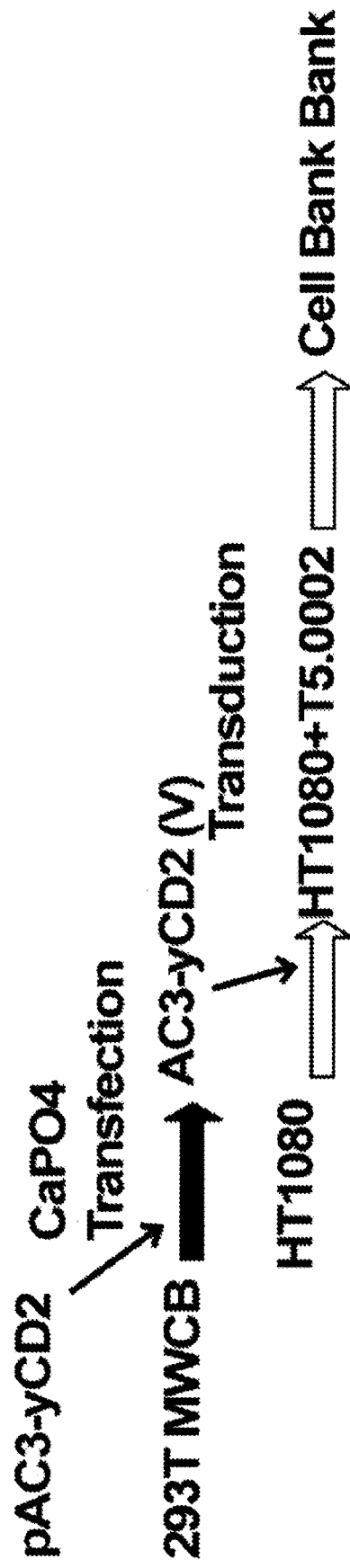


**FIGURE 1**

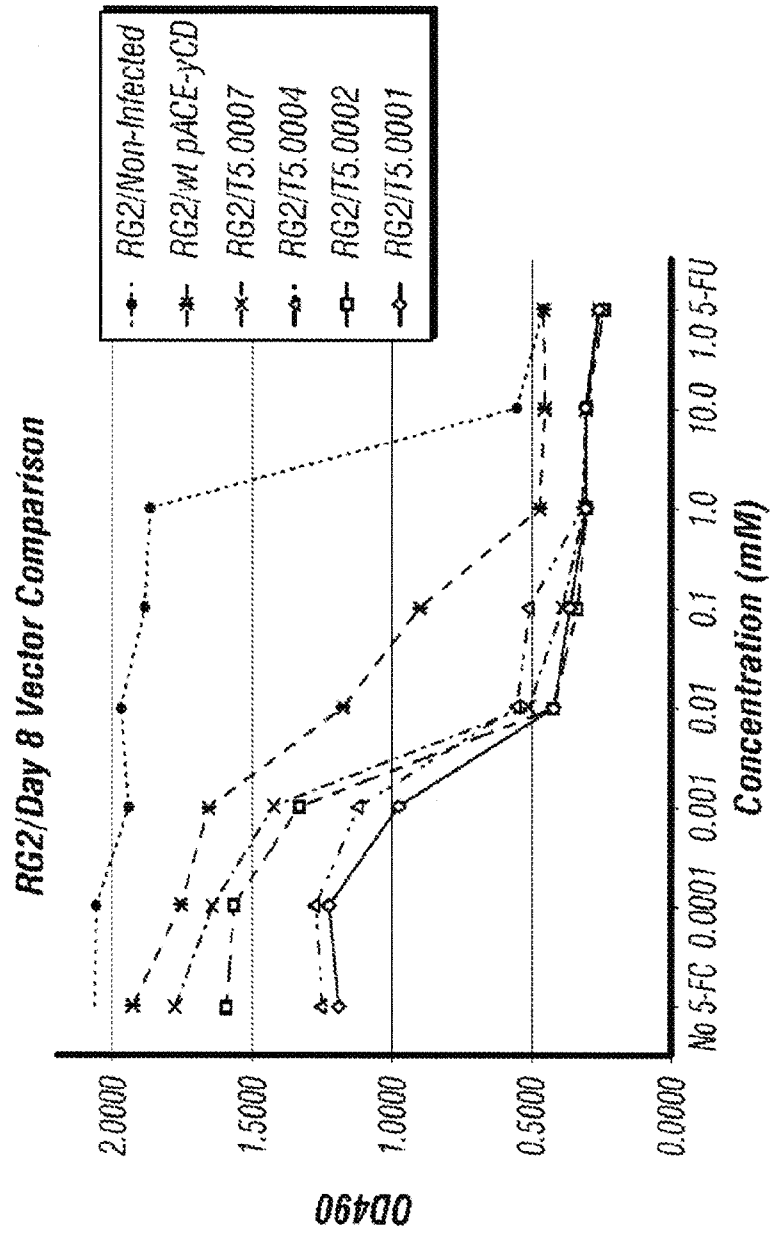


FIG. 2

Legend ref.	Reference name	Original Name	Other names	5' UTR PROMOTER	Envelope	Vector	IRES	Transgene	3'LTR	Notes
T5.0001	pAC3-yCD1	CDypt sequence		CMV	Ampho (40704)	pAC3- <i>end</i>	EMCV	yeastCD		hu codon
T5.0002	pAC3-yCD2	CDypt + 3pt		CMV	Ampho (40704)	pAC3- <i>end</i>	EMCV	yeastCD		hu codon + 3pt mutations
T5.0003	pAC3-yCD-U	CD-UPRT		CMV	Ampho (40704)	pAC3- <i>end</i>	EMCV	yeastCD		hu codon + 3pt mut UPRT fusion
T5.0004	pAC3-yCD2-O	CDypt + 3pt-OPRT		CMV	Ampho (40704)	pAC3- <i>end</i>	EMCV	yeastCD		hu codon + 3pt mut OPRT fusion
T5.0005	pAC3-yCD2-LO	CDypt + 3pt-LINK-OPRT		CMV	Ampho (40704)	pAC3- <i>end</i>	EMCV	yeastCD		hu codon + 3pt mut-LINKOPRT fusion
T5.0006	pAC3-eGFP	pACE- <i>end</i>	pACE-GFP	CMV	Ampho (40704)		EMCV	Emerald GFP	MLV U3	Emerald GFP
T5.0007	pAC3-yCD			CMV	Ampho (40704)		EMCV	Wt yeast CD	MLV U3	

FIG. 2 (Cont'd)

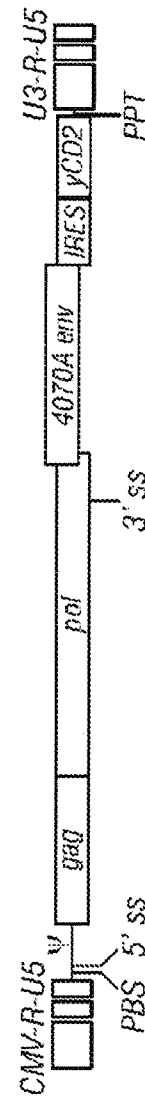


FIG. 34

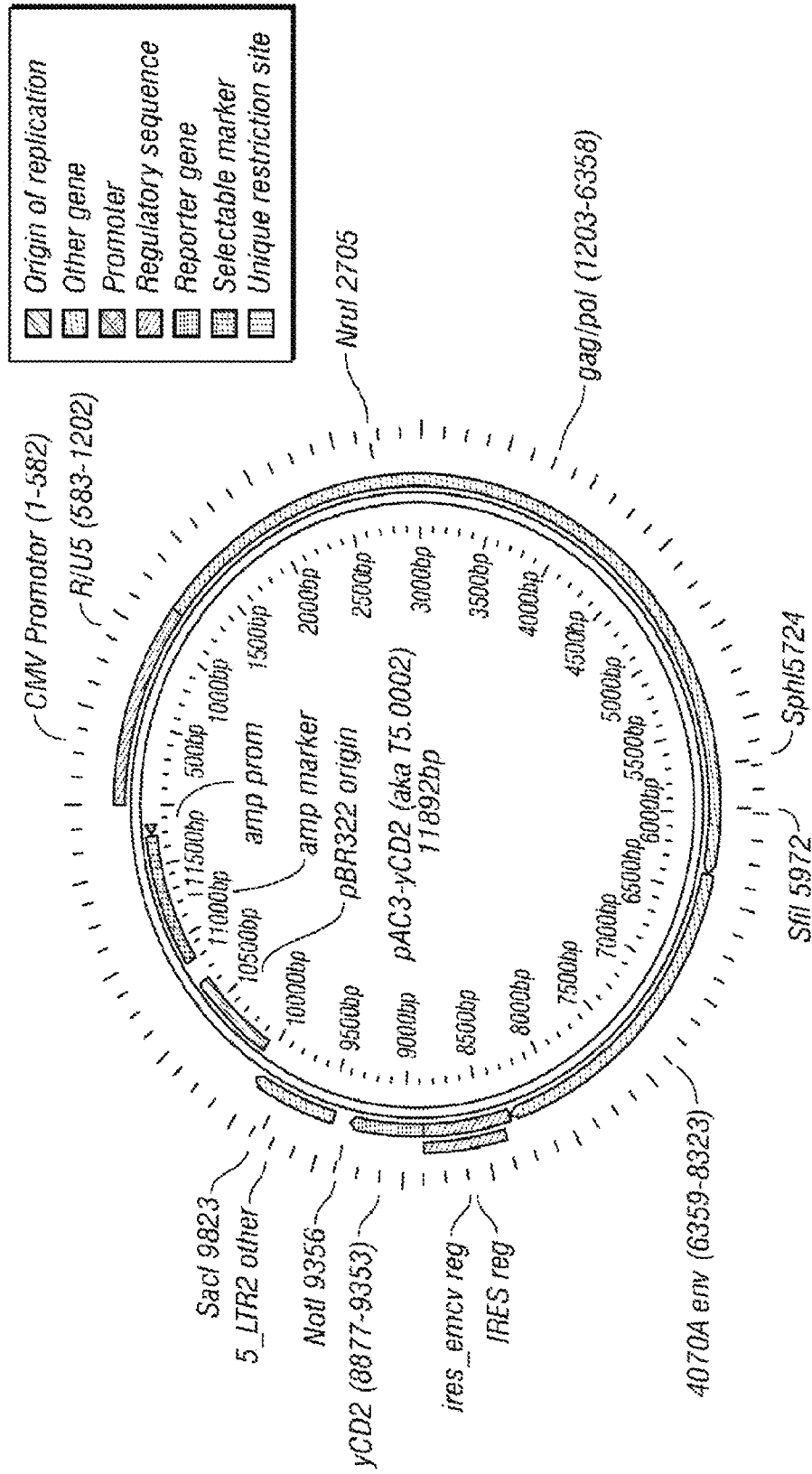


FIG. 3B

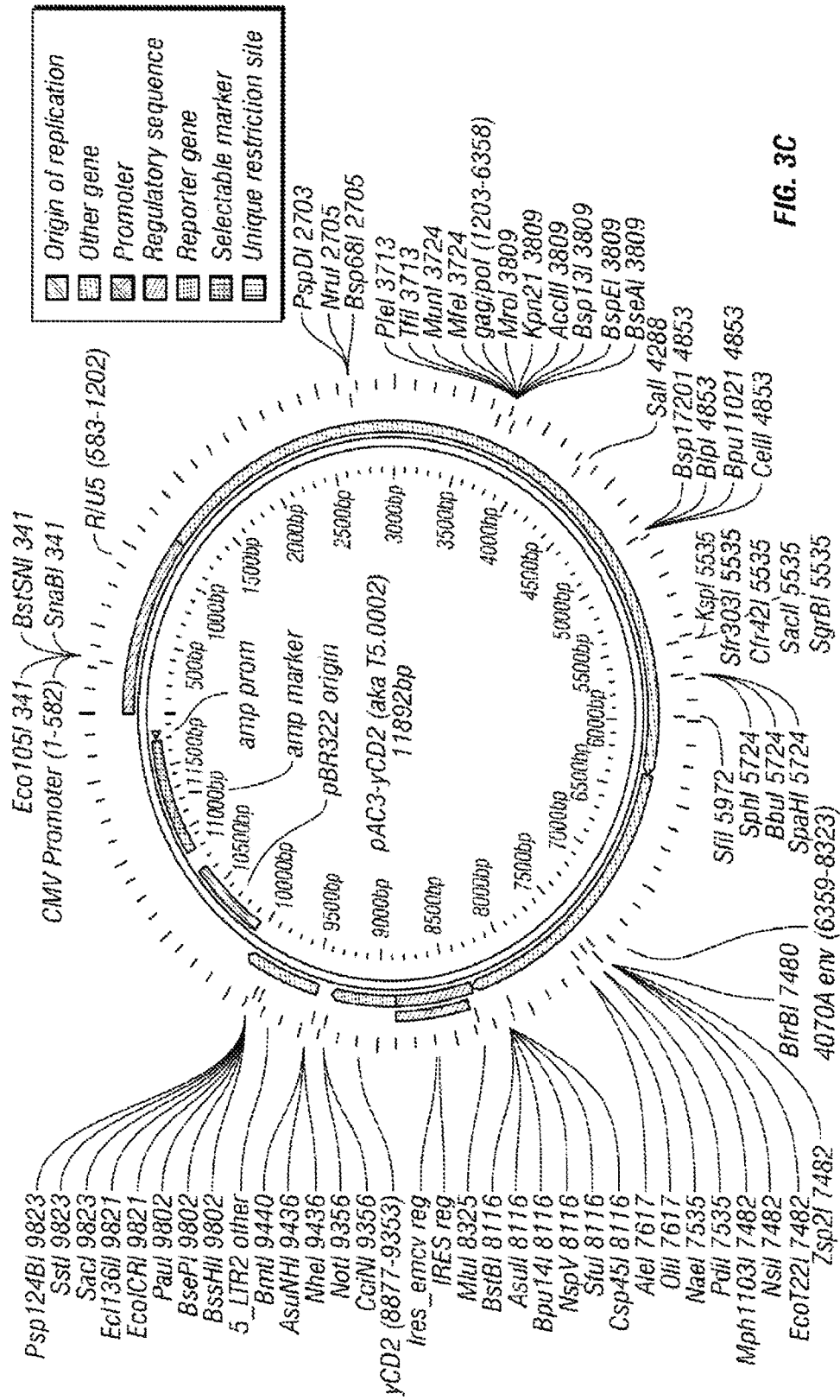


FIG. 3C

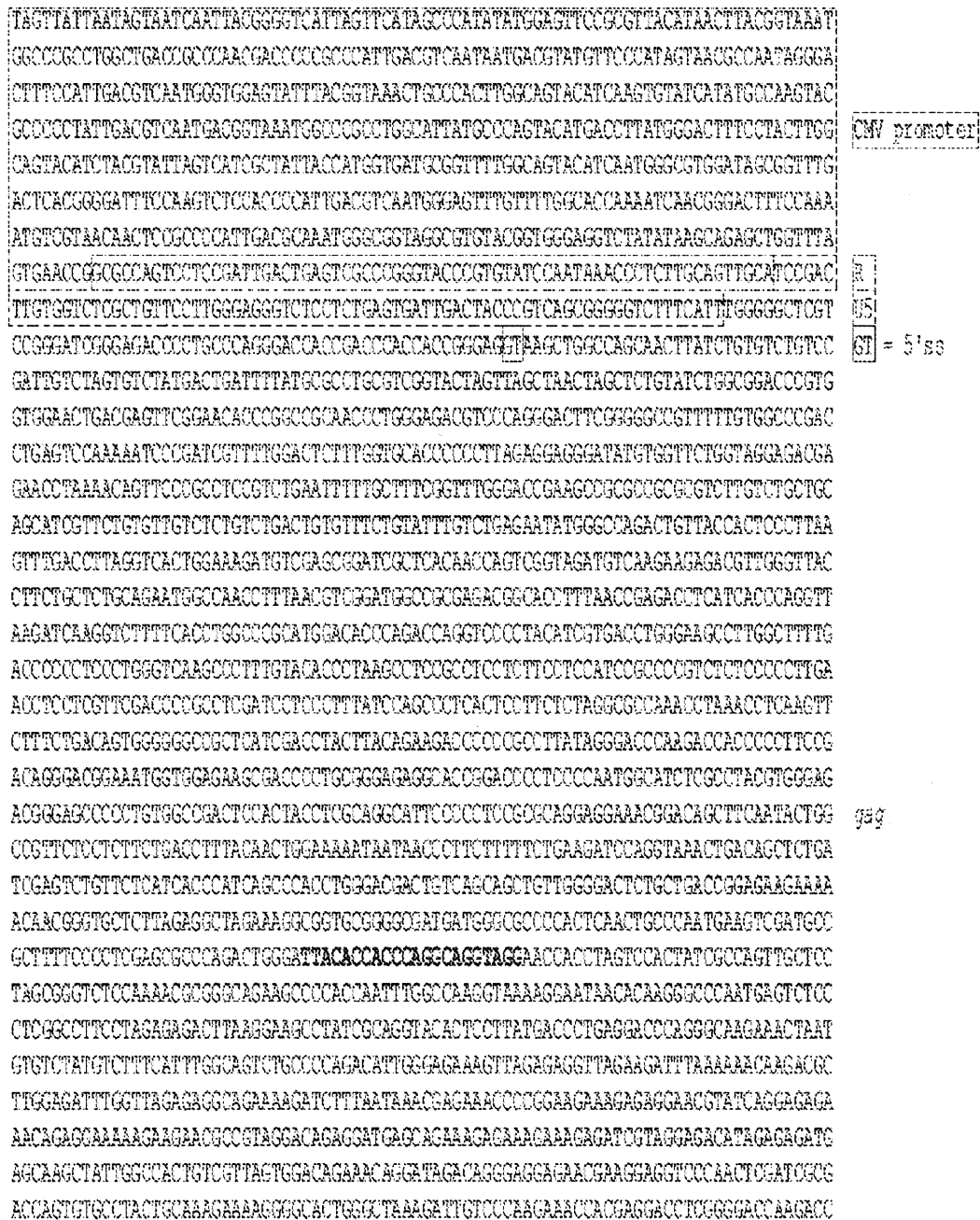


FIGURE 3D

CCAGACCTCCCTCCTGACCTAGATGACTAGGAGGTGAGGTGAGGAGCCCCCTGAAACCCAGGATACCCCTCAAAGTC
 GGGGGGCAACCCGTCACCTTCCTGGTAGATACTGGGGCCCAACACTCCGTGCTGACCCAAAATCCTGGACCCCTAAGTGATA
 AGTCTGCCTGGGTCCAAAGGGCTACTGGAGCAAGCGGTATCCTGGACCAAGATCGCAAAGTACATCTAGCTACCGTTAA
 GGTCCACCACTCTTCTCCATGTACAGACTGTCCCTATCTCTGTTAGGAAGAGATTGCTGACTAAACTAAAGGCCAA
 ATCCACTTTGAGGGATCAGGAGCCAGGTATGGGACCAATGGGGCAGCCCTGCAAGTGTGAGCCCTAAATATAGAGATG
 AGCATCGCTACATGAGACCTCAAAAGAGCCAGATGTTCTCTAGGGTCCACATGGCTGTCTGATTTCCTCAGGCCCTGGGC
 GGAAACCGGGGATGGGACTGGCAGTTGGCAAGCTCTCTGATCATACCTGTGAAGCAACCTCTACCCCGGTGTCATTA
 AAACATATACCCATGTCAAGAGAGCCAGACTGGGGATCAAGGCCACATACAGAGACTGTGGACCAAGGATACCTGGTAC
 CTTGCCAGTCCCTCTGCAACAGCCCTGTACCCCTTAAGAAAACAGGGAATTAATGATTATAGGCTGTCCAGGATCTGAG
 AGAAGTCAACAGCGGTGGAGAGATCCACCCACCGTCCACACCTTACAACTCTTGAGCGGGCTCCACCGTCCAC
 CAGTGGTACACTGTGCTTGATTAAAGGATGCCCTTTTCTGCTGAGACTCCACCCACAGTCAAGCTCTCTCTGGCTTTG
 AGTGGAGAGATCCAGAGATGGGAATCTCAGGACAAITGACCTGGACAGACTCCACAGGGTTTCAAAGCAGTCCACCT
 GTTGTGATGAGGCACTGCAAGAGACCTAGCAGACTTCGGATCCAGCAGCCAGACTTGATCTGTGATCAGTACGTGGATGAC
 TTAAGTCTGGCGGCACTCTGAGCTAGACTGCACCAAGGTACTGGGGCTGTTCACAAACCTAGGGAACCTGGTATC
 GGGCTCTGGGCAAGAAAGCCAAATTTGCCAGAAACAGGTCAAGTATCTGGGGTATCTTCTAAAGAGGCTCAGAGATGGCT
 GACTGAGGCCAGAAAGAGACTGTGATGGGGCAGCTACTCCAGAGCCCTGGACACCTAAGGAGTTCTAGGGAGGGCA
 GGGTCTGTGCTGCTCTGATCCCTGGTTTGCAAGATGGCAGCCCTTGTACCTCTCACCAAAACGGGACTCTGTTTA
 ATTGGGGCCAGACCAACAAAGGCTATCAAGAAATCAAGCAAGTCTTCTAAGTCCCGAGCCCTGGGGTTGCCAGATT
 GACTAAGCCCTTTGAAGTCTTTGTGACAGAGAGCAGGGCTACGGCAAGGTGTCTAACGCAAAACTGGGACCTTGGGT
 CGGCCGTTGGCTAGCTGTCCAAAAGCTAGATCCAGTAGCAGCTGGGTGGCCCTTGCCTAGGGATGGTAGCAGCCATTG
 CCGTACTGACAAAGATGCAAGGCAAGCTAACCATGGGACAGCCACTAGTCACTTCTGGCCCTCATGCASTAGAGGCACTAGT
 CAACCAACCCCGACCGCTGGCTTTCCAGCGCCCGGATGACTACTATCAGGCTTGGCTTTGGACACGGACCGGCTCCAG
 TTGGGACCGGTGCTAGCTCTGAAACCGGCTACGCTGCTCCACTGCTTGAAGAGGGCTGCAACACAGCTGCTTGTATCC
 TGGCGAGAGCCCGGAAACCGGACCTAACGGACAGCGCTCCAGAGCGCGACCAACCTGGTACAGGATGGAG
 CAGTCTCTTACAGAGAGGACAGCTAAGCGGCAAGCTGCGGTCAACACCGAGGCGAGTAACTCTGGGCTAAAGCCCTGCCA
 GCCGGGACATCCGCTCAGCGGGCTGAAGTATAGCACTCAGCCAGGCCCTAAAGATGGCAGAGGTAAGAAGCTAAATGTTT
 ATACTGATAGCCCTTATGCTTTTCTACTGCCCATATCATGAGAAATATACAGAGGCGTGGGTGCTCAGATCAGAAAG
 CAAAGAGTCAAAAATAAAGACGAGATCTTGGCTTACTAAAGCCCTCTTCTGCCAAAAGACTTAGCATATCCATTCT
 CCAGGACATCAAAAGGACACAGCGCGGCTAGAGGCAAGCGGATGGCTGACCAAGCGGCCGAAAGGACAGCATCAG
 AGACTCAGACACTCTACCTCTCATAGAAATTCATCACCTACACCTCAGAACATTTTCATTACACAGTGAATAT

[p1]

FIGURE 3D (cont'd)



FIGURE 3D (cont'd)

CMV Promotor (1-582)>>>

```

1  TAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCG 60
   ATCAATAATTATCATTAGTTAATGCCCCAGTAATCAAGTATCGGGTATATACCTCAAGGC

61  CGTTACATAACTTACGGTAAATGGCCCCGCTGGCTGACCGCCCAACGACCCCGGCCATT 120
   GCAATGTATTGAATGCCATTTACCGGGCGGACCGACTGGCGGGTTGCTGGGGGGGGGTAA

121  GACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCA 180
   CTGCAGTTATTACTGCATACAAGGGTATCATTCGCGTTATCCCTGAAACGTAACCTGCACT

181  ATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCC 240
   TACCCACCTCATAAATGCCATTTGACGGGTGAACCGTCATGTAGTTCACATAGTATACGG

241  AAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTTATGCCAGTA 300
   TTCATGCGGGGGATAACTGCAGTTACTGCCATTTACCGGGCGGACCGTAATACGGGTCAT

```

Eco105I

|

SnaBI

|

EcoSNI

|

```

301  CATGACCTTATGGGACTTTCTTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTAC 360
   GTACTGGAATACCCGAAAGGATGAACCGTCATGTAGATGCATAATCAGTAGCGATAATG

361  CATGGTGATGCGGTTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGAATCAGGGG 420
   GTACCACTACGCCAAAACCGTCATGTAGTTACCCGCACCTATCGCCAAACTGAGTCCCCC

421  ATTTCCAACTCTCCACCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACG 480
   TAAAGGTTCAAGAGGTGGGTAACCTGCAGTTACCCCTCAAACAAAACCGTGGTTTTAGTTGC

481  GGACTTTCCAAAATGTGTAACAACTCCGCCCCATTGACGCCAATGGGCGGTAGGCGTGT 540
   CCTGAAAGGTTTTACAGCATTGTTGAGGCGGGGTAACCTGCGTTTACCGCCCATCCGCACA

```

R region (583-650)>>>

|

```

541  ACGGTGGCAGGTCTATATAAGCAGAGCTGTTTAGTGAACCGCGGCCACTCCTCCCATTC 600
   TGCCACCCCTCCAGATATATTGCTCTGACCAAATCACTTGGCCGCGGTGAGGAGGCTAAC

```

FIGURE 3E

05 region (651-1202)>>>

601 ACTGAGTCGCCCCGGGTACCCGTGTAATCCAAATAAACCCCTCTTGCAAGTTGCATCCGACTTGT 660
TGAATCAGCGGGGCCCATGCGGCACATAGGTTATTTGGGAGAACGTCACGTTAGGCTGAACA

661 GGTCTCGCTGTTCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTC 720
CCAGAGCGACAAGGAACCCCTCCAGAGGAGACTCACTAAGTATGGGAGTCCGCCCCAG

721 TTTCATTTGGGGGCTCGTCCGGGATCGGGAGACCCCTGCCAGGGACACCGACCCACCA 780
AAAGTAAACCCCCGAGCAGGCCCTAGCCCTCTGGGGAGGGTCCCTGCTGGCTGGGTGGT

5'SS (788)

781 CCGGGAGGTAAGCTGGCCAGCAACTTATCTGTGTCGTCCGATTGCTAGTGTCTATGAC 840
GGCCCTCCATTCCAGCCGGTCTGTAATAGACACAGACAGGCTAACAGATCACAGATACTG

841 TGATTTTATGCGGCTGGGTCCGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCG 900
ACTAAAATACGGCGACCCAGCCATGATCAATCGATTGATCGAGACATAGACCGCCTGGGC

901 TGGTGGAACTGACGAGTTCCGAAACACCGGGCCCAACCCCTGGGAGACGTCCAGGGACTT 960
ACCTCCTTGACTGCTCAAGCTTTGTGGGCCGGCGTTGGGACCTCTGCGAGGGTCCCTGAA

961 CCGGGGCCCTTTTGTGGCCCGACCTGAGTCCAAAATCCCGATCGTTTGGACTCTTTG 1020
GCCCCCGGCAAAACACCGGGCTGGACTCAGGTTTTTAGGGCTAGCAAAACCTGAGAAAC

1021 GTGCACCCCTTASAGGAGGATATCTGGTCTCGGTAGGAGACGAGAACCTAAACAGT 1080
CAGCTGGGGGAATCTCTCCCTATACACCAAGACCATCTCTCTCTTGGATTTTGTCA

1081 TCCCGGCTCCGCTCTGAATTTTGGCTTTGGGTTTGGGACCGAAGCCGGCCGGCGGCTCTG 1140
AGGGCTGAGGCAGACTTAAAAACCAAGCCAAACCCCTGGCTTCGGCGGGCGGCGAGAAC

1141 TCTGCTGCAGCATCTTTCTGTGTTGTCTCTGCTGACTGTGTTCTGTATTTGTCTGAGA 1200
AGACGACTCTGTAGCAAGACACAACAGAGACAGACTGACACCAAGACATTAACAGACTCT

gag (1203, 2819)>>>

1201 ATATGGGCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAGATGTGG 1260
TATACCCGCTCTGCAATGCTCAGGGAATTCAAACTGCAATCCAGTGAACCTTTCTACAGT

1261 AGCGGATCCCTCACAAACAGTCCGTAGATGTCAAGAGAGAGGTTGGGTTACCTTCTGCT 1320
TCGCTTAGCGAGTGTGTGTCAGCCATCTACAGTTCTTCTCTGCAACCCANTGGAAGCGA

1321 CTGCAGATGGCCAAACCTTTAAGCTCGGATGCCCCGAGACGGCACCTTTAAGCGAGACC 1380
GAGCTCTTACCGGTTGGAANTTGCAGCCTACCGGGCTCTGCCGTGGAATTTGCTCTGG

1381 TCATCACCCAGGTTAAGATCAAGGCTCTTTTCACTGCCCCGCTTGGACACCCAGACCCAGG 1440
AGTAGTGGGTCCAATTTCTAGTTCCAGAAAGTGGACCGGGGTACCTGTGGGTCTGGTCC

1441 TCCCTACATCGTGACCTGGGAGGCTTGGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCT 1500
AGGGATGTAGCACTGGACCTTCGGAACCGAAACTGGGGGAGGGACCCAGTTCCGGG

FIGURE 3E (cont'd)

1501 TTGTACACCCCTAAGCCTCCGCTCCTCTTCCCTCCATCCGCCCCGTCTCTCCCCCTTGAAC 1560
 AACATGTGGGATTCCGAGGCGCAGGAGAAGGAGCTAGGCGGGGCAGAGAGGGGGAACCTG
 1561 CTCCTCGTTCCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCACTCCTTCTCTAGGCG 1620
 GAGGAGCAAGCTGGGGCGGAGCTAGGAGGGAATAGGTCCGGAGTGAGGAAGAGATCCGC
 1621 CCAAACCTAAACCTCAAGTTCTTTCTGACAGTGGGGGGCCGCTCATCGACCTACTTACAG 1680
 GGTTTTGGATTGGAGTTCAGAAAGACTGTCACCCCCCGGCGAGTAGCTGGATGAATGTU
 1681 AAGACCCCCCGCTTATAGGGAACCAAGACCACCCCCCTCCGACAGGGACGGAANTGGTG 1740
 TTCTGGGGGCGGAATATCCCTGGGTCTGGTGGGGGAAGGCTGTCCCTGCCTTTACCAC
 1741 GAGAAGCGACCCCTCGGGGAGAGGCACCGACCCCTCCCAATGGCATCTCGCTACGTG 1800
 CTCTTCGCTGGGGACGCCCTCTCCGTGGCTGGGGAGGGGTTACCGTAGAGCGGATGCAC
 1801 GGAGACGGGAGCCCCGTGTGGCGGACTCCACTACCTCGCAGGCATTCCCCCTCCGCGCAG 1860
 CCTCTGCCCTCGGGGACACCGGCTGAGGTGATGGAGCGTCCGTAAGGGGGAGGCGCGTC
 1861 GAGGAAACGGACAGCTTCAATACTGGCGGTTCTCCTCTTCTGACCTTTACAACTGGAAAA 1920
 CTCCTTTGCCTGTGGAAGTTATGACCGGCAAGAGGAGAAGACTGGAAATGTTGACCTTTT
 1921 ATAATAACCCCTTCTTTTTCTGAAGATCCAGGTAAACTGACAGCTCTGATCGAGTCTGTTT 1980
 TATTATTGGGAAGAAAAAGACTTCTAGGTCCATTGACTGTCGAGACTAGCTCAGACAAG
 1981 TCATCACCCTATCAGCCACCTGGGACGACTGTCAGCAGCTGTTGGGGACTCTGCTGACCG 2040
 AGTAGTGGGTAGTCGGGTGGACCTGCTGACAGTCTGTCGACAACCCCTGAGACGACTGGC
 3121 ACTTTGAGGGATCAGGAGCCAGGTTATGGCACCAGTGGGGCAGCCCTGCAAGTGTGA 3180
 TGAAACTCCCTAGTCTCGGGTCCAATACCCCTGCTTACCCCGTCGGGGACGTTCAAACT
 3181 CCTAAATATAGAAGATGAGCATCGGCTACATGAGACCTCAAAAGAGCCAGATGTTTCTC 3240
 GGGATTATATCTTCTACTCGTAGCCGATGTACTCTGGAGTTTTCTCGGTCTACAAAGAG
 3241 TAGGCTCCACATGGCTGTCTGATTTTCTCAGGCCTGGGCGGAAACCGGGGGCATGGGAC 3300
 ATCCCAGGTGTACCGACAGACTAAAAGGAGTCCGGACCCGCTTTGGCCCCGTACCCCTG
 3301 TGGCAGTTCCGCAAGCTCCTCTGATCATACCTCTGAAAGCAACCTCTACCCCGGTGCCA 3360
 ACCGTCAAGCGGTTCGAGGAGACTAGTATGCAGACTTTCGTTGGAGATGGGGGCACAGGT
 3361 TAAACAATACCCCATGTCAAGAAGCCAGACTGGGGATCAAGCCCCACATACAGAGAC 3420
 ATTTTGTATGGGGTACAGTGTCTTCGGTCTGACCCCTAGTTGCGGGGTGTATGTCTCTG
 3421 TGTTGGACCAAGGAATACTGGTACCTGCCAGTCCCCCTGGAACAGGCCCTGTACCCG 3480
 ACAACCTGCTCCCTTATGACCATGGGACGCTCAGGGGGACCTTGTGCGGGGACGATGGGC
 3481 TTAAGAAACCAAGGACTAATGATTATAGGCCTGTCCAGSATCTGAGAGAAGTCAACAAGC 3540
 AATTCCTTGGTCCCTGAATTAATATCCGACAGGTCTTAGACTCTCTTCAGTTGTTCTG

3' SS (3314)

FIGURE 3E (cont'd)

```

3541 GGGTGGGAAGACATCCACCCACCGTGCCCAACCCCTTACAACCTCTTGAGCGGGCTCCCAC 3600
    CCCACCTTCTGTAGGTGGGGTGGCACGGGTTGGGAATGTTGGAGAAGTCCGCCGAGGGTG

3601 CGTCCCAACAGTGGTACACTGTGCTTGATTAAAGGATGCCCTTTTCTGCCTGAGACTCC 3660
    GCAGGGTGGTCACCATGTGACACGAAGTAAATTTCTACGGAAAAAGACGGACTCTGAGG

                                     PfeI
                                     |
                                     TfiI
                                     |
3661 ACCCCACCAAGTCAGCCTCTCTTGGCCTTTGAGTGGAGAGATCCAGAGATGGGAATCTCAG 3720
    TGGGGTGGTCAGTCGGAGAGAAGCGGAAACTCACCTCTCTAGCTCTCTACCCCTTAGAGTC

    MfeI
    |
    MunI
    |

3721 GACAAATTGACCTGGACCAGACTCCCACAGGGTTTCAAAAACAGTCCCACCCCTGTTTGATG 3780
    CTGTTAACTGGACCTGGTCTGAGGGTGTCCCAAAGTTTTGTCAGGGTGGGACAAACTAC

                                     MroI
                                     |
                                     BseAI
                                     |
                                     Bsp13I
                                     |
                                     BspEI
                                     |
                                     Kpn2I
                                     |
                                     AccIII
                                     |

3781 AGGCACTGCACAGAGACCTAGCAGACTTCCGGATCCAGCACCCAGACTTGATCCTGCTAC 3840
    TCCGTGACGTGTCTCTGGATCGTCTGAAGGCCTAGGTGCTGGGTCTGAAGTAGGACGATG

3841 AGTACGTGGATGACTTACTGCTGGCGGCCACTTCTGAGCTAGACTGCCAACAGGTACTC 3900
    TCATGCACCTACTGAATGACGACCGGCGGTGAAGACTCGATCTGACGGTTGTTCCATGAG

3121 ACTTTGAGGGATCAGGAGCCCAAGTTATGGGACCAATGGGGCAGCCCTGCAAGTGTGTA 3180
    TGAAACTCCCTAGTCCTCGGGTCCAATACCCTGGTTACCCCGTCGGGGACGTTACAACT

3181 CCCTAAATATAGAAGATGAGCATCGGCTACATGAGACCTCAAAAGAGCCAGATGTTTCTC 3240
    GGCATTTATATCTTCTACTCGTAGCCGATGTAATCTGGAGTTTTCTCGGTCTACAAAGAG

3241 TAGGGTCCACATGGCTGTCTGATTTTCTCAGGCCTGGGCGGAAACGGGGGCATGGGAC 3300
    ATCCCAGGTGTACCGACAGACTAAAAGGAGTCCGGACCCGCTTTGGCCCCCGTACCTG

```

FIGURE 3E (cont'd)

3' SS (3314)

3301 TGGCAGTTCGCCAAGCTCCTCTGATCATACTCTGAAAGCAACCTCTACCCCCGTGTCCA 3360
 ACOGTCAAGCGGTTCGAGGAGACTAGTATGGAGACTTTTCGTTGGAGATGGGGGCACAGGT

3361 TAAAACAATACCCCATGTCAACAAGAAGCCAGACTGGGGATCAAGCCCCACATACAGAGAC 3420
 ATTTTCTTATGGGCTACAGTGTTCCTTCGGTCTGACCCCTAGTTTCGGGTGTATGTCTCTG

3421 TGTTCGACACAGGGAATACTGGTACCCCTGCCAGTCCCCCTGGAAACACGCCCTGCTACCCG 3480
 ACAACCTGGTCCCTTATGACCATGGGACGGTCAGGGGGACCTTGTGCGGGACGATGGGC

3481 TTAAGAAACCAGGACTAATGATTATAGGCCTGTCCAGGATCTGAGAGAAGTCAACAAGC 3540
 AATTCTTTGGTCCCTGATTACTAATATCCGGACAGGTCTAGACTCTCTTCAGTTGTTTCG

3541 GCGTGGAAAGACATCCACCCCACTGCCCCAACCCCTTACAACCTCTTGAGGGGGCTCCAC 3600
 CCCACCTTCTGTAGGTGGGGTGGCAGGGTTGGGATGTTGGAGAACTCGCCCCAGGGTG

3601 CGTCCCACAGTGGTACACTGTGCTTGATTTAAAGGATGCCTTTTTCTGCCTGAGACTCC 3660
 GCAGGGTGGTCACCATGTGACACGAATAAATTCCTACGGAAAAAGACGGACTCTGAGG

PfeI
 |
 TfiI
 |

3661 ACCCCACCACTCAGCCTCTCTTCGCCCTTTGAGTGGAGAGATCCAGAGATGGGAATCTCAG 3720
 TGGGGTGGTCAGTCGGAGAGAAAGCGGAAACTCACCTCTCTAGGTCTCTACCCCTAGAGTC

MfeI
 |
 MunI
 |

3721 GACAATTGACCTGGACACAGACTCCACAGGGTTTCAAAAACAGTCCCACCCCTGTTTGATG 3780
 CTGTTAACTGGACCTGGTCTGAGGGTGTCCCAAAGTTTTTGTGAGGGTGGGACAAACTAC

MroI
 |
 BseAI
 |
 Bsp13I
 |
 EspEI
 |
 Kpn2I
 |
 AccIII
 |

3781 AGGCACTGCACAGAGACCTAGCAGACTTCGGGATCCAGCACCCAGACTTGATCCTGCTAC 3840
 TCCGTGACGTGTCTCTGGATCGTCTGAAGGCCTAGGTCTGGGTCTGAAGTAGGACGATG

FIGURE 3E (cont'd)

3841 AGTACGTGGATGACTTACTGCTGGCCGCCACTTCTGAGCTAGACTGCCAACAAGCTACTC 3900
 TCATGCACCTACTGAATGACGACCGGCGGTGAAGACTCGATCTGACGGTTGTTCCATGAG
 3901 GGGCCCTGTTACAAACCCTAGGGAACCTCGGGTATCGGGCCTCGGCCAAGAAAGCCCAAA 3960
 CCGGGGACAATGTTTGGGATCCCTTGGAGCCCATAGCCCGGAGCCGGTCTTTTGGGGTTT
 3961 TTTGCCAGAAACAGGTCAAGTATCTGGGCTATCTTCTAAAAGAGGGTCAGAGATGGCTGA 4020
 AAACGGTCTTTGTCCAGTTCATAGACCCCATAGAAGATTTTCTCCAGTCTCTACCGACT
 4021 CTGAGGCCAGAAAAGAGACTGTGATGGGGCAGCCTACTCCGAAGACCCCTCGACAATAA 4080
 GACTCCGGTCTTTTCTCTGACACTACCCCGTCGGATGAGGCTTCTGGGGAGCTGTTGATT
 4081 GGGAGTTCTTAGGGACGGCAGGCTTCTGTGCCTCTGGATCCCTGGGTTTGCAGAAATGG 4140
 CCTCAAGGATCCCTGCCGTCCGAAGACAGCGGAGACCTAGGGACCCAAACGTCTTTACC
 4141 CAGCCCCCTTGTACCCCTCTCACCAAAACGGGGACTCTGTTTAAATTGGGGCCAGACCAAC 4200
 CTCGGGGGAACATGGGAGAGTGGTTTTGCCCTGAGACAAATTAACCCCGGCTCTGGTTG
 4201 AAAAGGCCTATCAAGAAATCAAGCAAGCTCTTCTAACTGCCCCAGCCCTGGGGTTGCCAG 4260
 TTTTCCGGATAGTTCTTTAGTTGTTTCGAGAAGATTGACGGGGTCGGGACCCCAACGGTC

SalI
|

4261 ATTTGACTAAGCCCTTTGAACCTCTTTGTGACGAGAGCAGGGCTACGCCAAAGGTGTCC 4320
 TAAACTGATTCCGGGAAACTTGAGAAACAGCTGCTCTTCGTCCCGATGCGGTTTCCACAGG
 4321 TAACGCCAAAAACTGGGACCTTGGCGTCGGCCGGTGGCCTACCTGTCCAAAAGCTAGACC 4380
 ATTGCGTTTTTTGACCCCTGGAACCGCAGCCGGCCACCGGATGGACAGGTTTTTCGATCTGG
 4381 CAGTAGCAGCTGGGTGGCCCCCTTGCCCTACGGATGGTAGCAGCCATTGCCGTACTGACAA 4440
 GTCATCGTCGACCCACCGGGGGAACGGATGCCTACCATCGTCGGTAACGGCATGACTGTT
 4441 AGGATGCAGGCAAGCTAACCATGGGACAGCCACTAGTCATTCTGGCCCCCATCGCAGTAG 4500
 TCCTACGTCCGTTGCGATTGGTACCCTGTGCGTGATCAGTAAGACCGGGGGGTACGTCATC
 4501 AGGCACTAGTCAAACAACCCCCCGACCGCTGGCTTTCCAACGCCCGGATGACTCACTATC 4560
 TCCGTGATCAGTTTGTGGGGGGCTGGCGACCGAAAGGTTGCGGGCTACTGAGTGATAG
 4561 AGGCCTTGCTTTTGGACACGGACCGGGTCCAGTTCGGACCGGTGGTAGCCCTGAACCCGG 4620
 TCCGGAACGAAAACCTGTGCCTGGCCAGGTCAAGCCTGGCCACCATCGGSACTTGGGCC
 4621 CTACGCTGCTCCCACTGCCTGAGGAAGGGCTGCAACACAACCTGCCTTGATAATCCTGGCCG 4680
 GATGCGACGAGGGTGACGGACTCCTTCCCGACGTTGTGTTGACGGAACATAGGACCGGC
 4681 AAGCCACGGAACCGACCCGACCTAACGGACCGCGCTCCAGACGCCGACCCACACCT 4740
 TTCCGGTGCCCTTGGGCTGGGCTGGATTGCCTGGTCGGCGAGGCTCTGCGGCTGGTGTGGA
 4741 GGTACACGGATGGAAGCAGTCTCTTACAAGAGGGACAGCGTAAGGCGGGAGCTGCGGTGA 4800
 CCATGTGCCTACCTTCGTGAGAGAATGTTCTCCCTGTGCGCATTCGCCCTCGACGCCACT

FIGURE 3E (cont'd)

HspI
 |
 CclII
 |
 Bpu1102I
 |
 Bsp1720I
 |
 4801 CCACCGAGACCGAGGTAATCTGGGCTAAAGCCCTGCCAGCCGGGACATCCGCTCAGCGGG 4860
 GGTGGCTCTGGCTCCATTAGACCCGATTTCCGGACGGTGGGCCCCGTAGGCGAGTCCGCC
 4861 CTGAACCTGATAGCACTCAGCCAGGCCCTAAAGATGCCAGAGGTAAGAAGCTAAATGTTT 4920
 GACTTGACTATCGTGAGTGGTCCGGGATTTCTACCGCTCTTCCATTCTTCGATTTCACAA
 4921 ATACTGATAGCGGTTATGCTTTTGGTACTGCCCATATCCATGGAGAAATATACAGAGGC 4980
 TATGACTATCGGCAATATGAAAACGATGACGGGTATAGGTACCTCTTTATATGTCTTCCG
 4981 GTGGGTTGCTCAGATCAGAGGCAAGGAGATCAAAATAAAGACGAGATCTTGGCCCTAC 5040
 CACCCAAAGAGTGTAGTCTTCCGTTTCTCTAGTTTTATTTCTGCTTATAGAACCGGGATG
 5041 TAAAGCCCTCTTTCTGCCCAAAGACTTAGCATAATCCATTGTCCAGGACATCABAAGG 5100
 ATTTTCGGGAGAAAGACGGGTTTTCTGAATCGTATTAGGTAACAGGTCCGTAGTTTTCC
 5101 GACACAGCGCCGAGGCTAGAGGCCAACCGGATGGCTGACCAAGCGGCCCGAAAGGCAGCCA 5160
 CTGGCTCGCGGCTCCGATCTCCGTTGGGCTACCGACTGGTTCCGCCGGCTTTCCGTCGGT
 5161 TCACAGAGACTCCAGACACCTCTACCCCTCTCATAGAAAATTCATCACCTTACACCTCAG 5220
 AGTGTCTCTGAGGCTCTGTGGAGATGGGAGGATATCTTTAAGTAGTGGGATGTGGAGTC
 5221 AACATTTTCATTACACAGTGAATGATATAAGGACCTAACCAAGTTGGGGGCCATTTATG 5280
 TTGTAAGTAATGTGTCACTGACTATATTTCCCTGGATTGGTTCAACCCCGGTAATAC
 5281 ATAAACAAAGAGTATTGGGCTACCAAGGAAACCTGTGATGCTGACCACTTTACTT 5340
 TATTTTGTTCCTTCATACCCAGATGGTTCTTTTGGACACTACGGACTGGTCAAAATGAA
 5341 TTGAATTATTAGACTTTCTTCATCAGCTGACTCACCTCAGCTTCTCAAAAATGAAGGCTC 5400
 AACTTAATAATCTGAAGCAAGTACTCGACTGAGTGGAGTCGAGAGCTTTTACTTCCGAG
 5401 TCCTAGAGAGAGCCACAGTCCCTACTACATGCTGAACCGGGATCGAACACTCAAAATA 5460
 AGGATCTCTCTTCEGTGTCAGGGATGATGTACGACTTGGCCCTAGCTTGTGAGTTTTTAT
 5461 TCAGTGAAGCTGCAAGCTTGTGCACAAGTCAACGCCAGCAAGTCTGCCGTTAAACAGG 5520
 AGTCACTCTGACGTTTCCAAACAGTGTTCAGTTGCCGTCGTTTCAGACGCCAATTTGTCC
 SacII
 |
 SgrBI
 |
 Cfr42I
 |
 Sfr593I
 |
 KspI
 |

FIGURE 3E (cont'd)

5521 GAACTAGGGTCCGCGGGCATCGGGCCGGCACTCATTGGGAGATCGATTTCAACCGAGATAA 5580
 CTTGATCCCAGCGCGCCCGTAGCCGGGCGGTGAGTAACCCCTCTAGCTAAAGTGGCTCTATT

 5581 AGCCCGGATTGTATGGCTATAAATATCTTCTAGTTTTTATAGATACCTTTTCTGGCTGGA 5640
 TCGGGCCTAACATACCGATATTTATAGAAGATCAAAAATATCTATGGAAAAGACCGACCT

 5641 TAGAAGCCTTCCCAACCAAGAAAGAAACCGCCAAGGTCGTAACCAAGAAGCTACTAGAGG 5700
 ATCTTCGGAAGGGTTGGTTCTTTCTTTGGCGGTTCCAGCATTGGTTCTTCGATGATCTCC

PaeI
 |
 BbuI
 |
 SpaHI
 |
 SphI
 |

 5701 AGATCTTCCCCAGGTTCCGGCATGCCTCAGGTATTGGGAAGTGAACAATGGGCCTGCCTTCG 5760
 TCTAGAAGGGGTCCAAGCCGTACGGAGTCCATAACCCCTTGACTGTTACCCGGACGGAAGC

 6901 CTTCCAAGGGGCTACTCGAGGGGGCAGATGCAACCCCTCTAGTCCTAGAATTCAGTGATGC 6960
 GAAGGTTCCCCGATGAGCTCCCCCGTCTACGTTGGGAGATCAGGATCTTAAGTACTAGTACG

 6961 AGGAAAAAAGGCTAACTGGGACGGGCCAAATCGTGGGGACTGAGACTGTACCGGACAGG 7020
 TCCTTTTTTCCGATTGACCCCTGCCCGGGTTTAGCACCCCTGACTCTGACATGGCCTGTCC

 7021 AACAGATCCTATTACCATGTTCTCCCTGACCCGGCAGGTCCTTAATGTGGGACCCCGAGT 7080
 TTGTCTAGGATAATGGTTACAAGAGGGAAGTGGGCGGTCCAGGAATTACACCCCTGGGGCTCA

 7081 CCCCATAGGGCCCAACCCAGTATTACCGAGCCAAAGACTCCCTTCCCTACCAATAGAGAT 7140
 GGGGTATCCCGGTTGGGTCATAATGGGCTGGTTTCTGAGGGAAGGAGTGGTTATCTCTA

 7141 TGTACCGGCTCCACAGCCACCTAGCCCCCTCAATACCAAGTACCCCCCTTCCACTACCAG 7200
 ACATGGCCGAGGTGTCGGTGGATCGGGGGAGTTATGGTCAATGGGGGAAGGTGATGGTC

 7201 TACACCCTCAACCTCCCTACAAGTCCAAGTGTCCCACAGCCACCCCCAGGAACTGGAGA 7260
 ATGTGGGAGTTGGAGGGGATGTTCAAGGTTACAGGGTGTGGGTGGGGTCCCTTGACCTCT

 7261 TAGACTACTAGCTCTAGTCAAAGGAGCCTATCAGGCGCTTAACCTCACCAATCCCGACAA 7320
 ATCTGATGATCGACATCAGTTTCCCTCGGATAGTCCGCGAATTGGAGTGGTTAGGGCTGTT

 7321 GACCCAAGAATGTGGCTGTCTTACTGTGCGGACCTCCTTATTACGAAGGAGTAGCGGT 7380
 CTGGGTTCTTACAACCGACACGAATCACAGCCCTGGAGGAATAATGCTTCCCTCATCGCCA

 7381 CGTGGGCACTTATACCAATCAATCCACCGCTCCGGCCAACTGTACGGCCACTTCCCAACA 7440
 GCACCCGTGAATATGGTTAGTAAAGTGGCGAGGCGGTTGACATGCCGGTGAAGGGTTGT

FIGURE 3E (cont'd)

```

                                EcoT22I
                                |
                                NsiI
                                |
                                Mph1103I
                                |
                                Zsp2I
                                |
                                BfrBI
                                |
                                |

7441 TAAGCTTACCCTATCTGAAGTGACAGGACAGGGCCTATGCATGGGGGCAGTACCTAAAAC 7500
    ATTCCAATGGGATAGACTTCACTGTCTCTGTCCCGGATACGTACCCCGTCATGGATTTTG

                                NaeI
                                |
                                PdiI
                                |
                                MroNI
                                |
                                NgoMIV
                                |
                                |

7501 TCACCAGGCCTTATGTAACACCACCCAAAGCGCCGCTCAGGATCCTACTACCTTGCAGC 7560
    AGTGGTCCGGAATACATTCTGGTGGGTTTCGCGGCCGAGTCCTAGGATGATGGAACTCG

                                AleI
                                |
                                OliI
                                |

7561 ACCCGCCGGAACAATGTGGGCTTGCAGCACTGGATTGACTCCCTGCTTGTCCACCACGGT 7620
    TGGGCGGCCTTGTTACACCCGAACGTCGTGACCTAACTGAGGGACGAACAGGTGGTGCCA

7621 GCTCAATCTAACCACAGATTATTGTGTATTAGTTGAACTCTGGCCCAGAGTAATTTACCA 7680
    CGAGTTAGATTGGTGTCTAATAACACATAATCAACTTGAGACCGGGTCTCATTAATGGT

6901 CTTCCAAGGGGCTACTCGAGGGGGCAGATGCAACCCCTCTAGTCCTAGAATTCAGTATGC 6960
    GAAGCTTCCCGATGAGCTCCCCCGTCTACGTTGGGAGATCAGGATCTTAAGTGACTACG

6961 AGGAAAAAAGGCTAACTGGGACGGGGCCAAATCGTGGGGACTGAGACTGTACCGGACAGG 7020
    TCCTTTTTTCCGATTGACCCCTGCCCGGGTTAGCACCCCTGACTCTGACATGGCCTGTCC

7021 AACAGATCCTATTACCATGTTCTCCCTGACCCGGCAGGTCCTTAATGTGGGACCCCGAGT 7080
    TTGTCTAGGATAATGGTACAAGAGGGACTGGGCCGTCCAGGAATTACACCCTGGGGCTCA

```

FIGURE 3E (cont'd)

7081 CCCCATAGGGCCCAACCCAGTATTACCCGACCAAAAGACTCCCTTCCTCACCAATAGAGAT 7140
 GGGGTATCCCGGGTTGGGTTCATAATGGGCTGGTTTCTGAGGGAAGGAGTGGTTATCTCTA
 7141 TGTACCGGCTCCACAGCCACCTAGCCCCCTCAATACCAGTTACCCCCCTTCCACTACCAG 7200
 ACATGCCCCGAGGTGTGGGTGGATCGGGGGAGTTATGGTCAATGGGGGGAAGGTGATGGTC
 7201 TACACCCCTCAACCTCCCCCTACAAGTCCAAGTGTCCCACAGCCACCCCCAGGAACTGGAGA 7260
 ATGTGGGAGTTGGAGGGCATGTTTCAGGTTACAGGGTGTGGGTGGGGTCCTTGACCTCT
 7261 TAGACTACTAGCTCTAGTCAAAGGAGCCTATCAGGCGCTTAACCTCACCAATCCCGACAA 7320
 ATCTGATGATCGAGATCAGTTTCCTCGGATAGTCCGCGAATTGGAGTGGTTAGGGCTGTT
 7321 GACCCAAGAATGTTGGCTGTGCTTAGTGTGGGACCTCCTTATTAAGAAGGAGTAGCGGT 7380
 CTGGGTTCCTTACAACUGACACGAATCACAGCCCTGGAGGAATAATGCTTCCTCATCGCCA
 7381 CTTGGGCACTTATACCAATCATTCCACCGCTCCGGCCAACTGTACGGCCACTTCCCAACA 7440
 GCACCCGTGAATATGGTTAGTAAGGTGGCGAGGCCGGTTACATGCCGGTGAAGGGTTGT

EcoT22I

|

NsiI

|

Mph1103I

|

Zsp2I

|

BfrBI

| |

7441 TAAGCTTACCCTATCTGAAGTGACAGGACAGGGCCTATGCATGGGGGACGTACCTAAAAC 7500
 ATTCGAATGGGATAGACTTCACGTGCTGTCCCGGATACGTACCCCGTCATGGATTTTG

NaeI

|

PdiI

|

MroNI

| |

NgoMIV

| |

7501 TCACCAGGCCTTATGTAACACCACCCAAAGCGCGGCTCAGGATCCTACTACCTTGCAGC 7560
 AGTGGTCCGGAATACATTGTGGTGGGTTTCGCGGCCGAGTCCTAGGATGATGGAACGTGC

FIGURE 3E (cont'd)

AlaI
|
OliI
|

7561 ACCCGCCGGACAAATGTGGGCTTGCAGCACTGGATTGACTCCCTGCTTGTCCACCACGGT 7620
TGGGCGGCCCTTGTACACCCGAACGTCGTCACCTAACTGAGGGACGAACAGGTGGTGCCA

7621 GGTCAATCTAACCACAGATTATTGTGTATTAGTTGAACTCTGGCCCAGAGTAATTTACCA 7680
CCAGTTAGATTGGTGTCTAATAACACATAATCAACTTCAGACCGGGTCTCATTAAATGCT

7681 CTCCCCCGATTATATGTATGGTCAGCTTGAACAGCGTACCAAATATAAAAGAGAGCCAGT 7740
GAGGGGGCTAATATACATACCAGTCGAACCTGTGCGCATGGTTTATATTTCTCTCGGTCA

7741 ATCATTGACCCCTGGCCCTTCTACTAGGAGGATTAACCATGGGAGGGATTGCAGCTGGAAT 7800
TACTAACTGGGACCGGGGAAGATGATCCTCTCTAATTTGGTACCCCTCCCTAACGTCGACCTTA

7801 AGGGACGGGGACCACTGCGCTTAATTAACCCAGCAGTTTGAGCAGCTTCATGCCGCTAT 7860
TCCCTGCCCCCTGGTGACGGAATTAATTTGGGGTCTCAAACCTGCTCGAAGTACGGCGATA

7861 CCAGACAGACCTCAACGAAGTCGAAAAGTCAATTACCAACCTAGAAAAGTCACTGACCTC 7920
GGTCTGTCTGGAGTTGCTTCAGCTTTTTCAGTTAATGGTTGGATCTTTTCAGTGACTGGAG

7921 GTTGTCTGAAGTAGTCTTACAGAACCGCAGAGGCTAGATTTGCTATTTCCTAAAGGAGGG 7980
CAACAGACTTCATCAGGATGTCTTGGCGTCTCGGGATCTAAACGATAAGGATTTCTCTCC

7981 AGGTCTCTGCGCAGCCCTAAAAGAAGAATGTTGTTTTATGCAGACCACACGGGGCTAGT 8040
TCCAGAGACGGCTCGGGATTTTCTTCTTACAACAAAAATACGTCTGGTGTGCCCCGATCA

8041 GAGAGACAGCATGGCCAAATTAAGAGAAAGGCTTAATCAGAGACAAAACTATTTGAGAC 8100
CTCTCTGTCTACCGGTTTAAATCTCTTTCCGAATTAGTCTCTGTTTTTGATAAACTCTG

NspV
|
BstBI
|
Bsp119I
|
AsuII
|
Csp45I
|
SfuI
|
Bpu14I
|
BspT104I
|

8101 AGGCCAAGGATGGTTTCGAAGGCTGTTTAATAGATCCCCCTGGTTTACCACCTTAATCTC 8160
TCCGGTTCTTACCAAGCTTCCCGACAAATTATCTAGGGGGACCAATGGTGAATTAGAG

FIGURE 3E (cont'd)

```

8161 CACCATCATGGGACCTCTAATAGTACTCTTACTGATCTTACTCTTTGGACCTTGCAATTCT 8220
      GTGGTAGTACCCGAGATTATCATGAGAATGACTAGAATGAGAAACCTGGAACCTAAGA

8221 CAATCGATTGGTCCAAATTTGTTAAAGACAGGATCTCAGTGGTCCAGGCTCTGGTTTTGAC 8280
      GTTAGCTAACCAGGTTAAACAATTTCTGTCTAGAGTCACCAGGTCCGAGACCAAAACTG

                                     IRES reg(8327,8876)>>>
                                     |
                                     MluI(8325)
                                     | |
8281 TCAGCAATATCACCAGCTAAAACCCATAGAGTACGAGCCATGAACGCCTTACTGGCCGAA 8340
      AGTCGTTATAGTGGTCGATTTTGGGTATCTCATGCTCGGTACTTGGCGCAATGACCGGCTT

                                     ires_emcv reg(8378,8876)>>>
                                     |
8341 GCGCGTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACCATATTGCCGT 8400
      CCGCGAACCTTATTCCGGCCACACGCAACAGATATAACAATAAAAGGTGGTATAACGGCA

8401 CTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTCTTGACGASCATTCTTAGGG 8460
      GAAACCGTTACACTCCCGGGCCTTTGGACCGGGACAGAAGAACTGCTCGTAAGGATCCC

8461 GTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCCTGAAGGAAGCAGTTC 8520
      CAGAAAGGGGAGAGCGGTTTCTTACGTTCCAGACAACCTTACAGCACTTCTCTCGTCAAG

8521 CTCTGGAAGCTTCTTGAAGACAAACAACGTCTGTAGCGACCCCTTGCAGGCAGCGGAACC 8580
      GAGACCTTCGAAGAACTTCTGTTTGTGTCAGACATCGCTGGGAAACGTCCGTGGCCTTGG

8581 CCCCACCTGGCGACAGGTGCCTCTGGCGCCAAAAGCCACGTGTATAAGATACACCTGCAA 8640
      GGGGTGGACCGCTGTCCACGGAGACGCGGTTTTCTGGTGCACATATTCTATGTGGACGTT

8641 AGGCGGCACAAACCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGC 8700
      TCCGCCGTGTTGGGGTCACGGTGCAACACTCAACCTATCAACACCTTTCTCAGTTTACCG

8701 TCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCAGAGGTACCCATTGTATGG 8760
      AGAGGAGTTGSCATAAGTTGTTCCCGCACTTCTACGGGTCTTCCATGGGGTAACATACC

8761 GATCTGATCTGGGGCCTCGGTGCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAC 8820
      CTAGACTAGACCCCGGAGCCACGTGTACGAAATGTACACAAATCAGCTCCAATTTTTTG

```

FIGURE 3E (Cont'd)

yCD2 (8877, 9353) >>>

PsiI (8874)

8821 GTCTAGGCCCCCGAACCACGGGGACGTGGTTTTTCCTTTGAAAAACACGATTATAAATGG 8880
 CACATCCGGGGGGCTTGGTGCCCTGCACCAAAAGGAAACTTTTTGTGCTAATATTTACC

8881 TGACCGGGCGCATGGCCTCCAAGTGGGATCAAAAGGGCATGGATATCCCTTACGAGGAGG 8940
 ACTGGCGGGCGTACCGGAGGTTCAACCTAGTTTTCCCGTACCTATAGCGAATGCTCCTCC

8941 CCCTGCTGGGCTACAAGGAGGGGGCGGTGCCATCGGGCGCTGTCTGATCAACAACAAGG 9000
 GGCACGACCCGATGTTCTCCCGCGCACGGATAGCCGCGACAGACTAGTTGTTGTTCC

9001 ACCGCAGTGTGCTGGGCAGGGGCCACAACATGAGGTTCCAGAAGGGCTCCGCCACCCTGC 9060
 TGCCGTCACACGACCCGTCCCGGTTGTTGTTACTCCAAGGTCTTCCCGAGGCGGTGGGACG

9061 ACCGCGAGATCTCCACCCTGGAGAACTGTGGCAGGCTGGAGGGCAAGGTGTACAAGGACA 9120
 TGCCGCTCTAGAGGTGGGACCTCTTGACACCGTCCGACCTCCCGTTCCACATGTTCTCTGT

9121 CCACCCTGTACACCACCCTGTCCCTTGTGACATGTGTACCGGCGCTATCATCATGTACG 9180
 GGTGGGACATGTGGTGGGACAGGGAACTGTACACATGGCCGCGATAGTAGTACATGC

9181 GCATCCCTAGGTGTGTGATCGGCGAGAACTGAACCTTCAAGTCCAAGGGCGAGAAGTACC 9240
 CGTAGGGATCCACACACTAGCCGCTCTTGCACTTGAAGTTCAGGTTCCCGCTCTTCATGG

9241 TGCAAACCAGGGGCCACGAGGTGGTGGTGTGTTGACGATGAGAGGTGTAAGAAGCTGATGA 9300
 ACGTTTGGTCCCGGTGCTCCACCACCAACAACCTGCTACTCTCCACATTCTTCGACTACT

NotI (9356)

CciNI

9301 AGCAGTTTCATCGACGAGAGGCCCTCAGGACTGGTTCGAGGATATCGGCGAGTANGCGGCG 9360
 TCSTCAAGTAGCTGCTCTCCGGAGTCTGACCAAGCTCCTATAGCCGCTCATTGCGCGGC

U3 Region(9405, 9854) >>>

9361 CAGATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCCAAC 9420
 GTCTATTTTATTTCTAAAATAAATCAGAGGTCTTTTCCCCCCTTACTTTCTGGGGTGG

BmtI

NheI

AsuNHI

5' LTR2 other (9447, 9998) >>>>

9421 TGTAGGTTTGGCAAGCTAGCTTAAGTAAAGCCATTTTGCAAGGCATGSAAAAATACATAA 9480
 ACATCCAAACCGTTGCATCGAATTCATTGCGGTAAAACGTTCCGTACCTTTTTATCTATT

FIGURE 3E (cont'd)

9481	CTGAGAATAGAGAAAGTTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCA	9540
	GACTCTTATCTCTTCAAGTCTAGTTCAGTCCCTTGTCTACCTTGTGCACTTATACCCGGT	
9541	AACAGGATATCTGTGGTAAGCAGTTCTTGCCCGGCTCAGGGCCAAGAACAGATGGAACA	9600
	TTGTCTATAGACACCATTCTGCAAGGACGGGGCCGAGTCCCGGTTCTTGTCTACCTTGT	
9601	GCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCTTGCCCGGCTCAGGGCCA	9660
	CGACTTATACCCGGTCTTGTCTATAGACACCATTCTGCAAGGACGGGGCCGAGTCCCGGT	
9661	AGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATG	9720
	TCTTGTCTACCAAGGGGTCTACGCCAGGTCCGGGAGTCTGCAAGATCTCTTGGTAGTCTAC	
9721	TTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAG	9780
	AAAGGTCCCACGGGGTTCTTGGACTTTACTGGGACACGGAATAAACTTGATTGTTAGTC	

		SacI	
		SstI	
	PauI	Esp124BI	
	BsePI	EcoICRI	
	BssHII	Ecl136II	
9781	TTCGCTTCTCGCTTCTGTTCGGCGGCTTCTGCTCCCGAGCTCAATAAAAGAGCCCACAA		9840
	AAGCGAAGAGCGAAGACAAGCGCGCGAAGACGAGGGGCTCGAGTTATTTTCTCGGGTGTT		

```
R Region(9855,9921)>>>
```

9841 CCCCTCACTCGGGGCGCCAGTCTCCGAFTGACTGAGTCGCCCGGGTACCCGTGTATCCA 9900
GGGGAGTGAGCCCCGCGGTGAGGAGGCTAACTGACTCAGCGGGGCCATGGGCACATAGGT

U5 Region (9922, 9998) >>>>

9901 ATAAACCCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCTCTTGGGAGGGTCTCCT 9960
TATTTGGGAGAACGTCAACGTAGGCTGAACACCAGAGCGACAAGGAACCCCTCCCAGAGGA

9961 CTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTTCATTACATGTGAGCAAAAGGCCAGCA 10020
GACTCACTAACTGATGGGCAGTCGCCCCCAGAAAGTAATGTACACTCGTTTTCCGGTCGT

```
pBR322  origin(10045,10664)<<<
```

10021 AAAGGCCAGGAACCGTAA¹⁰⁰⁰AAAGGCCGCGTTGCTGGCGT¹⁰⁰⁰TTTTCCATAGGCTCCGCCCCCC 10080
TTTTCCGCTCCTTGGCATTTTTCCGGCGCAACGACCGCAAAAAAGGTATCCGAGGCGGGGGG

10081 TGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATA 10140
ACTGCTCGTAGTGTGTTTTAGCTGCGAGTTCAGTCTCCACCGCTTTGGGGCTGTGCTGATAT

10141 AAGATACCAGGGCGTTTCCCCCTGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGAGCCCTGCC 10200
TTCTATGGTCCGCAAAAGGGGGACCTTCGAGGGAGCACGCGAGAGGACAAGGCTGGGACGG

FIGURE 3E (cont'd)

10201 GCTTACCGGATACCTGTCCGCCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTC 10260
 CGAATGGCCTATGGACAGGCGGAAAGAGGGAAGCCCTTCGCACCGCGAAAGAGTTACGAG
 10261 ACGCTGTAGGTATCTCAGTTCGGTGTAGGTCCGCTTCGGCTCCAAGCTGGGCTGTGTGCACGA 10320
 TCGGACATCCATAGAGTCAAGCCACATCCAGCAAGCGAGGTTCCACCCGACACACGTGCT
 10321 ACCCCCGGTTTCAGCCCGACCGCTGGCGCTTATCCGGTAACCTATCGTCTTGAGTCCAACCC 10380
 TGGGGGGCAAGTCGGGCTGGCGACGCGGAATAGGCCATTGATACCAAGTCAAGTTCAGGTTGGG
 10381 GGTAAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAG 10440
 CCATTCTGTGCTGAATAGCGGTGACCGTCTGTCGGTGACCAATTGTCTAATCTGTCTCGCTC
 10441 GTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAG 10500
 CATACATCCGCCACGATGTCCTCAAGAACTTCACCACCGGATTGATGCCGATGTGATCTTC
 10501 GACAGTATTTGGTATCTGGGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAG 10560
 CTGTCTATAAACCATAGACGCGAGAGGACTTCGGTCAATGGAAGCCTTTTTCTCAACCATC
 10561 CTCTTGATCCGGCAAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGCAGCAGCA 10620
 GAGAACTAGGCGGTTTTGTTTGGTGGCGACCATCGCCACCAAAAAACAAACGTTTCGTCT
 10621 GATTACGGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGA 10680
 CTAATGCGCGTCTTTTTTCTAGAGTTCTTCTAGGAACTAGAAAAGATGCCCCAGACT
 10681 CGCTCAGTGGAAACGAAAACTCAGCTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGAT 10740
 GCGAGTCACCTTGCTTTTGGAGTGCATTCCTTAAACCAGTACTCTAATAGTTTTCCTA
 10741 CTTCACCTAGATCCTTTTAAATTAATAATGAAGTTTAAATCAATCTAAAGTATATATGA 10800
 GAAGTGGATCTAGGAAAATTTAATTTTACTTCAAAATTTAGTTAGATTTTCATATATACT

 amp marker (10819,11679)<<<
 |
 10801 GTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTG 10860
 CATTTGAACCAGACTGTCAATGGTTACGAATTAGTCACTCCGTGGATAGAGTCGCTAGAC
 10861 TCTATTTGGTTCATCCATAGTTGCCTGACTCCCGTCTGTGTAGATAACTACGATACGGGA 10920
 AGATAAAGCAAGTAGGTATCAACGGACTGAGGGGCAGCACATCTATTGATGCTATGCCCT
 10921 GGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGCGAGACCCACGCTCACC GGCTCC 10980
 CCCGAATGGTAGACCGGGGTACCGAGTTACTATGGCGCTCTGGGTGCGAGTGGCCGAGG
 10981 AGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCTCTCAAC 11040
 TCTAAATAGTCGTTATTTGGTGGGTGGGCTTCCCGGCTCGCGTCTTCACCAGGACGTTG

FIGURE 3E (cont'd)

11041 TTTATCCGCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCCGCC 11100
 AAATAGGCGGAGGTAGGTGAGATAATTAACAACGCCCTTCGATCTCATTTCATCAAGCGG
 11101 AGTTAATAGTTTGGGCAACGTTGTTGCCATTGCTGCAGGCATCGTGGTGTCAAGCTCGTC 11160
 TCAATTATCAAACGCGTTGCAACAACGGTAACGACGTCGGTAGCACACAGTGGCAGCAG
 11161 GTTTGGTATGGCTTCATTTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCC 11220
 CAAACCATAACGAAGTAAGTCGAGGCCAAGGGTTGCTAGTTCCGCTCAATGTACTAGGGG
 11221 CATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCCTCCGATCGTTGTCAGAAGTAAGTT 11280
 GTACAACACGTTTTTTTCGCCAATCGAGGAAGCCAGGAGGCTAGCAACAGTCTTCATTCAA
 11281 GGCUCGAGTGTATCACTCATGGTTATGGCAGCACTGCATAATTCCTTACTGTCTATGCC 11340
 CCGGCGTCACAATAGTGAGTACCAATACCGTCGTGACGTATTAGAGAATGACAGTACGG
 11341 ATCCGTAAGATGCTTTTCTGTGACTGGTGAAGTACTCAACCAAGTCATTCTGAGAATAGTG 11400
 TAGGCATTCTACGAAAAGACACTGACCACTCATGAGTTGGTTCAGTAAGACTCTTATCAC
 11401 TATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAACACGGGATAATACCGCGCCACATAG 11460
 ATACGCGGCTGGCTCAACGAGAACGGGCGCAGTTGTGCCCTATTATGGCGCGGTGTATC
 11461 CAGAAGTTTAAAAGTGCTCATCTTGGAAAACGTTCTTCGGGGCGAAAAGTCTCAAGGAT 11520
 GTCTTGAAATTTTACGAGTAGTAACCTTTTGCAAGAAGCCCCGCTTTTGAGAGTTCCTA
 11521 CTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGC 11580
 GAATGGCGACAACTCTAGGTCAAGCTACATTGGGTGAGCAGCTGGGTGACTAGAAGTCC
 11581 ATCTTTTACTTTCACACAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAA 11640
 TAGAAAATGAAAGTGGTTCGCAAGACCCACTCGTTTTTGTCTTCCGTTTTACGGCGTTT
 11641 AAAGGGAATAAGGGGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTA 11700
 TTTCCCTTATTTCCCGCTGTGCCTTTTACAACCTATGAGTATGAGAAGGAAAAAGTTATAAT

 amp prom(11721,11749)<<<
 |
 11701 TTGAAGCATTTATCAGGGTTATTTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAA 11760
 AACTTCGTAAATAGTCCCAATAACAGAGTACTCGCCTATGTATAAACTTACATAAATCTT
 11761 AAATAAACAAATAGGGGTTCCGCGCACATTTCCCGAAAAAGTGCCACCTGACGTCTAAGA 11820
 TTTATTTGTTTATCCCCAAGGCGCGTGTAAAGGGGCTTTTCACGGTGCAGTGCAGATTCT
 11821 AACCATTATTATCATGACATTAACTTATAAAAAATAGGCGTATCACGAGGCCCTTTCGTCT 11880
 TTGGTAATAATAGTACTGTAATTGGATATTTTATCCGCATAGTGTCCGGGAAAGCAGA
 11881 TCAAGAATTCAT 11892
 AGTTCTTAAGTA

FIGURE 3E (cont'd)

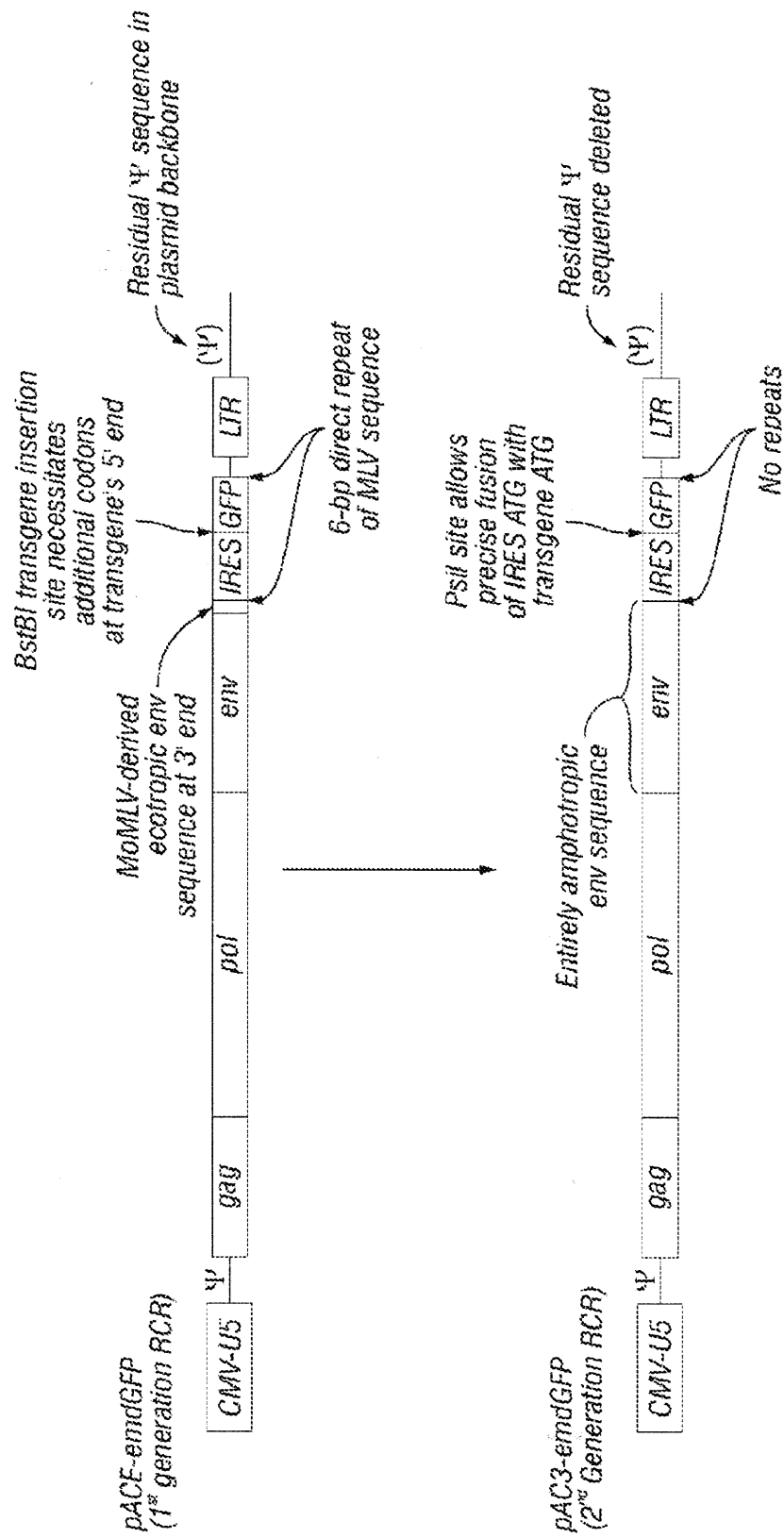
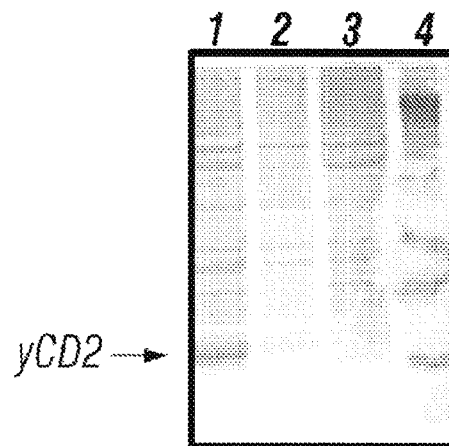


FIGURE 3F



- 1 - U87 + AC3-yCD2 (V)*
- 2 - U87 + ACE-yCD (V)*
- 3 - U87 (uninfected)*
- 4 - Molecular Weight Standards*

FIGURE 4

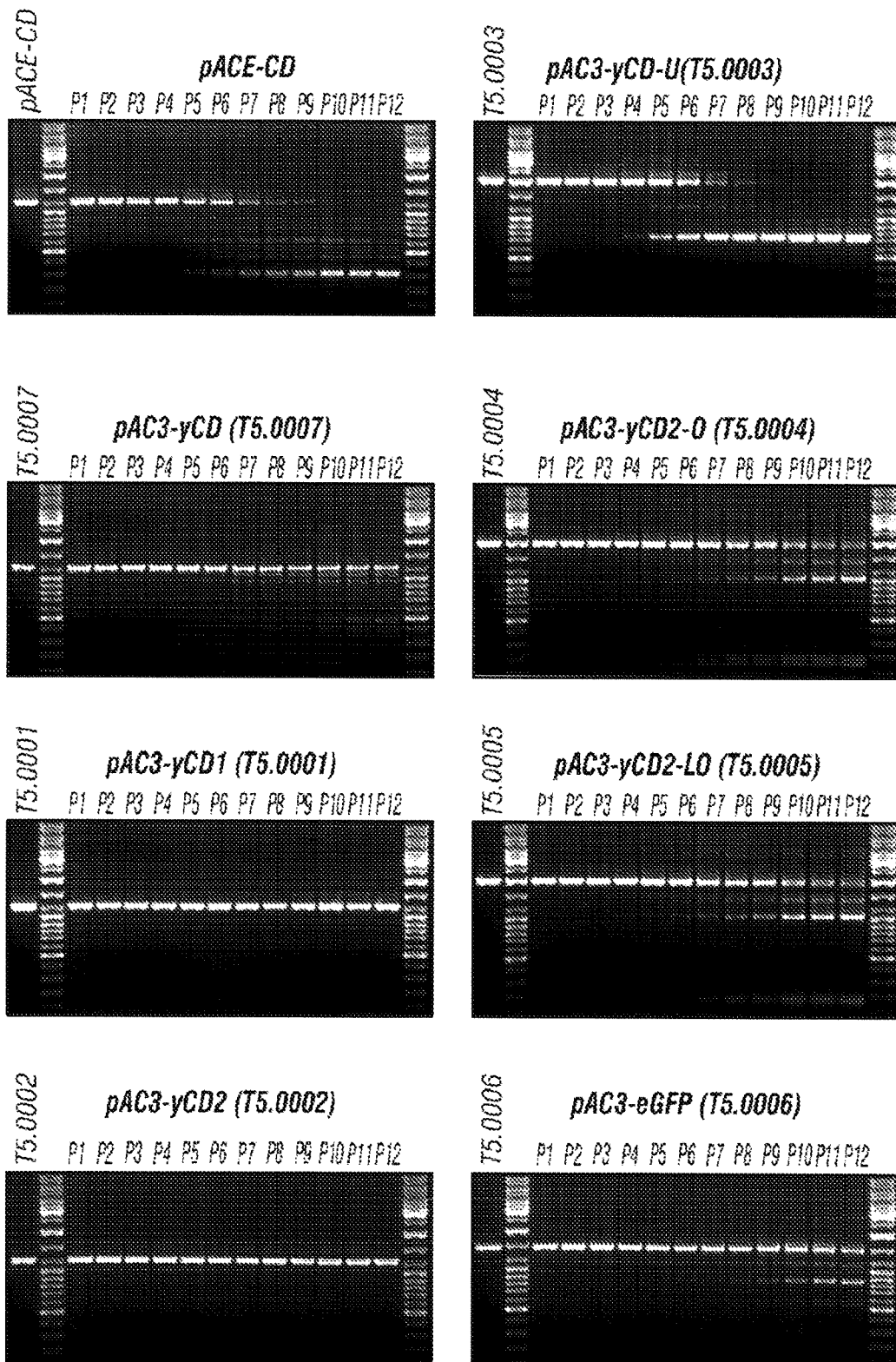


FIGURE 5

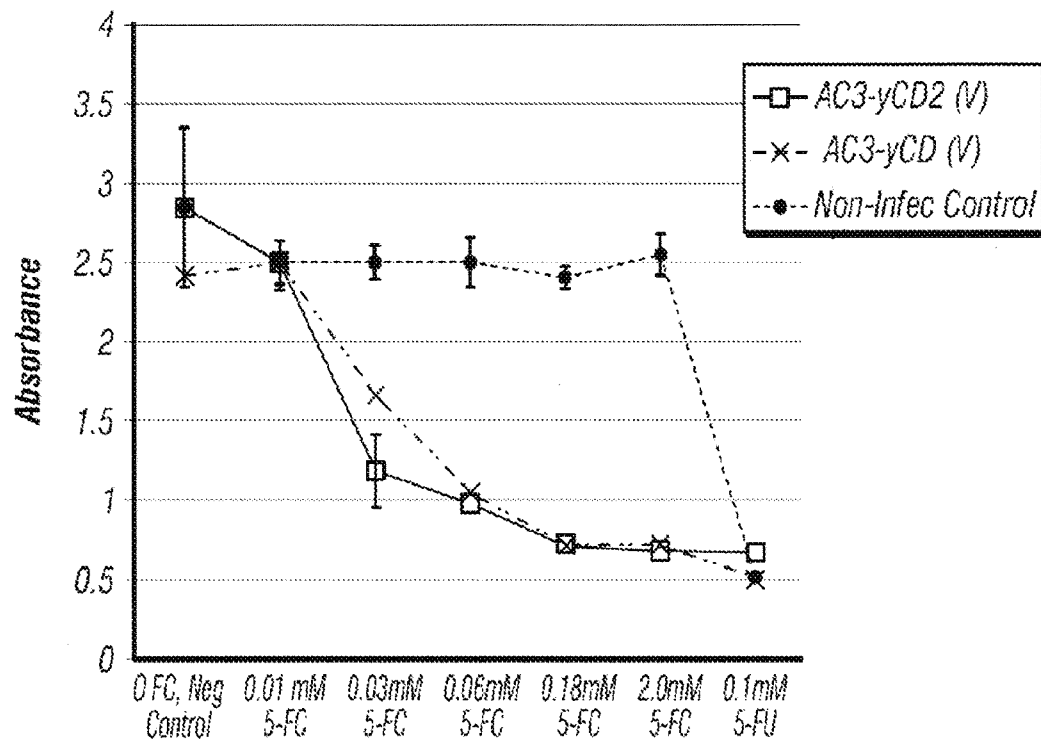


FIGURE 6A

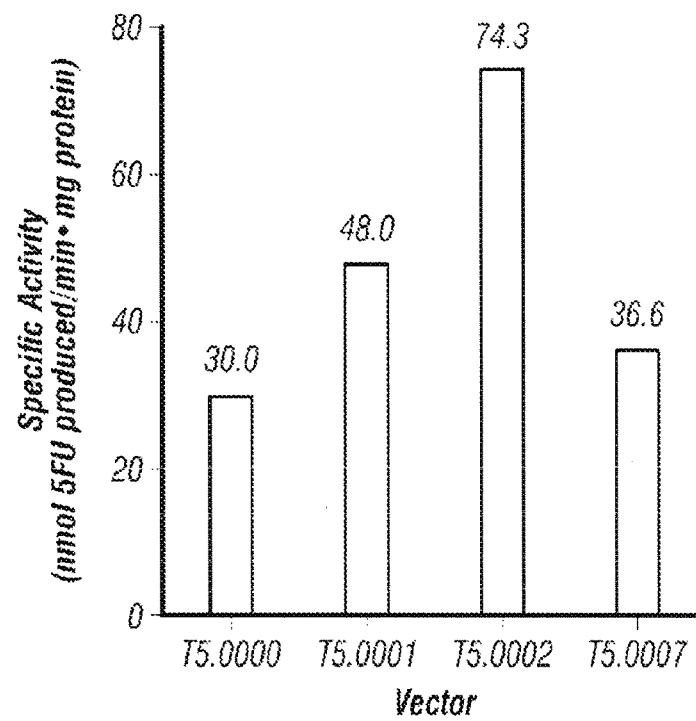


FIGURE 6B

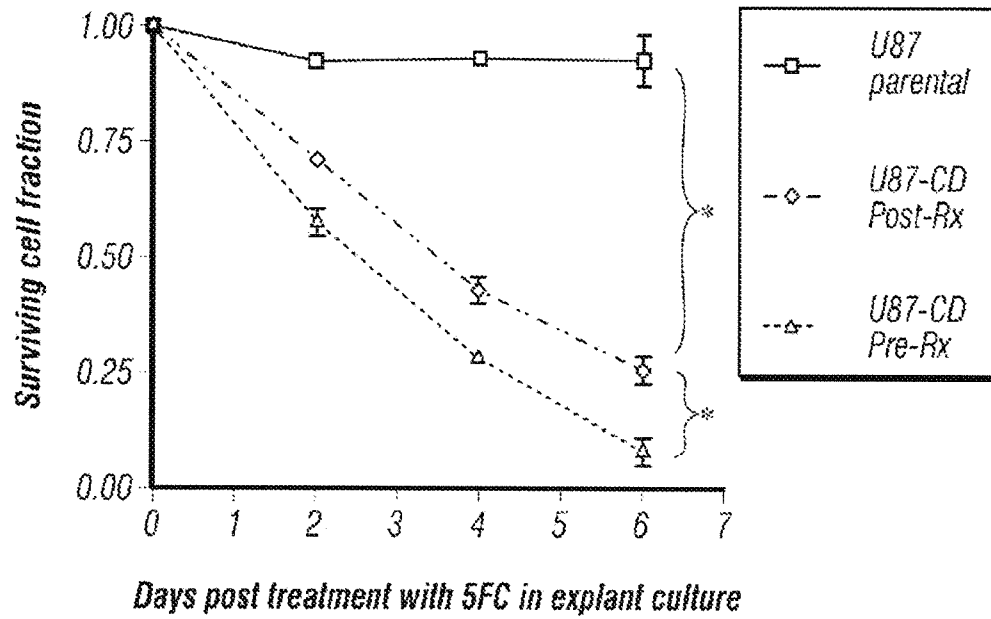


FIGURE 7

U-87 nude xenograft intracranial model-10 animals/group

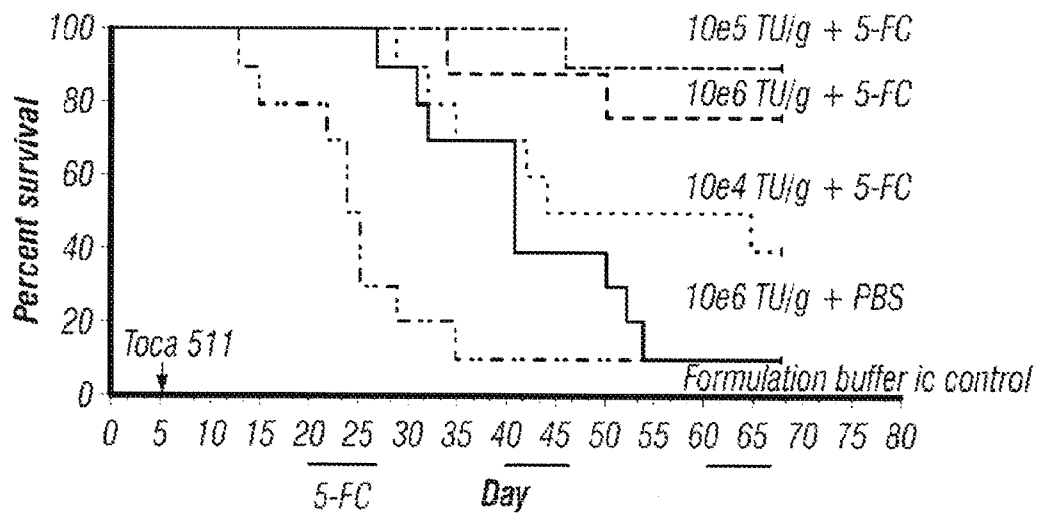


FIGURE 8

CT26 BALB/c syngeneic intracranial model - 10 animals/group

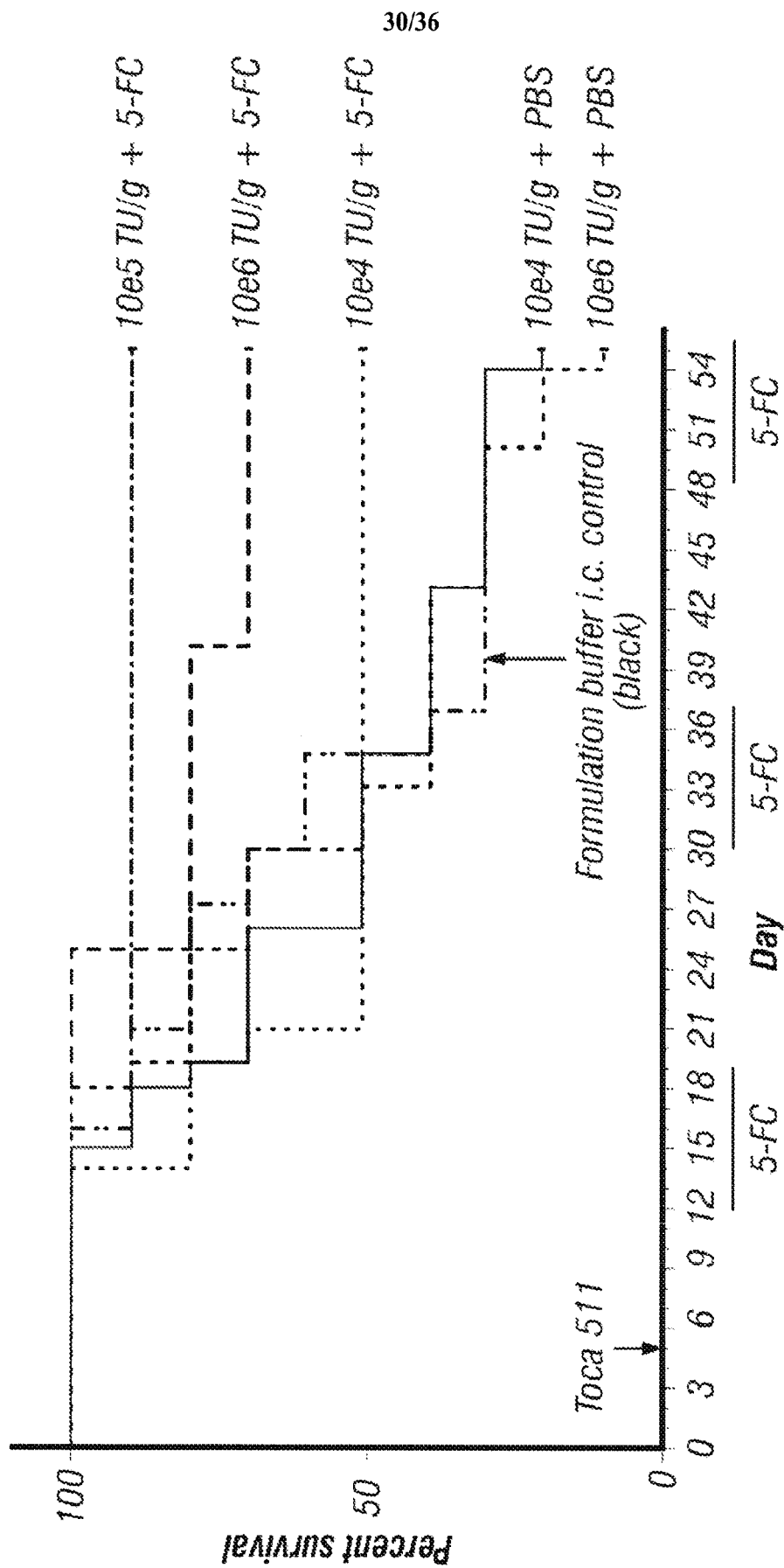


FIGURE 9

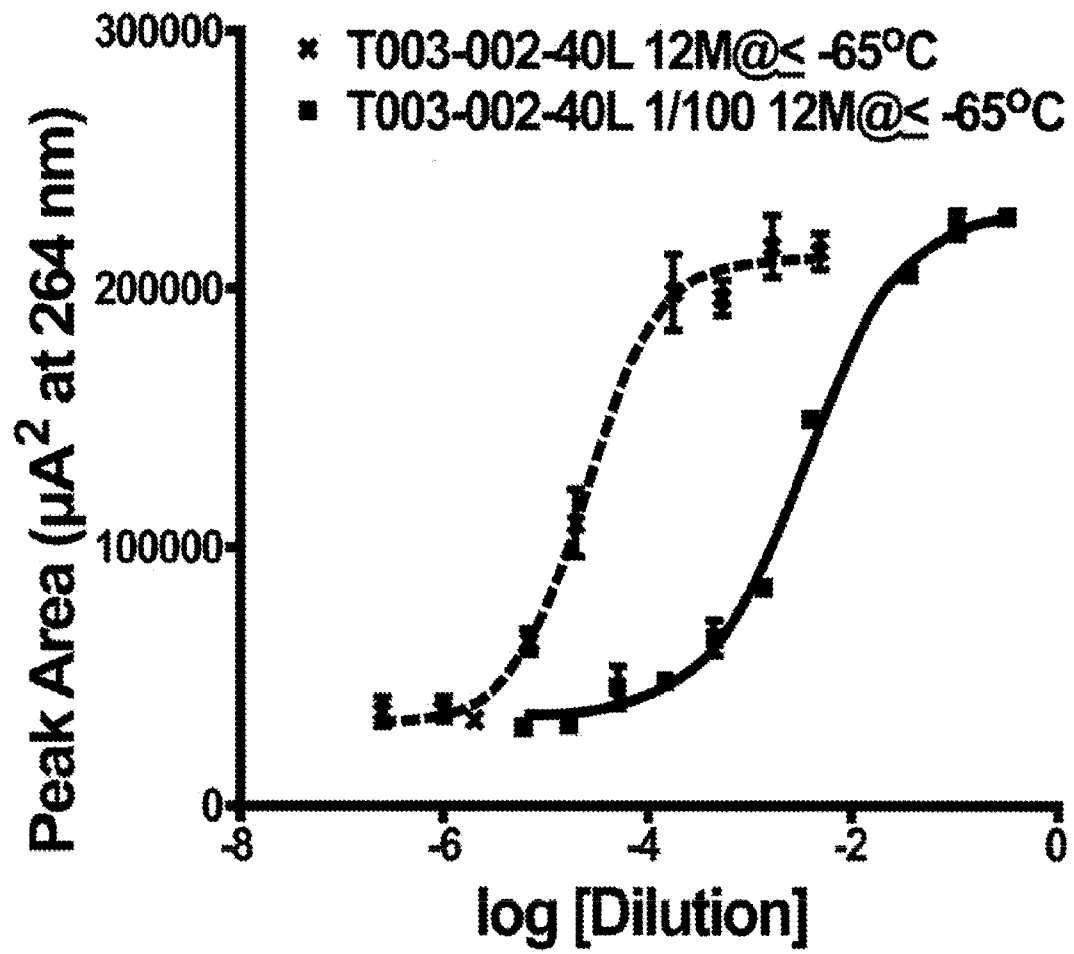


FIGURE 10

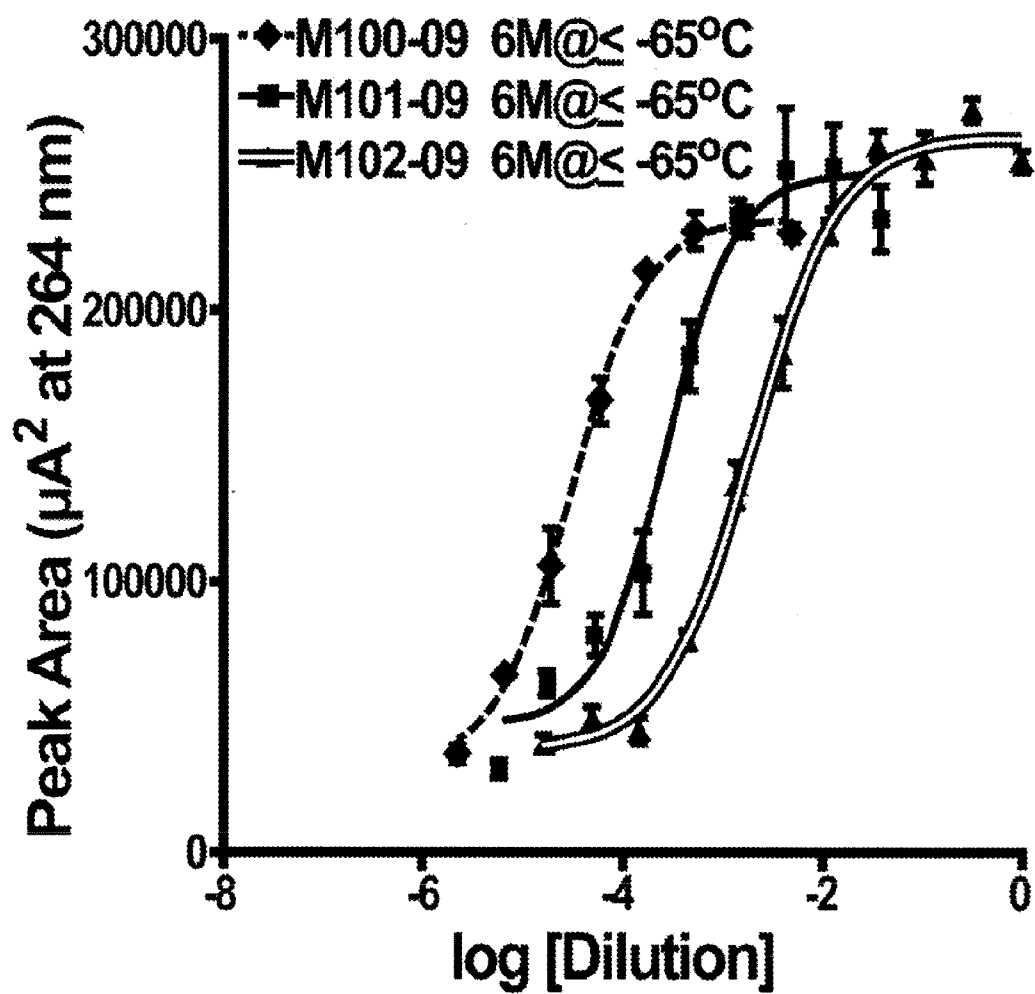


FIGURE 11

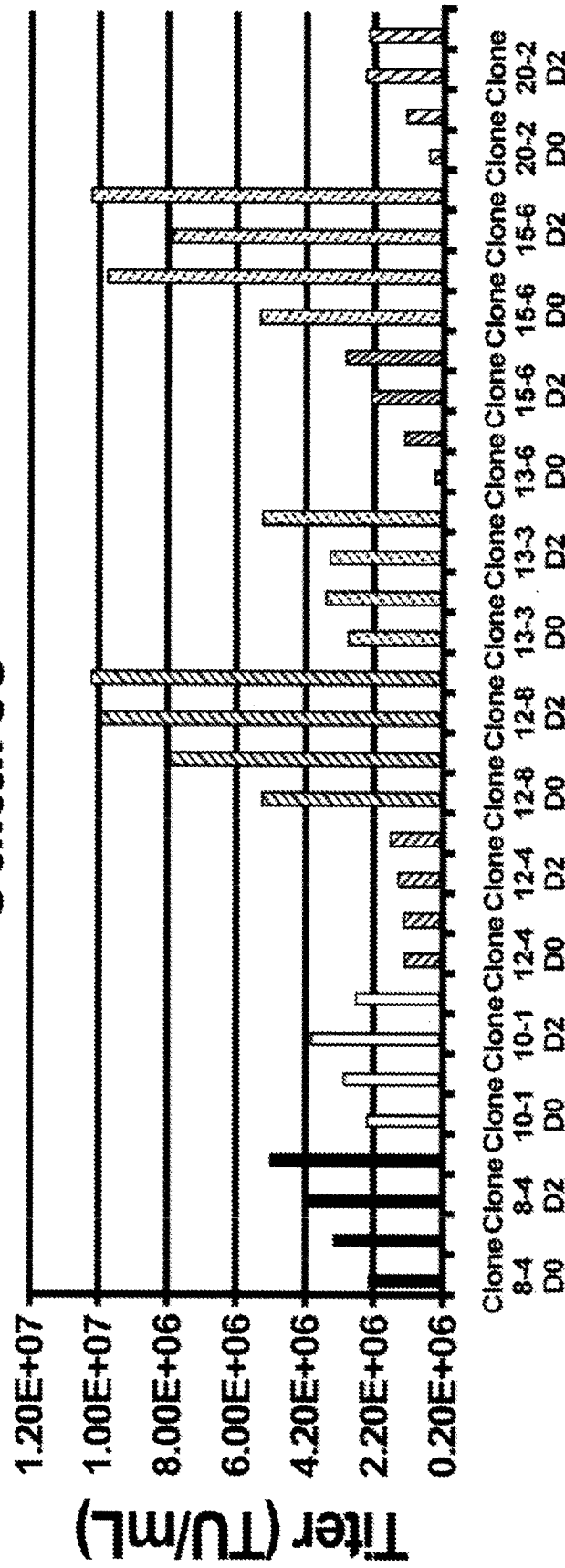


FIGURE 12

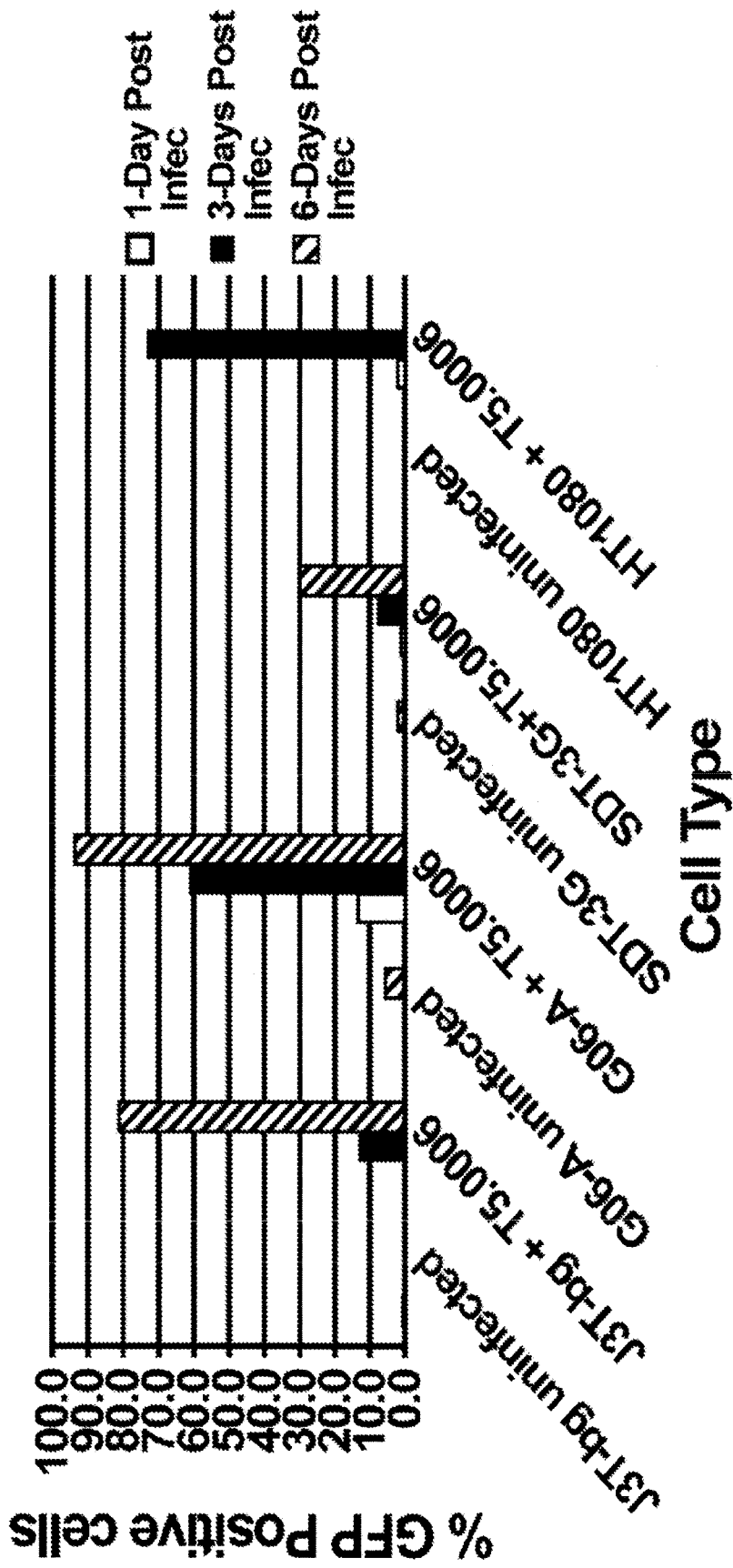


FIGURE 13

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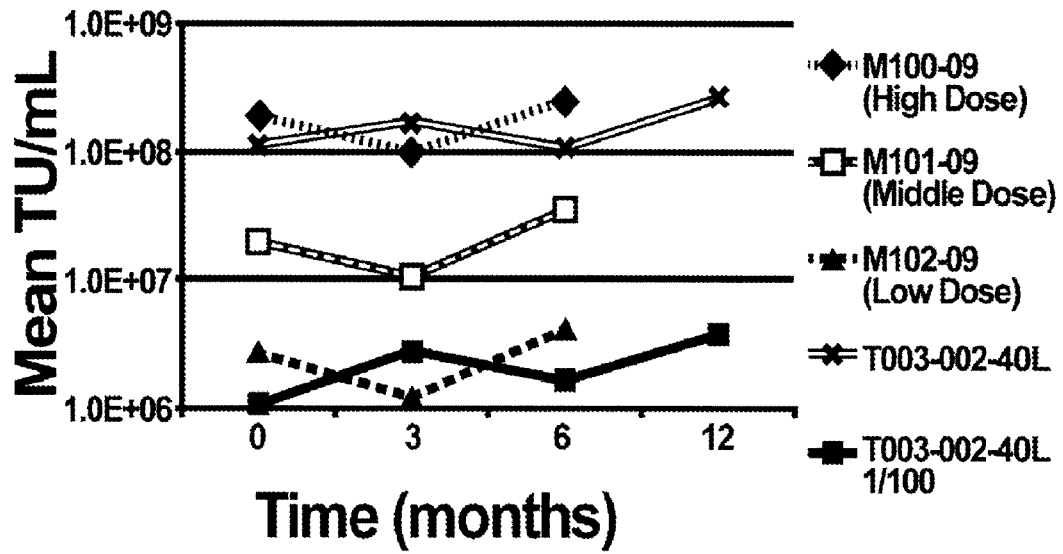


FIGURE 14

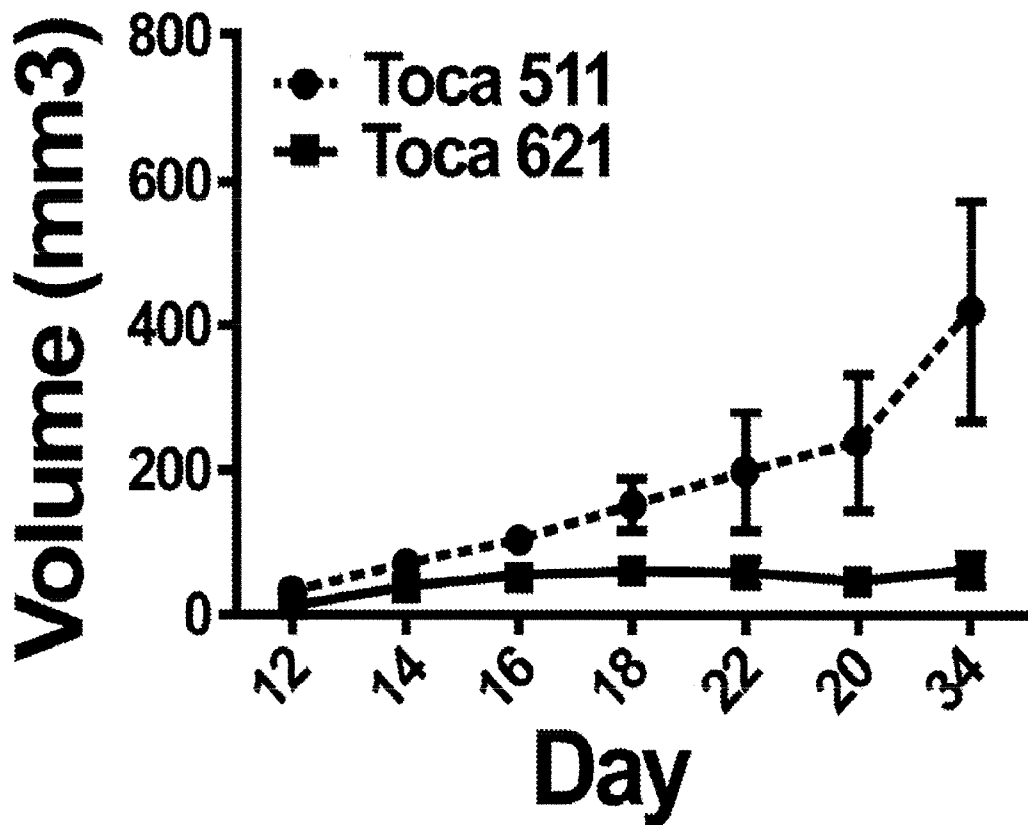


FIGURE 15

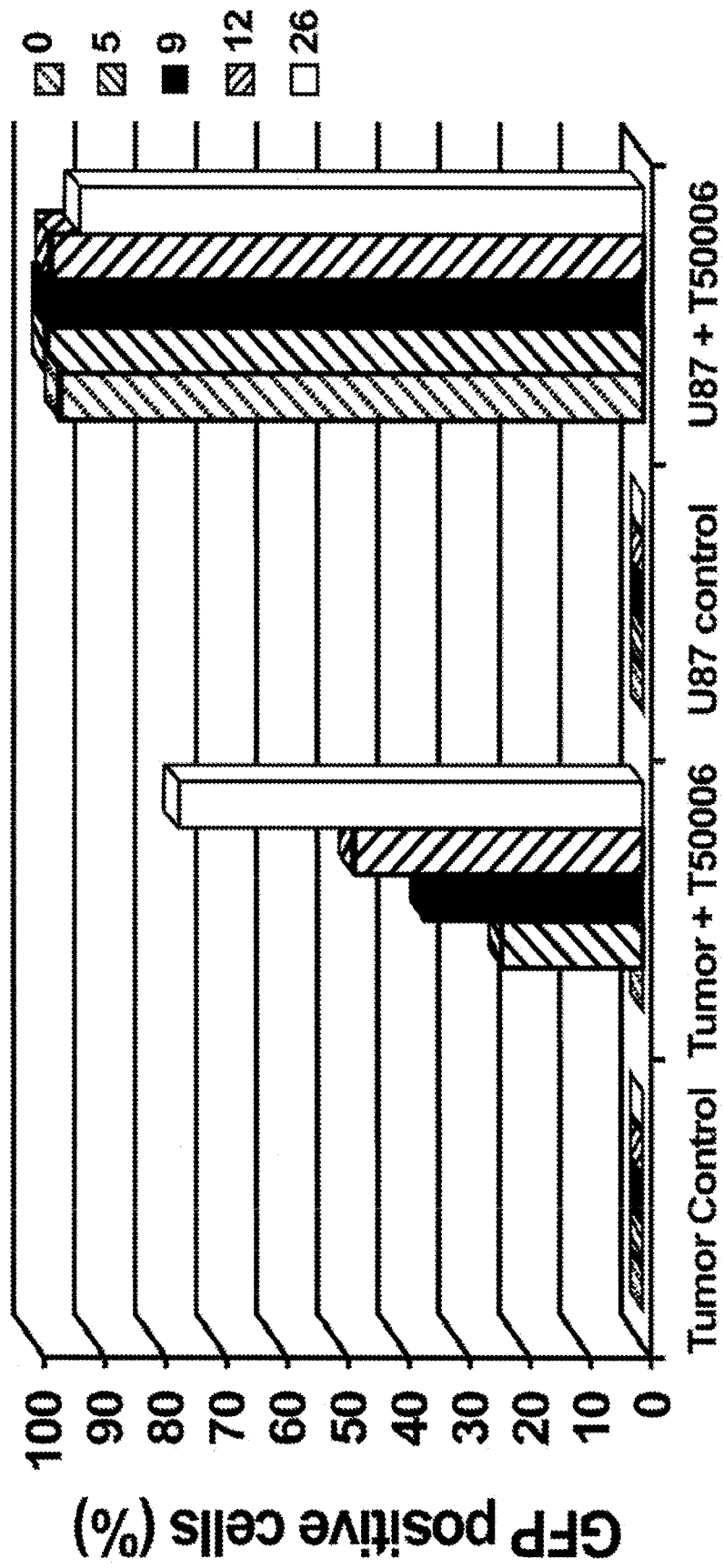


FIGURE 16