sequence 37 (247 aa)
Sequence 42 (246 aa)
Sequence 46 (252 aa)
Sequence 35 (256 aa)
Sequence 10 (249 aa)
Sequence 39 (255 aa)
Sequence 23 (244 aa)
Sequence 44 (248 aa)
Sequence 50 (245 aa)
Sequence 24 (244 aa)
Sequence 26 (251 aa)
Sequence 33 (242 aa)
Sequence 16 (248 aa)
Sequence 43 (246 aa)
Sequence 58 (249 aa)
Sequence 32 (254 aa)
Sequence 20 (247 aa)
Sequence 22 (249 aa)
Sequence 34 (250 aa)
Sequence 60 (256 aa)
Sequence 62 (251 aa)
Sequence 2 (247 aa)
Sequence 21 (247 aa)
Sequence 12 (248 aa)
Sequence 7 (246 aa)
Sequence 4 (248 aa)
Sequence 15 (251 aa)
Sequence 29 (245 aa)
Sequence 6 (250 aa)
Sequence 27 (251 aa)
Sequence 57 (248 aa)
Sequence 17 (243 aa)
Sequence 25 (251 aa)
Sequence 59 (249 aa)
Sequence 28 (245 aa)
Sequence 40 (249 aa)
Sequence 49 (249 aa)
Sequence 9 (259 aa)
Sequence 45 (248 aa)

FIG. 3

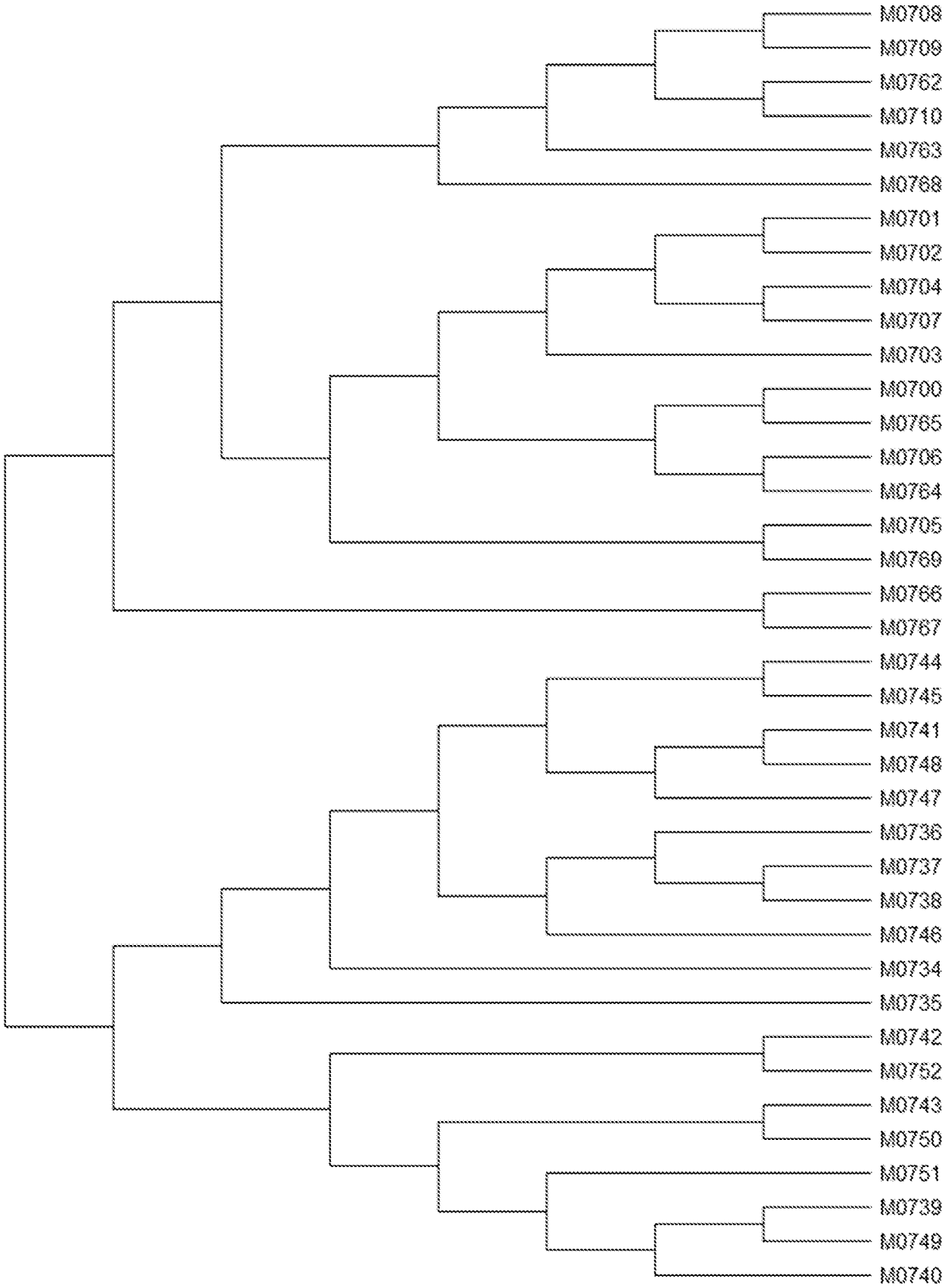

M0708
M0709
M0762
M0710
M0763
M0768
M0701
M0702
M0704
M0707
M0703
M0700
M0765
M0706
M0764
M0705
M0769
M0766
M0767
M0744
M0745
M0741
M0748
M0747
M0736
M0737
M0738
M0746
M0734
M0735
M0742
M0752
M0743
M0750
M0751
M0739
M0749
M0740

FIG. 4

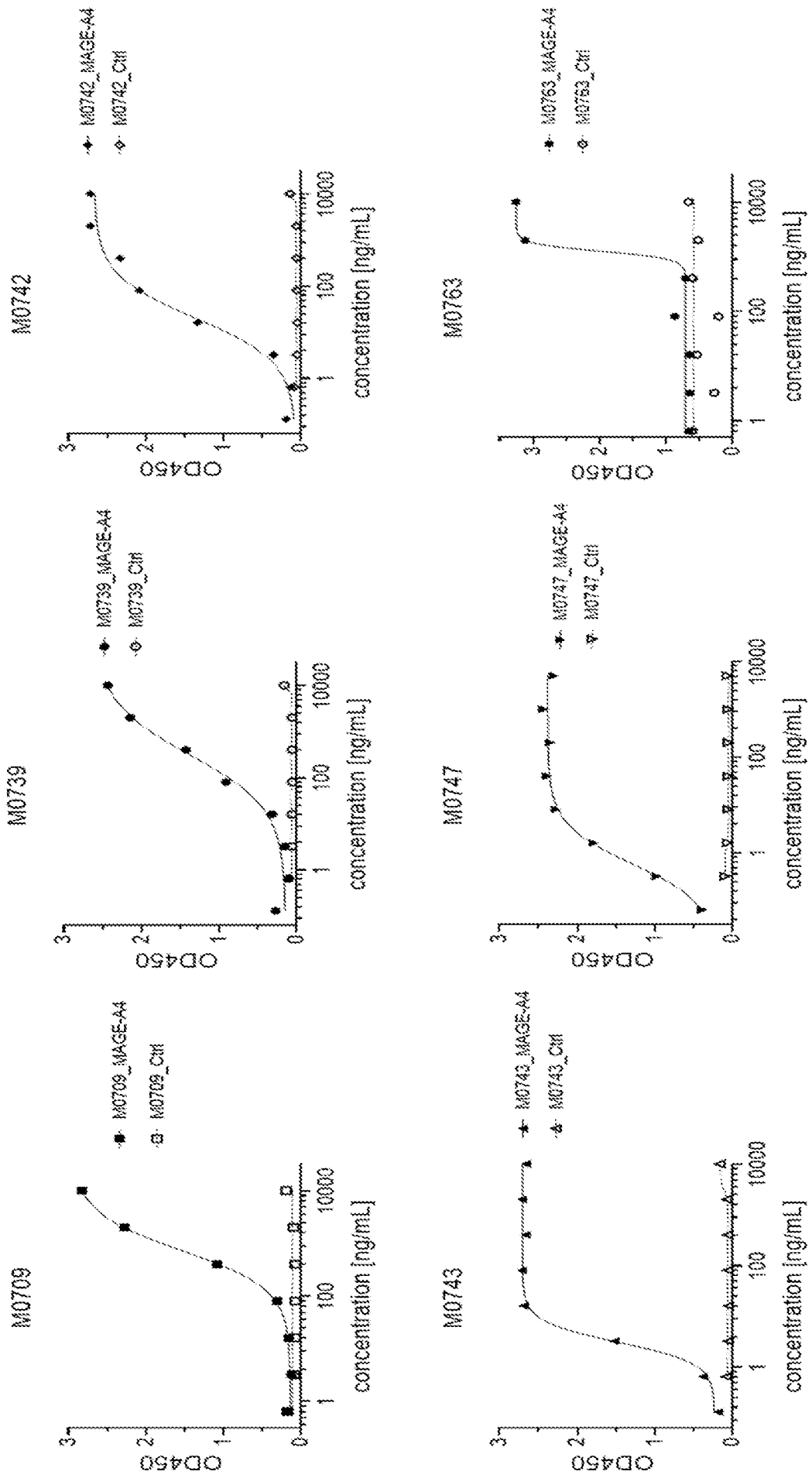

M0742
M0742_MAGE-A4
M0742_Ctrl
M0739
M0739_MAGE-A4
M0739_Ctrl
M0763
M0763_MAGE-A4
M0763_Ctrl
M0709
M0709_MAGE-A4
M0709_Ctrl
M0747
M0747_MAGE-A4
M0747_Ctrl
M0743
M0743_MAGE-A4
M0743_Ctrl
OD450
concentration [ng/mL]

FIG. 5A

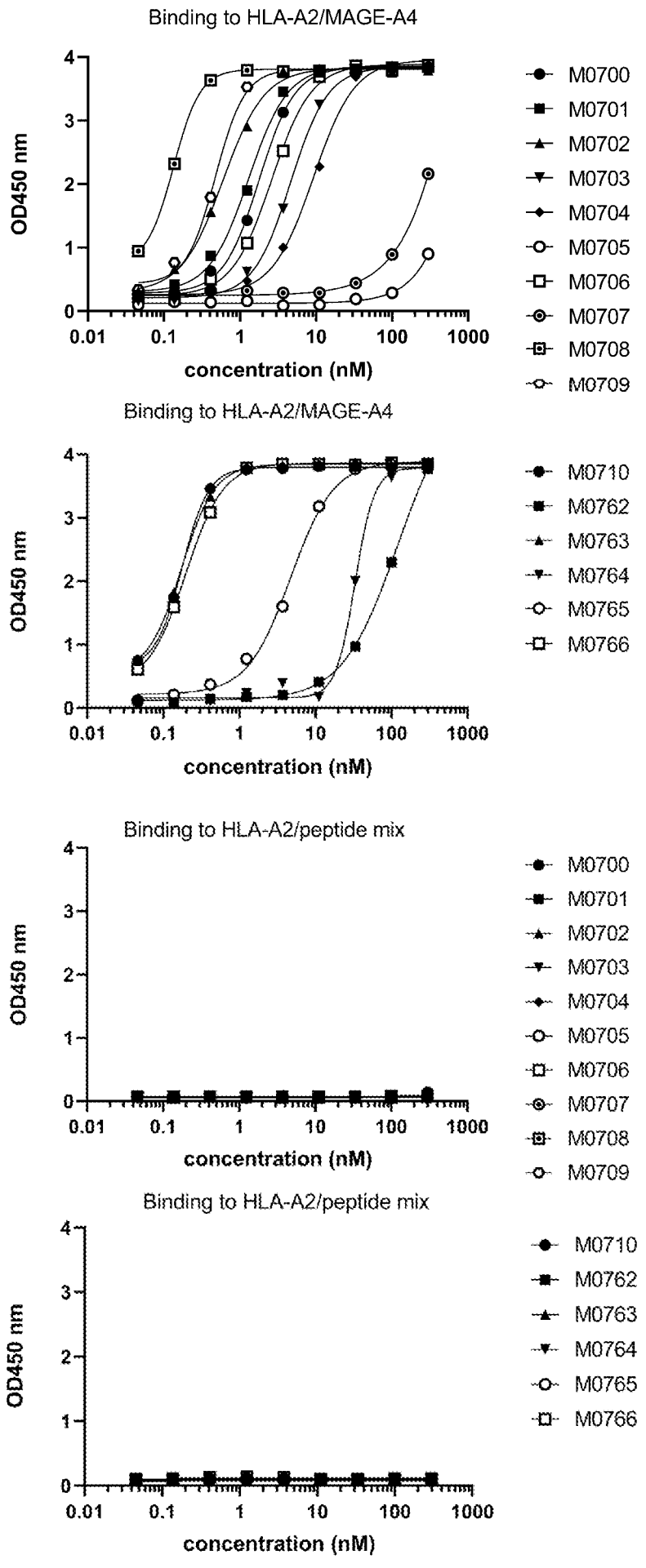

Binding to HLA-A2/MAGE-A4
OD450 nm
concentration (nM)
M0700
M0701
M0702
M0703
M0704
M0705
M0706
M0707
M0708
M0709
Binding to HLA-A2/MAGE-A4
OD450 nm
concentration (nM)
M0710
M0762
M0763
M0764
M0765
M0766
Binding to HLA-A2/peptide mix
OD450 nm
concentration (nM)
M0700
M0701
M0702
M0703
M0704
M0705
M0706
M0707
M0708
M0709
Binding to HLA-A2/peptide mix
OD450 nm
concentration (nM)
M0710
M0762
M0763
M0764
M0765
M0766

FIG. 5B

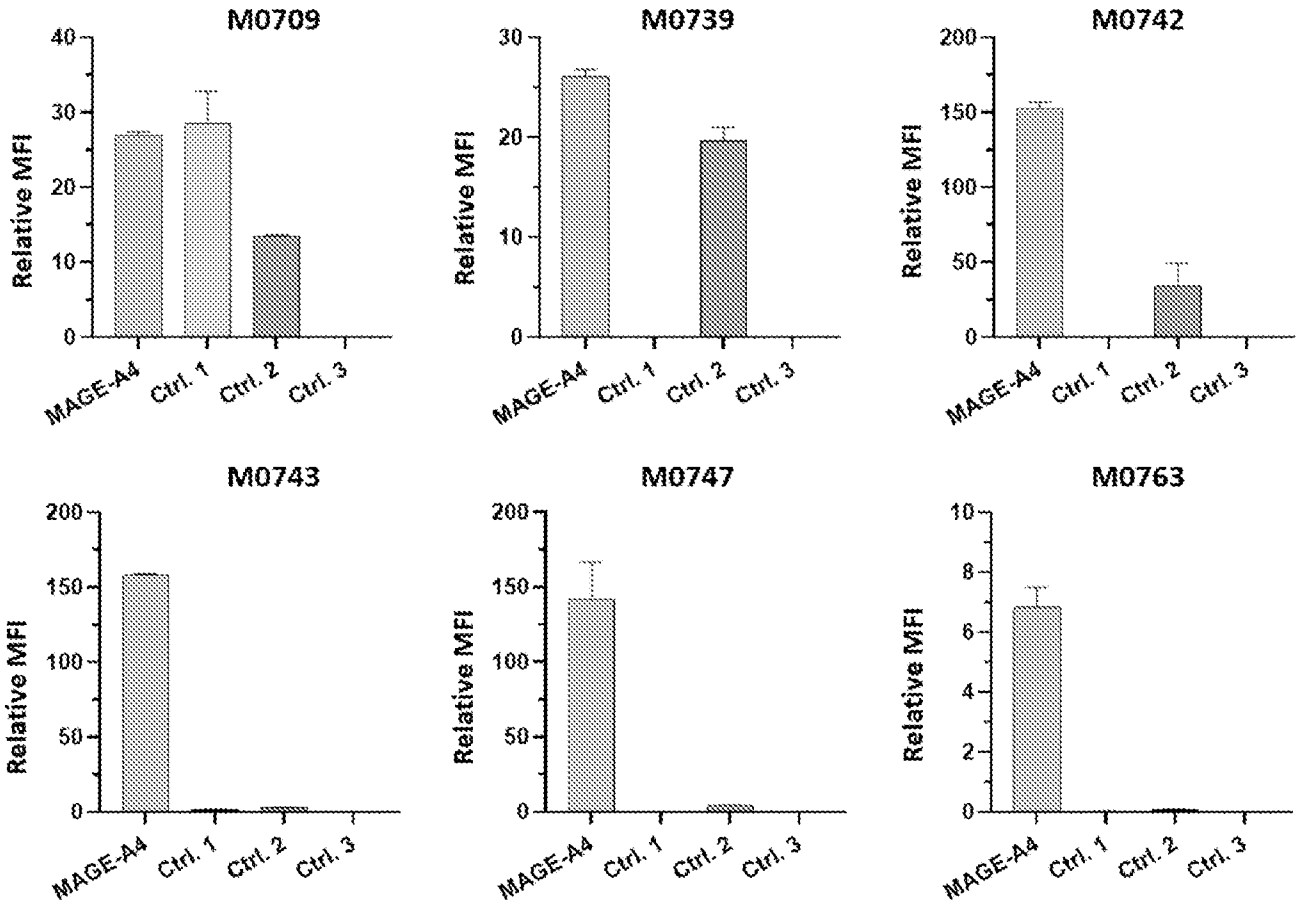

M0709
Relative MFI
40
30
20
10
0
MAGE-A4
Ctrl. 1
Ctrl. 2
Ctrl. 3
M0739
Relative MFI
30
20
10
0
MAGE-A4
Ctrl. 1
Ctrl. 2
Ctrl. 3
M0742
Relative MFI
200
150
100
50
0
MAGE-A4
Ctrl. 1
Ctrl. 2
Ctrl. 3
M0743
Relative MFI
200
150
100
50
0
MAGE-A4
Ctrl. 1
Ctrl. 2
Ctrl. 3
M0747
Relative MFI
200
150
100
50
0
MAGE-A4
Ctrl. 1
Ctrl. 2
Ctrl. 3
M0763
Relative MFI
10
8
6
4
2
0
MAGE-A4
Ctrl. 1
Ctrl. 2
Ctrl. 3

FIG. 6

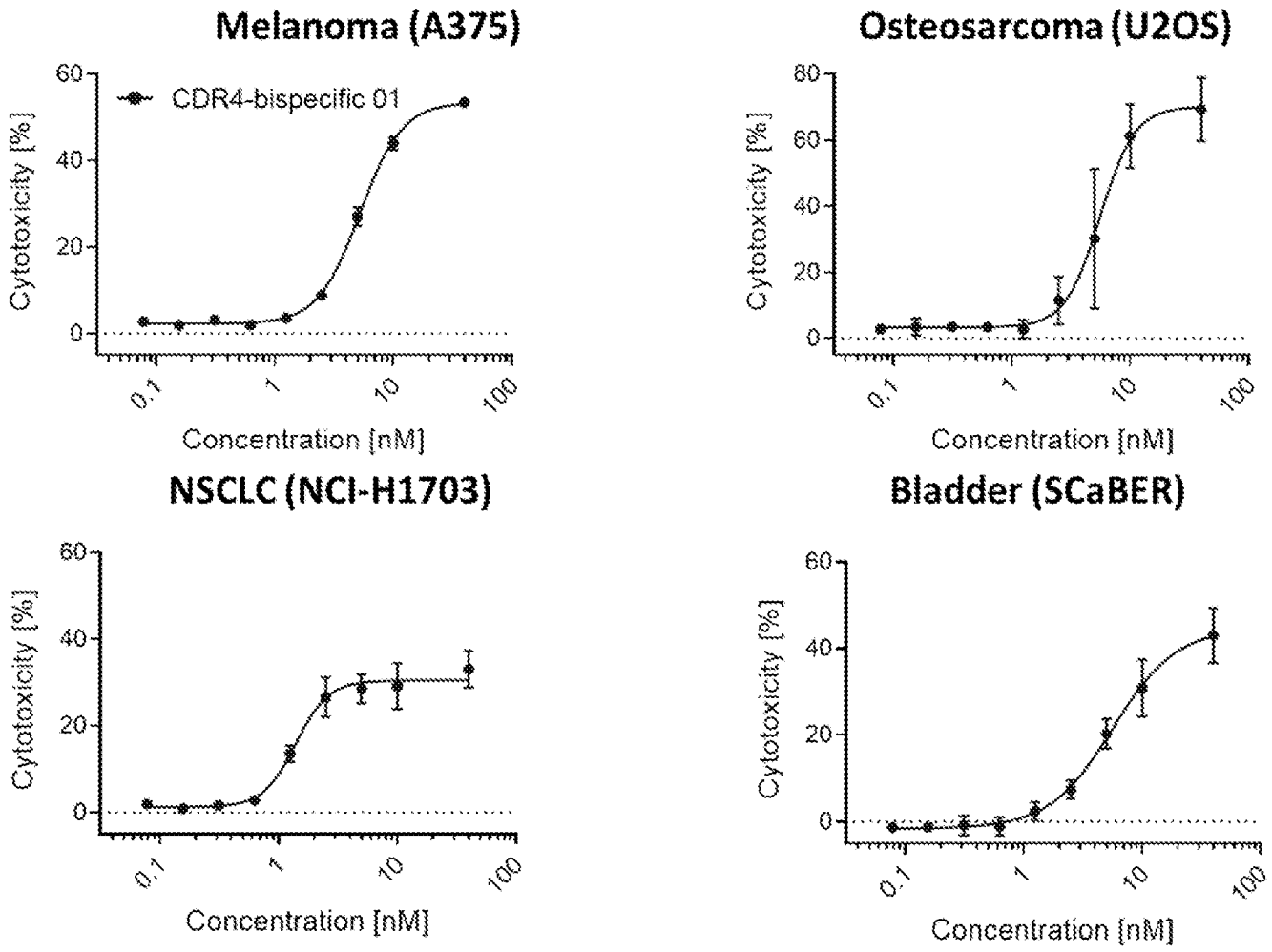

Melanoma (A375)
CDR4-bispecific 01
Cytotoxicity [%]
Concentration [nM]
Osteosarcoma (U2OS)
Cytotoxicity [%]
Concentration [nM]
NSCLC (NCI-H1703)
Cytotoxicity [%]
Concentration [nM]
Bladder (SCaBER)
Cytotoxicity [%]
Concentration [nM]

FIG. 7

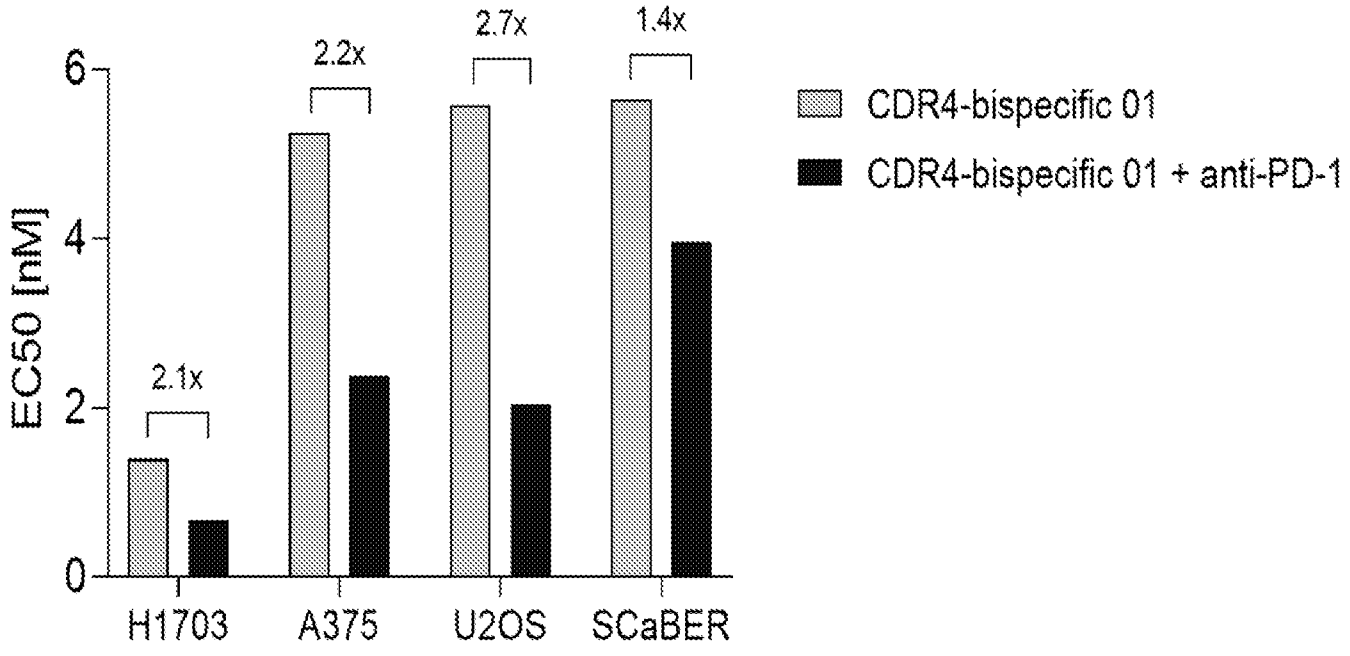

EC50 [nM]
6
4
2
0
2.1x
2.2x
2.7x
1.4x
H1703
A375
U2OS
SCaBER
CDR4-bispecific 01
CDR4-bispecific 01 + anti-PD-1

FIG. 8

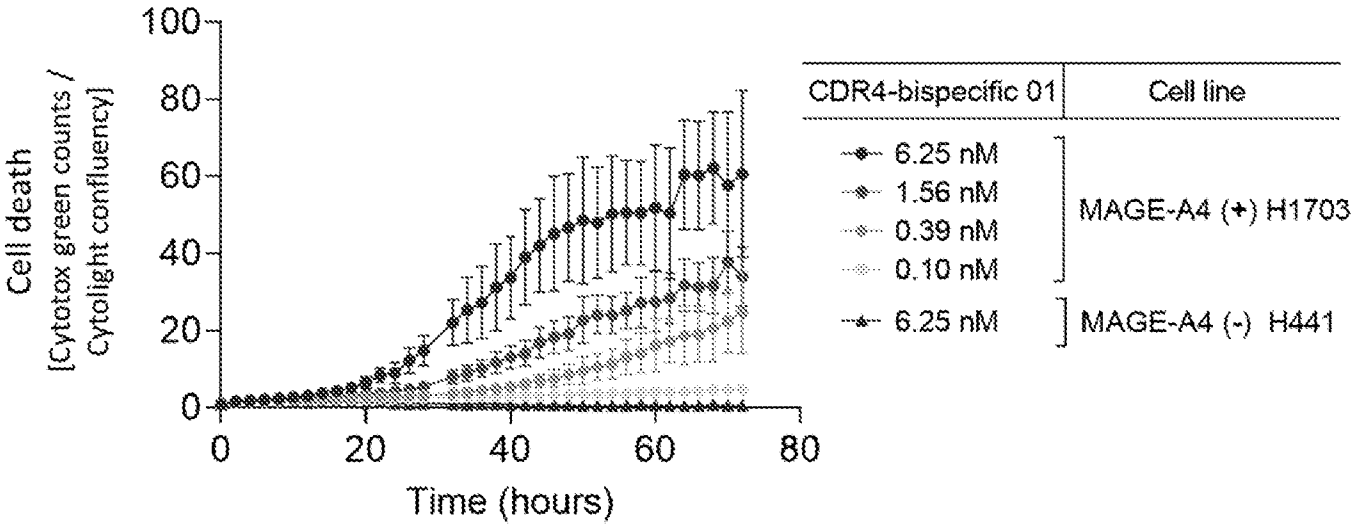

Cell death
[Cytotox green counts / Cytolight confluency]
100
80
60
40
20
0
0
20
40
60
80
Time (hours)
CDR4-bispecific 01
Cell line
6.25 nM
1.56 nM
0.39 nM
0.10 nM
MAGE-A4 (+) H1703
6.25 nM
MAGE-A4 (-) H441

FIG. 9

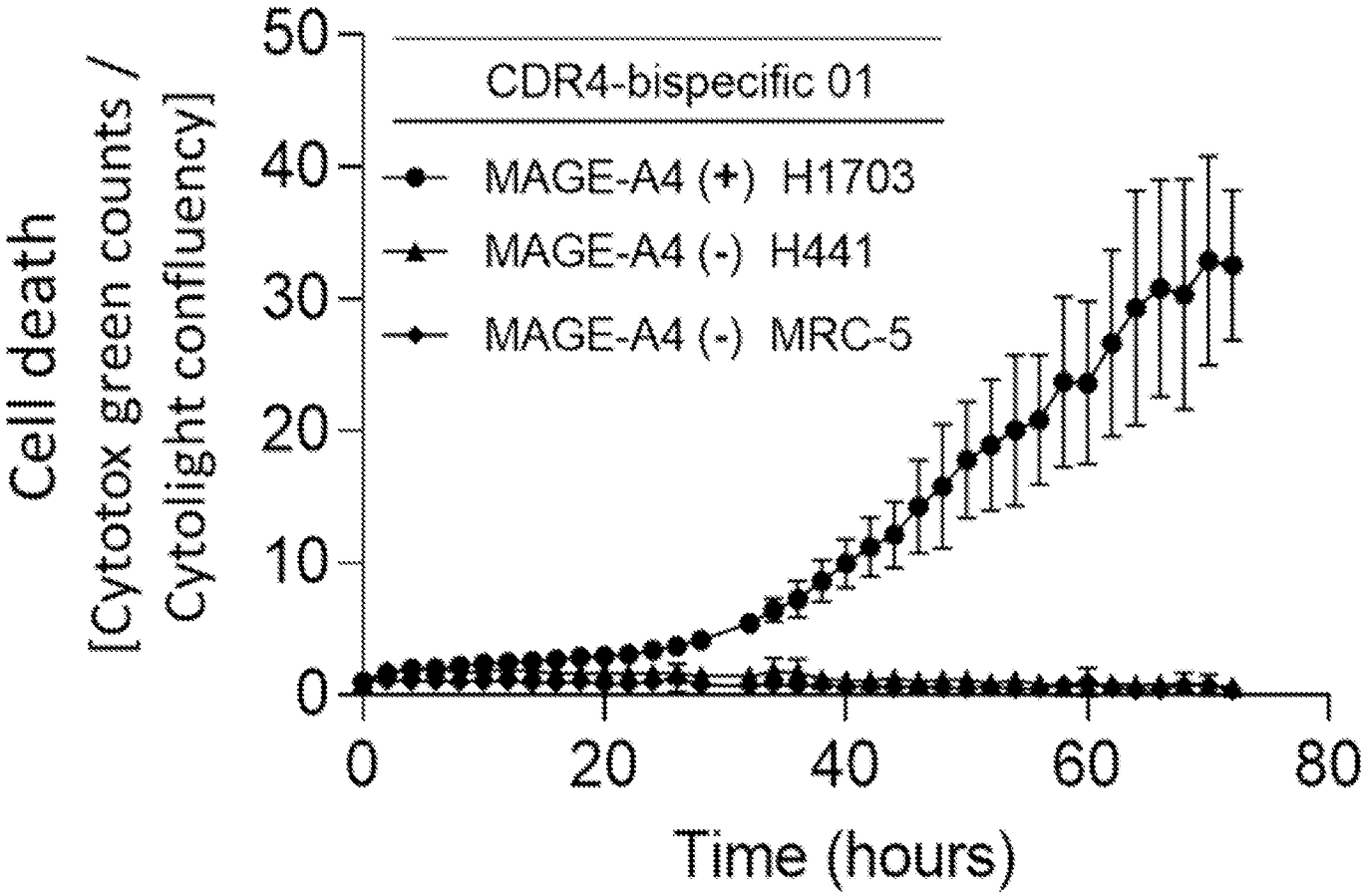

Cell death
[Cytotox green counts / Cytolight confluency]
50
40
30
20
10
0
0
20
40
60
80
Time (hours)
CDR4-bispecific 01
MAGE-A4 (+) H1703
MAGE-A4 (-) H441
MAGE-A4 (-) MRC-5

FIG.10

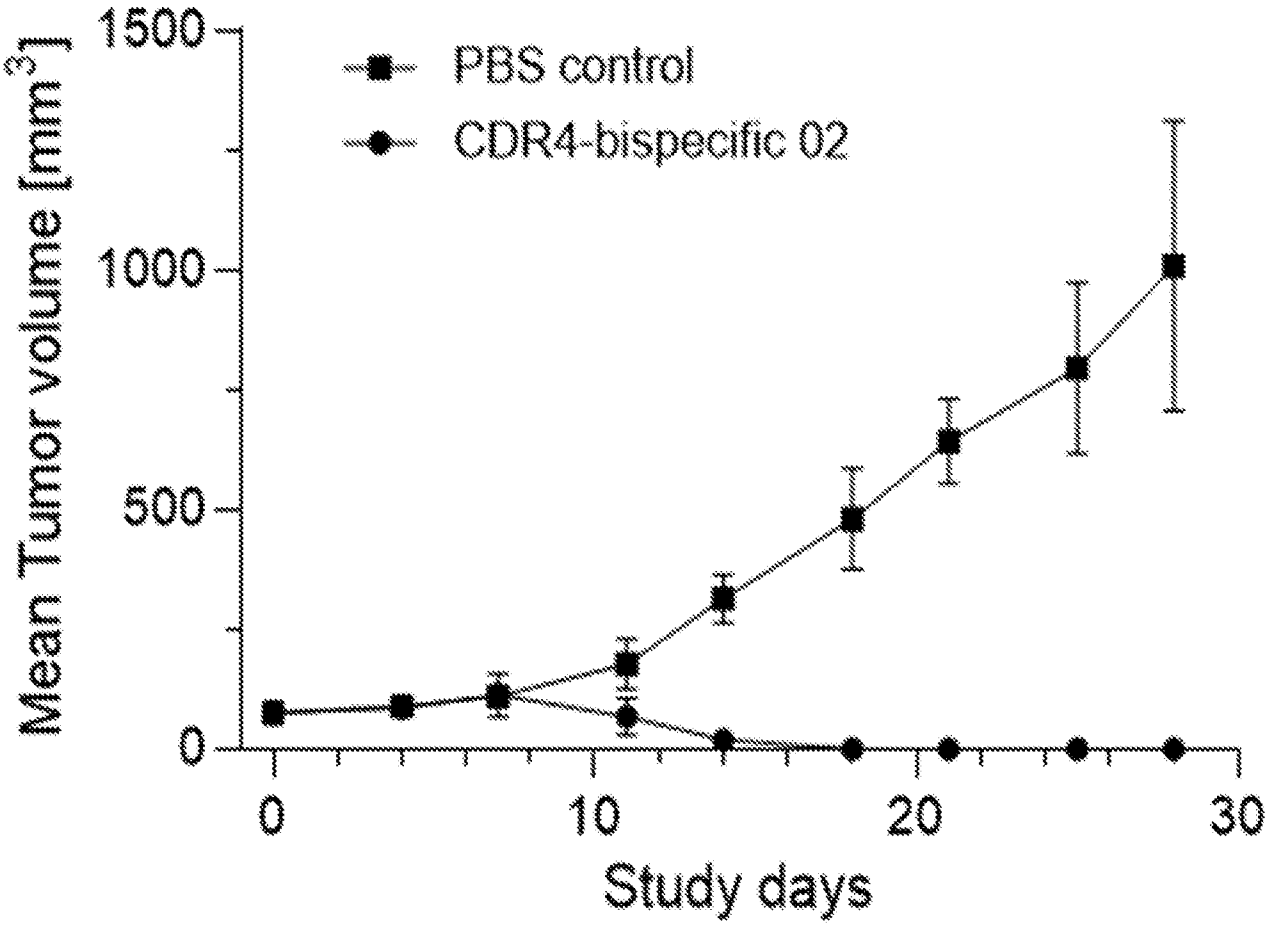

Mean Tumor volume [mm3]
1500
1000
500
0
PBS control
CDR4-bispecific 02
0
10
20
30
Study days

FIG.11