

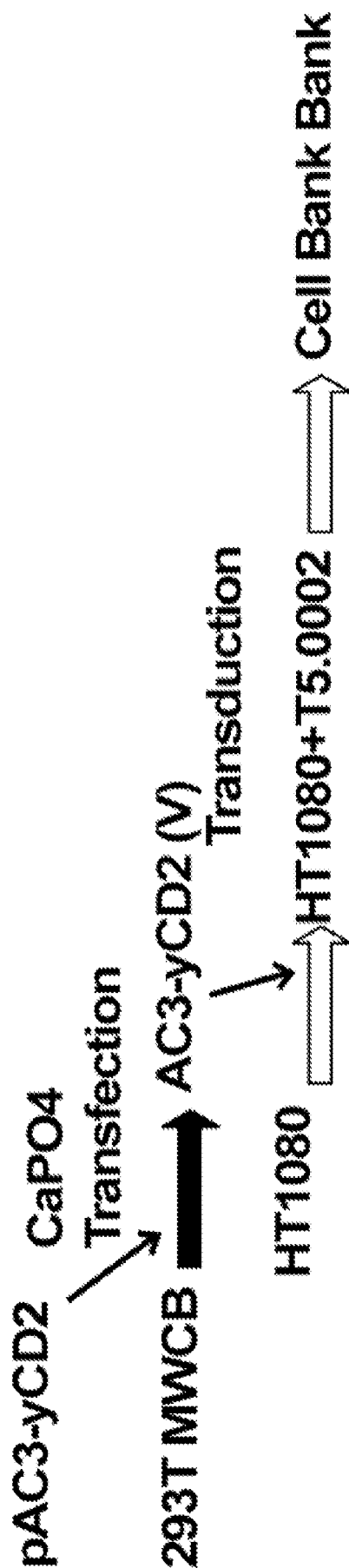


FIGURE 1

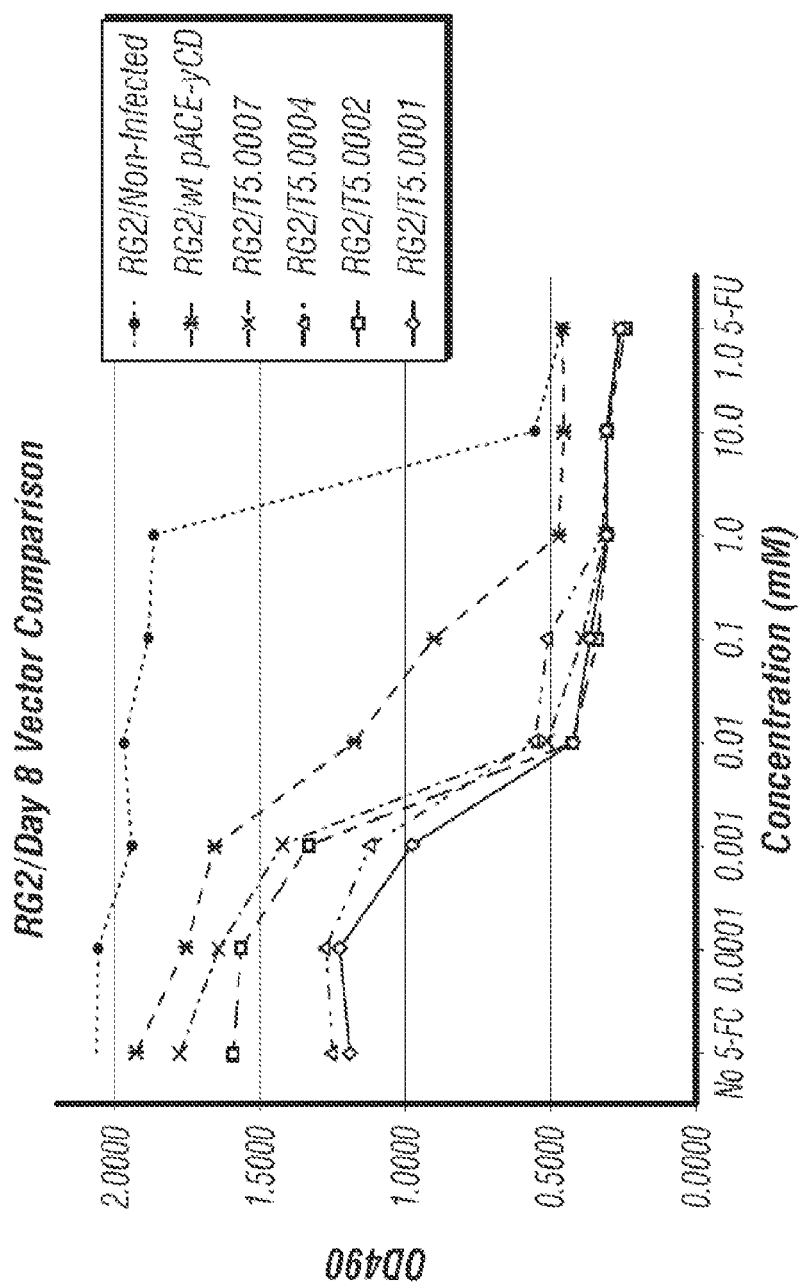


FIG. 2

3/36

Legend ref.	Reference name	Original Name	Other names	5'LTR PROMOTER	Envelope	Vector	IRES	Transgene	3'LTR	Notes
T5.0001	pAC3-yCD1	CD1 sequence		CMV	Ampho (4070A)	pAC3-end	EMCV	yeastCD		hu codon
T5.0002	pAC3-yCD2	CD2opt+3pt		CMV	Ampho (4070A)	pAC3-end	EMCV	yeastCD		hu codon + 3pt mutations
T5.0003	pAC3-yCD-U	CD-UPPT		CMV	Ampho (4070A)	pAC3-end	EMCV	yeastCD		hu codon + 3pt mut UPPT fusion
T5.0004	pAC3-yCD2-0	CD2opt+3pt-OPPT		CMV	Ampho (4070A)	pAC3-end	EMCV	yeastCD		hu codon + 3pt mut OPPT fusion
T5.0005	pAC3-yCD2-L0	CD2opt+3pt-LINK-OPPT		CMV	Ampho (4070A)	pAC3-end	EMCV	yeastCD		hu codon + 3pt mut-LINKOPPT fusion
T5.0006	pAC3-eGFP	pACE-end	pACE-GFP	CMV	Ampho (4070A)		EMCV	Emerald GFP	MLV U3	Emerald GFP
T5.0007	pAC3-yCD			CMV	Ampho (4070A)		EMCV	Wt yeast CD	MLV U3	

FIG. 2 (Cont'd)

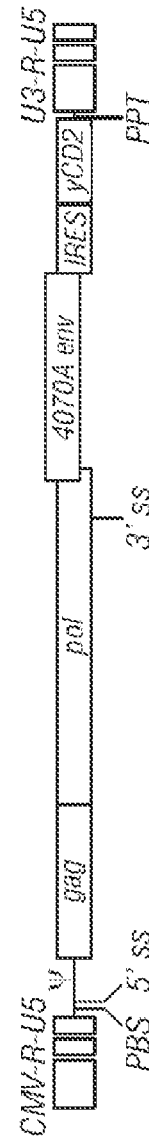


FIG. 3A

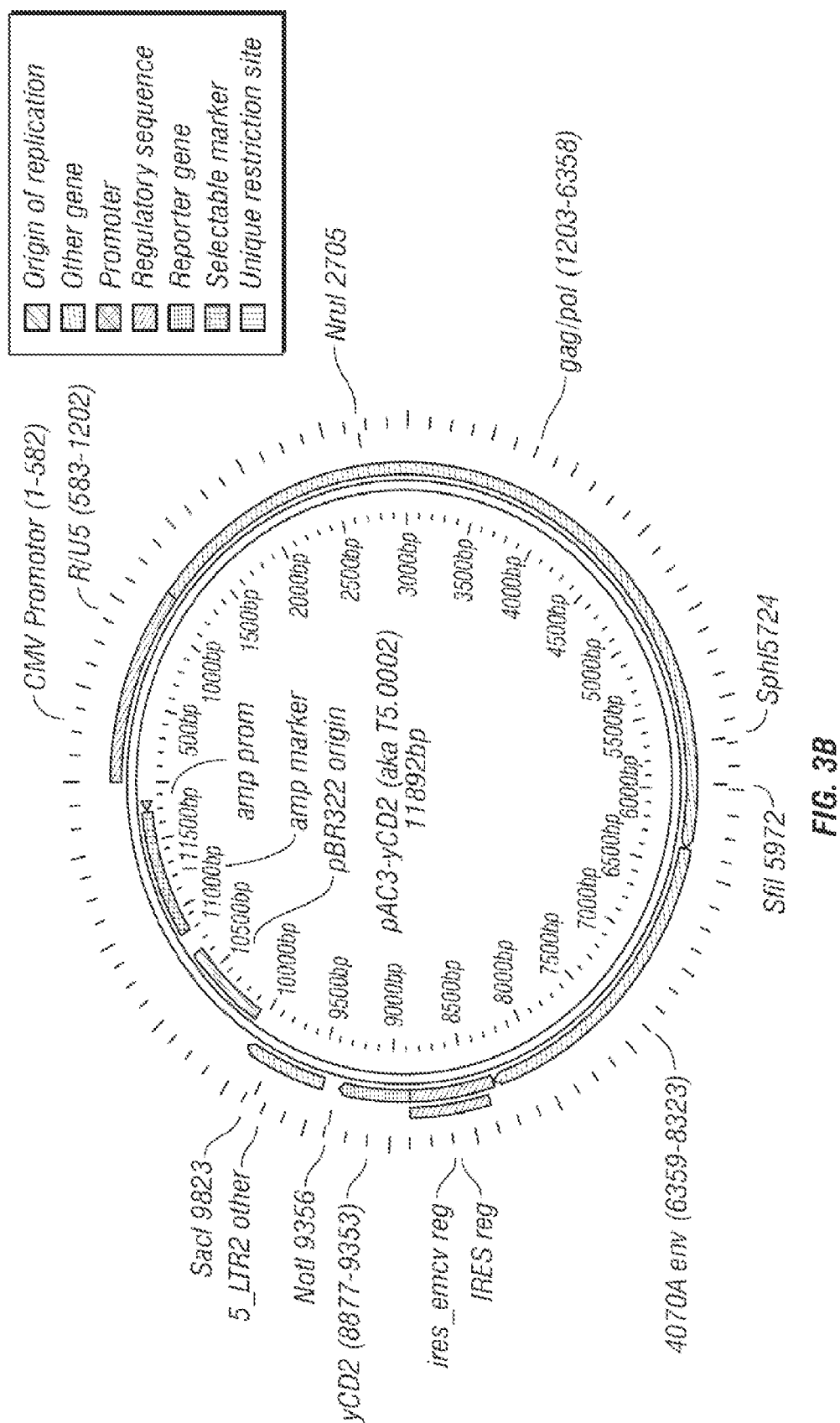


FIG. 3B

5/36

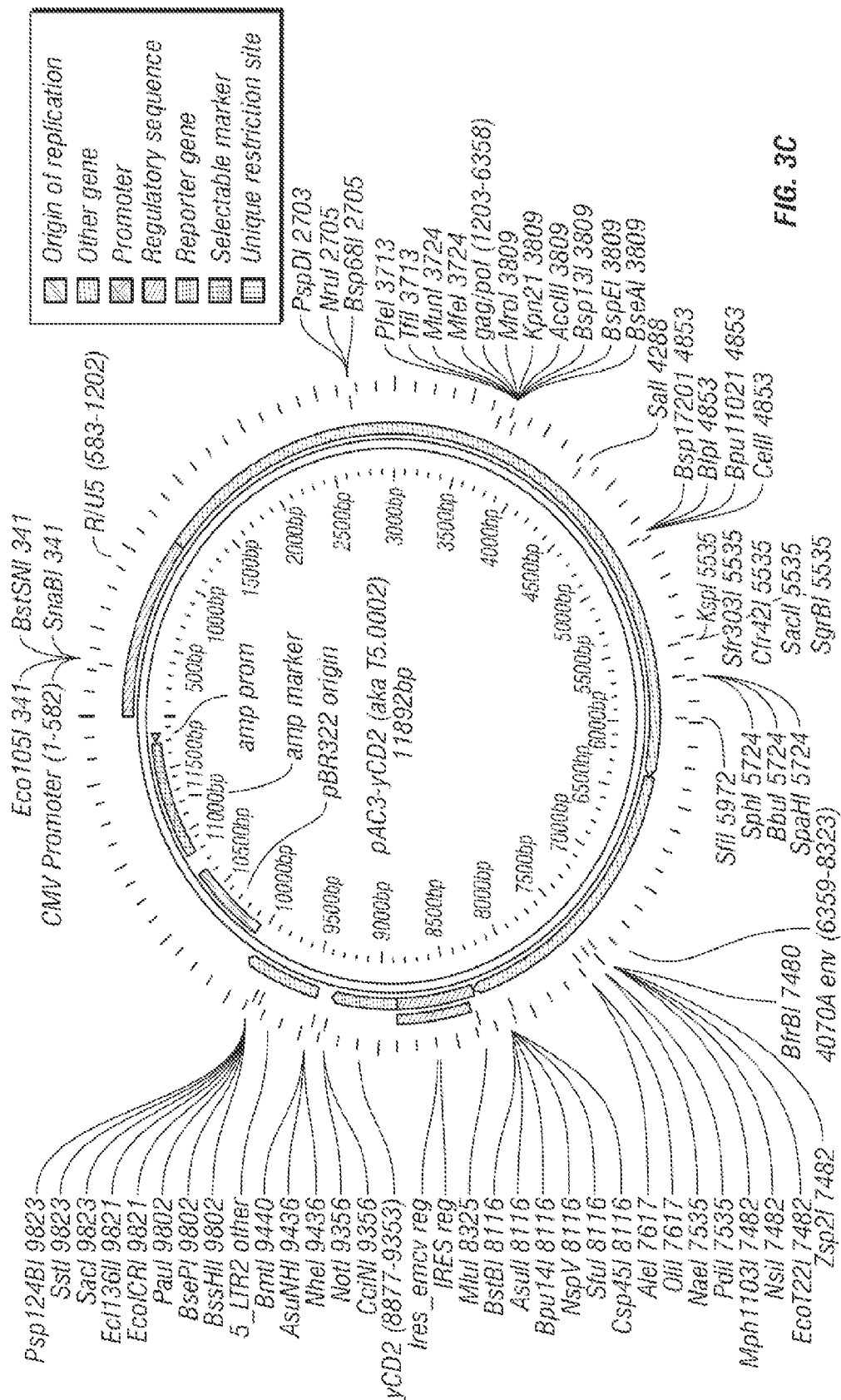


FIG. 3C

6/36

TAGTTATTAACTAATCAATTACGGGTCATTAGTTCATAGCCCATATATGGAGTTCGGGTACATAAATTACGGTAAAT
 GGCCCGCTTGGCTGACCGCCCAACGACCCCGCCCAATTGACGTCATTAATGACGTATGTTCCUATAGTAACGCCAATAGGGA
 CTTTCATTGACCTCAATGGGTGGAGTATTACGGTAAACTGCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTAC
 GCGCCCTATTGACGTCAATGACGCTAAATGGCCCGCTTGGCTATATGCCAGTACATGACCTTATGGGACTTTTCCACTTGG
 CAGTACATCTACGTATTAGTCATCGGTATTACCATGGTGATGCGGTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTG
 ACTCAGCGGGATTTCACAGTCTCCACCCCATTGACGTCATTAATGGGAGTTTGTGTTTGGCAGCAAAATCAACGGGACTTTCCAAA
 ATGTCTGTAAACAATCCGCCCATTGACGCAATGGGCGGTAGCGGTGTACGGTGGGAGGTTTATATAAGCAGAGCTGGTTTA
 GTGAACCGGGCGCAGTCTCCGATTGACTGAGTGGCCGGGTACCGGTGTATCCAAATAAACCTCTTGCAGTTGCAATCCGAC
 TTGTTGGTCTCGTGTTCCTTGGGAGGGTCTCTCTGAGTGATTGACTACCCGTCAGCGGGGCTCTTTCATTGGGGGCTCGT
 CCGGGATCGGGAGACCCCTGCCAGGGACCAACGACCCACCGGGAGGTTAAGCTGGCCAGCAACTTATCTGTGTCTGTCC
 GATTGCTTACTGTCTATGACTGATTTTATCGCCCTCGCTCGGTACTAGTTAGCTAAGTACTGTATCTGGCGGACCGGTG
 GTGGAAGTGAAGGTTGGGAACACCGGGCGGCAACCTGGGAGAGCTCCAGGGACTTCGGGGCGGTTTTTGTGTGGCCGAC
 CTGAGTCCAAAATCCCGATCGTTTGGGACTCTTTGGTGCACCCCTTAGAGGAGGATATGTGGTTCTGGTAGGAGAGGA
 GAACCTAAACAGTTCCCGCCCTCGCTGTGAATTTTGTCTTGGGTTGGGAACGAAGCGCGCGCGCTCTTGTCTGTCTGC
 AGCATCGTTCTGTGTGTCTCTGTGTGACTGTGTTTCTGTATTGTCTGAGAATAAGGGCCAGACTGTTACCACTCCCTTAA
 GTTTGACCTTAGGTCACCTGGAAGAATGTCGAGCGGATCGCTCACAACCACTCGGTAGATGTCAAGAAGAGAGCTTGGGTTAC
 CTTCTGCTCTGCAGAAATGGCCAACTTTAAGCTGGGATGGCCGCGAGACGGCACTTTAAGCGAGAGCTCATCACCCAGTT
 AAGATCAAGGTCTTTTCACTGGCCCGCATGGACACCCAGACCAAGGTCCCTACATGCTGAGCTGGGAACCTTGGCTTTTG
 ACCCCCTCCCTGGGTCAAGCCCTTTGTACACCTTAGGCTCCGCTCTCTTCTCTCCATCCGCCCCGTCTCTCCCTTGA
 AACTCTCGTTGGACCCCGCTCGATCCCTCTTTATCCAGCCCTCACTCTCTCTAGGCGGCAAACTTAAACCTCAAGTT
 CTTTCTGACAGTGGGGGGCTCTATCGACCTACTTACAGAGAGACCCCGCTTATAGGGAACCAAGACCAACCCCTTCC
 ACAGGAGCGAAATGCTGGAGAGCGACCCCTGGGGAGAGGACCGGACCCCTCCCAATGGCATCTCGCTACGTTGGGAG
 ACGGGAGCCCTCTGGCCGACTCCACTACCTCGCAGGCATTCCCTCTCCGCGCAGGAGGAACGGACAGCTTCAATACCTGG
 CCGTTCTCTCTCTCTGACCTTTACAACCTGGAAAAATAATAACCTCTCTTTTCTGAGATCCAGGTAAACTGACAGCTCTGA
 TCGAGTCTGTTCTCATACCCCATCAGCCCACTGGGAGGACTGTCAGCAGCTGTTGGGAGCTCTGCTGACCGGAGAGAAAA
 ACAACGGGTGCTCTTAGAGGCTAGAAAGCGGTGGCGGGGATGATGGGCGGCCACTCAACTGCCCAATGAAGTCCATGCC
 GCTTTTCCCTCGAGCGGCCAGACTGGGTTACACCAACCCAGGCAGGTAGGAACCACTAGTCCACTATCGCCAGTTGCTCC
 TAGCGGCTCTCCAAACCGGGCAGAGGCCCAACCAATTTGGCCAGGTAAGGAATAACACAGGGGCCAATGAGTCTCC
 CTCGGCTTCTAGAGAGACTTAGGAGAGCTATCGCAGGTACACTCTTATGACCTGAGGACCCAGGGCAAGAACTAAT
 GTGTCTATGTCTTTCAATTTGGGAGTGTGCCCCAGACATTGGGAGAAAGTTAGAGAGGTTAGAAAGATTAAAAACAAGAGGC
 TTGGAGATTTGTTAGAGAGGAGAGAAAGATCTTTAATAAACAGAAACCCCGAAGAAAGAGAGGAGCTATCAGGAGAGA
 AACAGAGGAAAAAGAAAGCCGTAGGACAGAGGATGAGCAGAAACAGAAAGAAAGAGATCGTAGAGACATAGAGAGATC
 AGCAAGCTATTGGCCACTGTCTTGTAGTGGACAGAAACAGGATAGACAGGGAGAGAGAGAGGAGGTCCCACTGATCGCG
 ACCAGTGTGCTACTGCAAGAAAAAGGGCAGTGGGCTAAGATTGTCCAGAAACCCAGGAGGCTCGGGGACCAAGACC

CMV promoter

R
 US
 GT = 5' ss

gag

FIGURE 3D

CCAGACCTCCCTCTGACCTAGATGACTAGGAGGTCAGGGTCAGGAGCCCCCCTGAAACCAGGATAACCCCTCAAAGTC
 GGGGGGCAACCCGTCACCTTCCTGTAGATACTGGGGCCACACTCCGTGCTGACCCAAAATCCTGGACCCCTAAGTGATA
 AGTCTGCTGGGTCCAGGGGCTACTGGAGGAAGCGGTATCCCTGGACTACGGATCGCAAAGTACATCTAGCTACCGTTAA
 GGTACCCACTCTTTCTCCATGTACAGAGCTCTCCCTATCCTCTGTTAGGAAGAGATTTCCTGACTAAACTAAAAGCCCAA
 ATCCACTTTGAGGGATCAGGAGCCAGGTTATCGGACCAATGGGGCAGCCCTGCAAGTGTGACCCTAATATAGAAGATG
 AGCATCGCTACATGAGACCTCAAAGAGCCAGATGTTCTCTAGGGTCCACATGGCTGTCTGATTTCCTCAGGCCCTGGG
 GGAAGCCGGGGCTGGGACTGGCAGTTCCGCAAGCTCCCTGATCATACCTCTGAAAGCAACCTTACCCCGTGTCCATA
 AAACRATACCCCATCTCACAAGAAAGCCAGACTGGGATCAAGCCCCACATACAGAGACTGTTGGACAGGGAACTACTGGTAC
 CCTGGCAGTCCCGCTGGAAACGCCCCCTGTACCCGTTAAGAAACAGGGACTAATGATTATAGCCCTGTCCAGGATCTGAG
 AGAAGTCAACAGCGGGTGGAGACATCCACCCACCGTGGCCACCCCTTACACCTCTTGAGCGGGCTCCACCGTCCAC
 CAGTGGTACACTGTGCTTGATTAAAGGATGCTTTTCTGCTGAGACTCCACCCCAAGCTCAGGCTCTCTTGGCTTTG
 AGTGGAGAGATCCAGAGATGGGAATCTCAGGACAAATGACCTGGACAGACTCCACAGGGTTTCAAAAACAGTCCACCT
 GTTTGATGAGGCACTGCACAGACCTAGCAGACTTCGGATCCAGCACCCAGACTTGATCCCTGCTACAGTACGTGGATGAC
 TTACTGCTGGCGGCCTCTCTGAGTAGACTGCCAACAAGTACTCGGGCCCTGTACAAACCTTAGGGAACTCGGTATC
 GGGCTCGGCCAAGAAAGCCCAATTTGCCAGAAACAGGTCAAGTATCTGGGTATCTTTCTAAAGAGGGTCAAGATGGCT
 GACTGAGGCCAGAAAAGAGACTGTGATGGGGCGCTACTCCGAGACCCCTCGACACTAAGGGAGTTCTTAGGGACGGCA
 GGGTTCTGTCCCTCTGGATCCCTGGGTTTGAGAAATGGCAGCCCCCTTGTAACCTCTCACAAAACGGGACTCTGTTTA
 ATTGGGGCCAGACCAACAAAGGCTATCAAGAAATCAAGCAAGCTCTTTCTAACTGCCCCAGCCCTGGGGTTGCCAGATT
 GACTAAGCCCTTTGAACTCTTTGTGACGAGAGAGCAGGGCTACGCCAAGGTGTCTTAACGCCAAAACCTGGGACCTTGGCT
 CGGCCGTTGGCTACCTGTCCAAAAGCTAGACCCAGTAGCAGCTGGGTGGCCCCCTTGCCTAGGGATGGTAGCAGCCATTG
 CCGTACTGACAAAGGATGCAGGCAAGCTAACATGGGACAGCCACTAGTCACTTCTGCCCCCATGCASTAGAGGCACTAGT
 CAAACAACCCCGACCGTGTGCTTTCCACGCGCCGGATGACTCACTATCAGGCTTGCTTTGGACACGGACCGGTCAG
 TTGGACCCGTTGGTAGCCCTGAACCCGGTACCTGCTCCCACTGCTTAGGAGAGGCTGCACACACTGCTTGTATATCC
 TGGCCGAGGCCACGGAAACCGGACCGGACCTAACGGACAGCCGCTCCAGAGCCGACACACCTGTTACAGGATGGAG
 CAGTCTCTTACAAGAGGGACAGCGTAAGCGGGCAGCTGGGTGACCAAGAGACCGAGGTAATCTGGGCTAAAGCCCTGCCA
 GCCGGGACATCCGCTCAGCGGCTGAAGTATAGCACTCACCCAGGCCCTAAAGATGGCAGAGGTAAGAAGCTAAATGTTT
 ATACTGATAGCCGTATGCTTTTGTACTGCCATATCCATGAGAAATATACAGAAGGCGTGGGTTGCTCACATCAGAAGG
 CAAAGAGATCAAAAATAAAGACGAGATCTTGGCCCTACTAAAAGCCCTCTTTCTGCCAAAAGACTTAGCATATCCATTGT
 CCAGGACATCAAAAGGACACAGGCGGAGGCTAGAGGCAACCGGATGGCTGACCAAGGGGCCGAAAGGACGACATCACAG
 AGACTCCAGACCTCTACCTCTCTATAGAAATTCATCACCTACACCTCAGAACATTTTCATTACACAGTACTGATAT

[pol]

FIGURE 3D (cont'd)

8/36

AAAGGACCTAACCAAGTTGGGGGCCATTATGATATAAACAAGAAAGTATTTGGGTCATCCAGGAAAACCTGTGATGCTGAC
 CAGTTTACTTTTGAATATTAGACTTTCTTCATCAGCTGACTCACCCTCAGCTTCTCAAATAATGAAGGCTCTGCTAGAGAGAA
 GTCACAGTCCCTACTTACACTGCTGAACCGGGATCGAACTCTCAAAATATATCAGTCAGACCTGCAAAAGCTTTGTGCACAACTCAA
 GCGCAGCAAGTCTGCGCTTAACACCGCAACTAGGCTTCCCGGGCATCCGCGCGCACTATTTGGGAGATCCATTTCAACGAG
 ATAAAGCCCGGATTTGTATGGCTATAAATATCTTCTAGTTTTTATAGATACCTTTTCTGGCTGGATAGAAGCTTTCCCAACCA
 ACAAAGAAACCCCAAGCTCTTAACCAAGAGCTACTAGAGAGATCTTCCCAAGCTTGGCATGCTCAAGTATTGGCAAC
 TGACAAATGGGCTTGGCTTCTTCCAGGCTGAGTCAGACAGTGGCGGATCTGTGGGGATTGATTGGAAATTACATTGTGCA
 TACAGACCCCAAGGCTCAGGCTAGGAGAGAAATGAATAGAACCATCAAGGAGACTTTAACTAAATTAAGGCTTGCACCTG
 GCTCTAGAGACTGGGTGCTCTACTTCCCTTAGCTTCTGACCGAGCCCGAACACGCTGGGCTCCCATGGCTTCAACCCATA
 TGAGATCTTATATGGGCAACCCCGCCCTTTGTAACTTCCCTGACCTGACATGACAAGCTTACTAACCAAGCCCTCTCTC
 CAAGCTCACTTACAGGCTTCTTACTTACTTACAGCAAGCTCTGGAGACCTTGGCGGAGCTTACCAAGAACAATGGACC
 GACCGGTGGTACCTCAACCTTACCGAGTGGCGGACACAGTGTGGGTCCGCGACACAGACTAAGAACCTAGAACCTGCTG
 GAAAGGACCTTACACAGTCTTGTGACACACCCCACTGCGCTTCAAGTAGACGGCATCGCAGCTTGGATACACGCGCGCAU
 GTGAAGGCTGCGACCCCGGGGGTGGACCATCTCTAGACTGACCTGGCGGTTCACGCTCTCAAAACCCCTCAAGATAA
 GATTAAACCCGTGGAGCCCTTAATAGTCACTGGAGTCTGTAGAGTAGGATGGCAGAGAGUCCCATCAGTCTTTTAAT
 GTAACTGGAGAGTCAACCAACCTGATGACTGGGCTACCGCAATGCCACCTCCCTCTGGGAAGTGTACAAGATGCTTCC
 CAAAATATATTTTGTATCTATGTGATCTGGTGGAGAGAGTGGGACCCCTCAGAACAGGAACCGTATGTGGGTATGGCTG
 CAAGTCCCTCCGAGGGGAGACAGCGGACCCGACTTTTGACTTTTACGTGTGCTGGGCTATACCGTAAAGTGGGGTGTGGG
 GCAACAGAGAGGGCTACTCTGTAAATGGGCTGTCAAAACAGTGCACAGCTTACTGCAAGCCACATCATCTGGGACC
 TAATCTCTTTAAGCGGCTAATACCCCTGGGACACGGGATGCTCTAAAGTTGCTGTGGCTCCCTGCTACGACTCTCTCA
 AGTATCAATTCCTTCAAGGGGCTACTCGAGCGGGCAGATGCAACCTCTAGTCTCTAGAAATCACTGATGCAAGAAAG
 GCTAACTGGGAGGGGCCAATCTGTGGGACTGAGACTGTACGGGACAGGAACAGATCTATTACCATGTTCTCCCTGACCC
 GGCAGGTCTTAAATGTGGGACCCCGAGTCCCACTAGGCGCCCAACCCAGTATTACCGGACCAAGAGCTCCCTTCTCACCAT
 AGAGATTGTACCGGCTCCACAGCTCACTAGCCCTCTCAATACAGTATTACCTCCCTTCCACTACAGTACACCTCAACCTCT
 CCTCAAGTCTCAAGTCTCCACAGCTCACTCCCGGAAGTGGAGATAGACTACTAGTCTAGTCTCAAGGAGGCTATCAGGCG
 TTAACCTCACCATCTCCAGACAGACCCCAAGAAATGTGGCTGTCTTACTGTCTGGGACCTCTTATTACGAGGAGTACGCT
 CGTGGGCACTTATACCAATCATCTCCCGGCTCTGGGCAAGCTGTAGGCGCTCTCCCAACATAAGCTTACCTATCTGAAGTG
 ACAGGACAGGGCTATGCTGGGCGGCTAGTCTCAAACTCACCAGGCTTATGTAAACACCAACCAAGGCGCGGCTCAGGAT
 CTTACTACTTGTGACGACCCCGCGCAAAATGTGGGCTTGCAGCACTGATTTGACTCTCTGCTTGTCCACACCGGCTCTAA
 TCTAACCACAGATTATTTGTATTTAGTTCAACTCTGGGCGCAGTAAATTTACCACTCTCCCGATATATGATGCTGCTG
 GAACAGCGTACCAAAATATAAAGAGAGCCAGTATCTATTGACCCCTGGCTTCTTACTAGCAGGATTAACCTGGGAGGCTTC
 CAGCTGGAATAGGAGCGGGGACCTGCTTAAATTAAGCCAGCAGTTTGAAGCAGCTTCACTGCGGCTATCCAGACAGCT
 CAACGAAGTCCAAAGTCAATTAACCACTAGAAAAGTCACTGACCTCTGTTGTCTGAGTAGTCTTACAGAACCGCAGAGGC
 CTAGATTCTGATTTCTTAAAGGAGGGAGGCTCTGGCGCAGCCCTAAAGGAAGATGTTGTTTTTATGCAAGACACACGGGCT
 TAGTGAGAGACAGGATGGCCAAATTAAGAGAAAGGCTTAATCAGAGACAAAAGTATTTGAGACAGGCTAAGGATGGTTCGA
 AGGCTCTTTAATAGATCCCGCTGGTTAACCCTTATATCTCCACCATCATGGGACCTCAATAGTACTCTTACTGATCTTA
 CTCTTTGGACCTTGCATTCTCAATTCGATTTGCTCAATTTGTTAAAGACAGGATCTCAGTGGTCCAGGCTTGTGTTTGA
 AGCAATATCACCGCTTAAACCCATAGAGTACGAGGCTATGAAGCTTACTGGCCGAGCGCTTGAATAGGCGGCTGTG
 CGTTTGTCTATATGTTATTTTCCACCATATTCGCGCTTTTGGCAATCTGAGGCGCCGGAACCTGGCCCTTCTCTTGTGAC
 GAGCATTCCTAGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGCTCTGTTGAATGTGTGAAGGAAGCAGTCTCTCTGGAA
 GCTCTTGAAGACAAACACCTCTGTAGCGAUCCTTTGCAAGCAGCGGAACCTCCACCTGGGACAGGCTCTCTGCGGCT
 AAAAGCCACGCTGATATAGATACACCTGCAAGGCGGACAAACCCAGTGGCAGCTTGTGAGTTGGATAGTTGTGGAAGAGT
 CAAATGGCTCTCTCAAGCGTATTCAACAAGGGCTGAAGGATGCCCAGAGGATACCCATTTGTATGGGATCTGATCTGGGG
 CCTCGGTGCACATGCTTTACATGTGTTTGTAGTCAGGTTAAAAAAGCTCTAGGCGCCCGCAACACGGGGACGTTGTTTCC
 TTTGAAAAACACCACTATAAATGCTCACCAGCGGATGGGCTTCAAGTGGGATCAAAAGGCGATGATATCGCTTACAGCA
 GGCCTGCTGGGCTACAGGAGGGCTGGGCTGCTATCGGCGGCTGTCTGATCAACAACAGGACGGCAGTGTCTGGGACGG
 GCGCACACATGAGGTTCCAGAGGGCTCCCGCACCTTGCACGGGAGATCTCCACCTGGAGAACTGTGCCAGCTGGAGG
 GCAAGGTGTACAGGACACACCTGTACACCTACCTGTCTCTTGTGACATGTGTACCGGCTATCATCATGTATGCGGCAT
 CCTAGGTGTGTGATCGCGGAGAGCGTGAACCTCAAGTCCAGGCGGAGAGTACCTGCAAAACAGCGGCGCAGAGGTGTG
 GTGTTGACGATGAGAGGTGTAAAGAGCTGATGAAGAGTTCACTGACAGAGGCTCAGGACTGGTTGAGATATCGGCTG

AG = 3' ss

4070A env1

Mbp1

EMCV IRES1

Psi1

yCD2

FIGURE 3D (cont'd)

9/36

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CMV Promotor (1-582)>>>
|
1   TAGTTATTAAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCGG 60
    ATCAATAATTATCATTAGTTAATGCCCCAGTAATCAAGTATCGGGTATATACCTCAAGGC

61   CGTTACATAACTTACGGTAATGGCCCCGCTGGCTGACCGCCCAACGACCCCCGCCCATT 120
    GCAATGTATTGAATCCCATTTACCGGGCGGACCGACTGGCGGGTTGCTGGGGGCGGGTAA

121  GACGTCATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCA 180
    CTGCAGTTAATTAATGCATACAAGGGTATCATTGCGGGTTATCCCTGAAAGCTAACTGCACT

181  ATGGGTGGAGTATTTACGGTAAACTGCCCCACTTGGCAGTACATCAAGTGTATCATATGCC 240
    TACCCACCTCATAAATGCCATTTGAAGGGTGAACCGTCATGTAGTTCACATAGTATACGG

241  AAGTACGCCCCCTATTGACGTCAATGACGGTAATGGCCCCGCTGGCATTATGCCCCAGTA 300
    TTCATCGGGGGATAACTGCAGTTACTGCCATTTACCGGGCGGACCGTAATAAGGGTCAT

                                     Eco105I
                                     |
                                     SnaBI
                                     |
                                     BstSNI
                                     |
301  CATGACCTTATGGCACTTTCCFACCTGGCAGTACATCTACGTATTASTCATCGCTATTAC 360
    GTACTGGAATACCTTGAAAGGATGAACCGTCATGTAGATGCATAATCAGTAGCGATAATG

361  CATGGTGATGCGGTTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGG 420
    GTACCACTACGCCAAAACCGTCATGTAGTTACCCGCACCTATCGCCAAACTGAGTGCCCC

421  ATTTCCAAGTCTCCACCCCAATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACG 480
    TAAAGGTTTACAGAGGTGGGGTAACCTGCAGTTACCCCTCAAACAAAACCTGGTTTTAGTTGC

481  GGACTTTCCAAAATGTGTAAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCSTGT 540
    CCTGAAAGGTTTTACAGCATTGTTGAGGCGGGGTAACCTGCGTTTACCCGCCATCCGCACA

                                     R region (583-650)>>>
                                     |
541  ACCGTGGCAGGTCTATATAAGCCAGAGCTCGTTTGTAGTCAACGGCGCCCACTCCTCCGATTC 600
    TGCCACCCCTCCAGATATATTGCTCTCGACCAATCACTTGGCCGCGGTCAGGAGGCTAAC

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FIGURE 3E

10/36

05 region (651-1202)>>>

|

601 ACTGAGTCGCCCCGGGTACCCGTGTATCCAAATAAACCCCTCTTGCAGTTGCATCCGACTTGT 660
TGA CTCAGCGGGCCCATGGGCACATAGGTTATTTGGGAGAACGTCAACGTAGGCTGAACA

661 GGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTGAGCGGGGGTC 720
CCAGAGCGACAAAGGAACCCCTCCAGAGGAGACTCACTA ACTGATGGGCAGTCGCCCCCAG

721 TTTCATTTGGGGGCTCGTCCGGGATCGGGAGACCCCTGCCAGGGACCAACGACCCACCA 780
AAAGTAAACUCCCGAGCAGGCCCTAGCCCTCTCGGGACGGGTCCCTGGTGGCTGGGTGGT

5'SS (788)

|

781 CCGGGAGGTAAGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGCTAGTGTCTATGAC 840
GGCCCTCCATTCCAGCCGTCGTTGAATAGACACAGACAGGCTAACAGATCACAGATACTG

841 TGATTTTATCGCCTGCTCGGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCG 900
ACTAAATACCGCGACCCAGCCATGATCAATCGATTGATCGAGACATAGACCGCCTGGGC

901 TGGTGGAACTGACGAGTTGGCAACACCGGGCCCAACCCCTGGGAGACGTCOCAGGGACTT 960
ACCACCTTGACTGCTCAAGCCTTGTGGGCCGGCGTTGGGACCCCTCTGCAGGGTCCCTGAA

961 CCGGGGCCCTTTTGTGGCCCGACCTGAGTCCAAAATCCGATCGTTTGGACTCTTTG 1020
GCCCCCGGCAAAAACACCGGGCTGGACTCAGTTTTTAGGGCTAGCAAAACCTGAGAAAC

1021 GTTCACCCCCCTTACAGGAGCGATATCTGGTTCCTGGTACGAGACGAGAACTAAACAGT 1080
CACCTGGGGGAATCTCCTCCCTATACACCAAGAACCATCCTCTGCTCTTGGATTTTGTCA

1081 TCCCGCCTCCGTCTGAATTTTGGCTTTGGGTTTGGGACCGAAGCCGGCCCGCGCGTCTTG 1140
AGGGCGGAGGCAGACTTAAAAACGAAGCCAAACCCCTGGCTTCGGCGCGCGCGCGAGAAC

1141 TCTGCTCGAGCATCGTTCTGTGTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAGA 1200
AGACGACGTCGTAGCAAGACACAAACAGAGACAGACTGACACAAAGACATRAACAGACTCT

gag (1203, 2819)>>>

|

1201 ATATGGGOCAGACTGTATCCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATGTG 1260
TATACCCGCTCTGACAATGCTGAGGGAATTCRAACTGGAATCCAGTGACCTTTCTACAGC

1261 AGCGGATCGCTCACAACCACTCGGTAGATGTCAAGAGAGAGAGGTTGGGTTACCTTCTGCT 1320
TCGCCTAGCGAGTGTGGTCAGCCATCTACAGTTCCTCTCTGCAACCCATGGAAGACGA

1321 CTGCAGAAATGGCCACCTTTAACCTCGGATGCGCCGAGACCGCACCTTTAACCGAGAGC 1380
GACGCTTTACCGGTTGGAAATTCAGCCCTACCGCGGCTCTGCCGTGGAAATTCGCTCTTG

1381 TCATCACCCAGGTTAAGACCAAGGTCTTTTCACCTGCCCCGCGATGGAACACCCAGACAGG 1440
AGTAGTGGGTCCAAATTCCTAGTTCAGAAAAGTGGACCGGGCGTACCTGTGGGTCTGGTCC

1441 TCCCCTACATCGTGACCTGGGAAGCCTTGGGCTTTTGACCTCCCTCCCTGGGTCAAGCCCT 1500
AGGGGATGTAGCACTGGACCCCTTCGGAACCGAAACTGGGGGAGGGACCCAGTTCCGGGA

FIGURE 3E (cont'd)

11/36

1501 TTGTACACCCCTAAGCCTCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCCTTGAAC 1560
 AACATGTGGGATTCGGAGCGGAGGAGAAGGAGGTAGGCGGGCAGAGAGGGGGAACCTG
 1561 CTCCTCGTTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCACTCCTTCTCTAGGCG 1620
 GAGGAGCAAGCTGGGGCGGAGCTAGGAGGGAAATAGGTGCGGAGTGAGGAAGAGATCCGC
 1621 CCAAACCTAAACCTCAAGTTCTTTCTGACAGTGGGGGGCCGCTCATCGACCTACTTACAG 1680
 GGTTTTGGATTTGGAGTTCAAGAAAGACTGTCACCCCCCGCGAGTAGCTGGATGAATGTC
 1681 AAGACCCCCCGCCTTATAGGGACCCAAGACCACCCCTTCCGACAGGGACGGAAATGGTG 1740
 TTCTGGGGGGCGGAATATCCCTGGGTTCTGTTGGGGGAAGCTGTCCCTGCCCTTTACCA
 1741 GAGAAGCGACCCCTGCGGGAGAGGCACCCGACCCCTCCCCAATGGCATCTCGCTACGTG 1800
 CTCCTCGCTGGGGACGCCCTCTCCGTGGCTGGGGAGGGGTACCGTAGAGCGGATGCAC
 1801 GGAGACGGGAGCCCCCTGTGGCCGACTCCACTACCTCGCAGGCATTCCCCCTCCGCGCAG 1860
 CCTCTGCCCTCGGGGACACCGGCTGAGGTGATGGAGCGTCCGTAAGGGGGAGGCGCGTC
 1861 GAGGAAACGGACAGCTTCAATACTGSCCCTTCTCCTCTTCTGACCTTTACAACTGAAAA 1920
 CTCCTTTGCCCTGTGCAAGTTATGACCGGCAAGAGGAGAAGACTGGAAATGTTGACCTTTT
 1921 ATAATAACCCCTTCTTTTTCTGAAGATCCAGGTAAACTGACAGCTCTGATCGAGTCTGTT 1980
 TATTATTGGGAAGAAAAAGACTTCTAGGTCCATTTGACTGTGAGACTAGCTCAGACAAG
 1981 TCATCACCACATCAGCCACCTGGGACGACTGTCAGCAGCTGTTGGGGACTCTGCTGACCG 2040
 AGTAGTGGGTAGTCGGGTGGACCTGCTGACAGTCTGTCGACAACCCCTGAGACGACTGGC
 3121 ACTTTGAGGGATCAGGAGCCCAGGTTATGGGACCAATGGGGCAGCCCCCTGCAAGTGTGTA 3180
 TGAAACTCCCTACTCCTCGGGTCCAATACCCCTGCTTACCCCGTCGGGGACGTTACAACT
 3181 CCCTAAATATAGAAGATGAGCATCGGCTACATGAGACCTCAAAAGAGCCAGATGTTTCTC 3240
 GGGATTTATATCTTCTACTCGTAGCCGATGTACTCTGGAGTTTTCTCGGTCTACAAAGAG
 3241 TAGGGTCCACATCGCTGTCTGATTTTCTCAGGCCTGGGCGGAAACCGGGGGCATGGGAC 3300
 ATCCCAGGTGTACCGACAGACTAAAAGGAGTCCGGACCCCGCTTTGGCCCCCGTACCCCTG
 3301 TGGCAGTTCGCCAAGCTCCTCTGATCATACCTCTGAAAGCAACCTCTACCCCCGTGTCCA 3360
 ACCGTCAGCGGTTCGAGGAGACTAGTATGGAGACTTTCGTTGGAGATGGGGGCACAGGT
 3361 TAAAACAATACCCCATGTCACAAGAAGCCAGACTGGGGATCAAGCCCCACATACAGAGAC 3420
 ATTTTGTATGGGGTACAGTGTCTCTCGGTCTGACCCCTAGTTGCGGGTGTATGTCTCTG
 3421 TGTTGGACCAGGGAATACTGGTACCCTGCCAGTCCCCCTGGAACACGCCCCCTGCTACCCG 3480
 ACAACCTGGTCCCTTATGACCATGGGACGGTCAGGGGGACCTTGTGCGGGGACGATGGGC
 3481 TTAAGAAACCAGGGACTAATGATTATAGGCCTGTCCAGGATCTGAGAGAAGTCAACAAGC 3540
 AATTCTTTGGTCCCTGATTACTAATATCCGACAGTCTTAGACTCTCTTCAGTTGTTGC

3' SS (3314)

FIGURE 3E (cont'd)

12/36

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3541  GGGTGGGAAGACATCCACCCACCGTGCCCAACCCCTTACAACCTCTTGAGCGGGCTCCCAC 3600
      CCCACCTTCTGTAGGTGGGGTGGCACGGGTTGGGAATGTTGGAGAACTCGCCCCAGGGTG

3601  CGTCCCACCAGTGGGTACACTGTGCTTGATTTAAAGCATGCCCTTTTCTGCCCTGAGACTCC 3660
      GCAGGGTGGTCACCATGTCACACGAACATAAATTCCTACCGAAAAAGACGGACTCTCAGG

                                     PfeI
                                     |
                                     TfiI
                                     |
3661  ACCCCACCAGTCAGCCTCTCTTCGCCCTTTGAGTGGAGAGATCCAGAGATGGGAATCTCAG 3720
      TGGGGTGGTCAGTCGGAGAGAAGCGGAAACTCACCTCTCTAGGTCTCTACCCCTTAGAGTC

      MfeI
      |
      MniI
      |

3721  GACAATTGACCTGGACCAGACTCCCACAGGGTTTCAAAAACAGTCCCACCTGTTTGATG 3780
      CTGTTAACTGGACCTGGTCTGAGGGTGTCCCAAAGTTTTTGTGAGGGTGGGACAAACTAC

                                     MroI
                                     |
                                     BseAI
                                     |
                                     BspI3I
                                     |
                                     BspEI
                                     |
                                     Kpn2I
                                     |
                                     AccIII
                                     |

3781  AGGCACTGCACAGAGACCTAGCAGACTTCGCGATCCAGCACCCAGACTTGATCCTGCTAC 3840
      TCCGTGACGTGTCTCTGGATCGTCTGAAGGCCCTAGGTGCTGGGTCTGAACCTAGGACGATG

3841  AGTACGTGGATGACTTACTGCTGGCCGCCACTTCTGAGCTAGACTGCCAACAAGGTACTC 3900
      TCATGCACCTACTGAATGACGACCGGCGGTGAAGACTCGATCTGACGGTTGTTCCATGAG

3121  ACTTTGAGGGATCAGGAGCCCAAGTTATGGGACCAATGGGGCAGCCCTGCAAGTGTGTA 3180
      TGAAACTCCCTAGTCCTCGGGTCCAATACCCTGCTTACCCCGTCGGGGACGTTACAACT

3181  CCCTAAATATAGAAGATGAGCATCGGGCTACATGAGACCTCAAAAGAGCCAGATGTTTCTC 3240
      GGCATTTATATCTTCTACTCGTAGCCGATGTAATCTGGAGTTTTCTCGGTCTACAAAGAG

3241  TAGGGTCCACATGGCTGTCTGATTTTCCTCAGGCCTGGGCGGAAACCGGGSGCATGGGAC 3300
      ATCCCAGGTGTACCGACAGACTAAAAGGAGTCCGGACCCGCCCTTTGGCCCCCGTACCCTG

```

FIGURE 3E (cont'd)

13/36



FIGURE 3E (cont'd)

14/36

```

3841 AGTACGTGGATGACTTACTGCTGGCCGCCACTTCTGAGCTAGACTGCCAACAGGTACTC 3900
    TCATGCACCTACTGAATGACGACCGGCGSTGAAGACTCGATCTGACGGTTGTTCCATGAG

3901 GGGCCCTGTTACAAACCCTAGGGAACCTCGGGTATCGGGCCCTCGGCCAAGAAAGCCCCAA 3960
    CCGGGACAATGTTTGGGATCCCTGGAGGCCATAGCCCGGAGCCGGTTCTTTGCGGTTT

3961 TTTGCCACAAACAGGTCAAGTATCTGGGSTATCTTCTAAAAGAGGGTCAGAGATGGCTGA 4020
    AAACGGTCTTTGTCCAGTTCATAGACCCCATAGAAGATTTTCTCCAGTCTCTACCGACT

4021 CTGAGGCCAGAAAAGAGACTGTGATGGGCGAGCCTACTCCGAAGACCCCTCGACAATAA 4080
    GACTCCGGTCTTTTCTCTGACACTACCCCGTCGGATGAGGCTTCTGGGGACCTCTTGATT

4081 GGGAGTTCCTAGGGACGGCAGGCTTCTGTGCCTCTGGATCCCTGGGTTTGCAGAAATGG 4140
    CCTCAAGGATCCCTGCCGTCCGAAGACAGCGGAGACCTAGGGACCCAAACGTCCTTTACC

4141 CAGCCCCCTTGTACCTCTCTACCAAAACGGGACTCTGTTTAAATTGGGGCCAGACCAAC 4200
    GTCGGGGGAACATGGGAGAGTGGTTTTGCCCTGAGACAAATTAACCCCGGGTCTGTTG

4201 AAAAGGCCTATCAAGAAATCAAGCAAGCTCTTCTAACTGCCCCAGCCCTGGGGTTGCCAG 4260
    TTTTCGGATAGTCTTTAGTTCGTTGAGAAGATTGACGGGGTCGGGACCCCAACGGTC

                                     SalI
                                     |
4261 ATTTGACTAAGCCCTTTGAACTCTTTGTGACGAGAAGCAGGGCTACGCCAAAGGTGTCC 4320
    TAAACTGATTGGGAAACTTGAGAAACAGCTGCTCTTCGTCCCGATGCGGTTTCCACAGG

4321 TAACGCAAAAACCTGGGACCTTGGCGTCGSCCGGTGGCCCTACCTGTCCAAAAGCTAGACC 4380
    ATTGCGTTTTTGAACCTGGAACCGCAGCCGGCCACCGGATGGACAGGTTTTTCGATCTGG

4381 CAGTAGCAGCTGGGTGGGCCCCCTTGCCCTACGATGGTAGCAGCCATTGCCGTACTGACAA 4440
    GTCATCGTCGACCCACCGGGGGAACGGATGCCTACCATCGTCGGTAACGGCATGACTGTT

4441 AGGATGCAGGCAAGCTAACCATGGGACAGCCACTAGTCATTCTGGCCCCCATGCAGTAG 4500
    TCCTACGTCCGTTGATTGGTACCCTGTGCGTGATCAGTAAGACCGGGGGTACGTCATC

4501 AGGCACTAGTCAAAACAACCCCCGACCGCTGGCTTTCCAACGCCCCGATGACTCACTATC 4560
    TCCGTGATCAGTTTGTGGGGGGCTGGCGACCGAAAGGTTGCGGGCCTACTGAGTGATAG

4561 AGGCCTTGCTTTTGGACACGGACCGGGTCCAGTTCCGGACCGGTGGTAGCCCTGAACCCGG 4620
    TCCGGAACGAAAACCTGTGCCTGGCCAGGTCAAGCCTGGCCACCATCGGGACTTGGGCC

4621 CTACGCTGCTCCCACTGCCTGAGGAAGGGCTGCAACACAACCTGCCTTGATATCCTGGCCG 4680
    GATGCGACGAGGGTGACGGACTCCTTCCCGACGTTGTGTTGACGGAATAAGGACCGGC

4681 AAGCCCACCGAACCCGACCCGACCTAACGGACCAAGCCGCTCCAGACCGCCGACCAACCT 4740
    TTCGGGTGCCTTGGGCTGGGCTGGATTGCCTGCTCGCGAGGGTCTGCGGCTGTTGTGGA

4741 GGTACACGGATGGAAGCAGTCTCTTACAAGAGGGACAGCGTAAGGCGGGAGCTGCGGTGA 4800
    CCATGTGCCTACCTTCGTGAGAGAATGTTCTCCCTGTGCAATTCCGCCCTGACGCCCACT

```

FIGURE 3E (cont'd)

15/36

BlnI
 |
 CclII
 |
 Bpu1102I
 |
 Bsp1720I
 |

4801 CCACCGAGACCGAGGTAATCTGGGCTAAAGCCCTGCCAGCCGGGACATCCGCTCAGCGGG 4860
 GGTGCTCTGCTCCATTAGACCCGATTCGGGACGGTUGGCCCTGTAGGGGAGTCCGCC

4861 CTGAACTGATAGCACTCAGCCAGGCCCTAAAGATGGCAGAAGGTAAGAAGCTAAATGTTT 4920
 GACTTGACTATCGTGAGTGGGTCCGGGATTTCTACCTCTCTCCATTCTTCGATTTACAAA

4921 ATACTGATAGCGGTTATGCTTTTGTACTGCCCATATTCATGGAGMAATATACAGAAGGC 4980
 TATGACTATCGGCAATACGAAACGATGACGGGTATAGGTACTCTTTATATGTCTTCCG

4981 CTGGGTTGCTCAGTCAGAGGGCAAGAGATCAAAAATAAAGACGAGATCTTGCCCTTAC 5040
 CACCCAAACGAGTGTAGTCTTCCGTTTCTCTAGTTTATTTCTGCTGTAGAACCGGGATG

5041 TAAAAGCCCTCTTTCTGCCAAAAGACTTAGCATAATCCATTGTCCAGGACATCAAAAGG 5100
 ATTTCCGGGAGAAAGACCGGTTTTCTGAATCGTATTAGGTAACAGGTCCTGTAGTTTTCC

5101 GACACAGCGCCGAGGCTAGAGGCCAACCGGATGGCTGAACCAAGCGGCCGAAAGGCAGCCA 5160
 CTGTGTCCGGCTCCGATCTCCGTTGGCCCTACCGACTGGTTCCGCCGGGCTTTCCGTCGGT

5161 TCACAGAGACTCCAGACACCTCTACCTCTCTCATAGAAAATTCATCACCTACACCTCAG 5220
 AGTGTCTCTGAGGTCTCTGCAGATGGGAGGAGTATCTTTTAAAGTAGTGGCATGTGAGTC

5221 AACATTTTCATTACACAGTCACTGATATAAAGGACCTAACCAAGTTGGGGGCCATTTATG 5280
 TTGTAAAAGTAATGTGTCACTGACTATATTTCTCTGGATTGGTTCAACCCCGGTAATAC

5281 ATRAAACAAGCAAGTATTGGCTCTAACAAGCAAAACCTGTGATGCTTCACCACTTTACTT 5340
 TATTTTGTCTTCTTCATAACCCAGATGGTTCTTTTGGACACTACGGACTGGTCAAAATGAA

5341 TTGAATTATTAGACTTTCTTTCATCAGCTGACTCACTEAGCTTCTCAAAAATGAAGECTC 5400
 AACTTAATAATCTGAAAGAAGTAGTCCACTGAGTGGAGTCCGAAGAGTTTTTACTTCCGAG

5401 TCCTAGAGAGAAGCCACAGTCCCTACTACATGCTGAACCGGATCGAACACTCAAAAATA 5460
 AGGATCTCTCTTCTGTGTCAGGGATGATGTACGACTTGGCCCTAGCTTGTGAGTTTTTAT

5461 TCACTCAGACCTGCAAAAGCTTGTGCACAAAGTCAAGCCAGCAAGTCTGCCGTTAAACAGG 5520
 AGTGACTCTGGACGTTTCGAACAGCTGTTTCAGTTGGGCTCGTTCCAGACGGCAATTTGTCC

SacII
 |
 SgrBI
 |
 Cfr42I
 |
 Sfr303I
 |
 KspI
 |

FIGURE 3E (cont'd)

16/36

5521 GAACTAGGGTCCGCGGGCATCGGGCCCGGCACTCATTGGGAGATCGATTTCAACCGAGATAA 5580
 CTTGATCCCAGGCGCCCGTAGCCGGGCGGTGAGTAACCCCTCTAGCTAAAGTGGCTCTATT

5581 AGCCCGGATTGTATGGCTATAAATATCTTCTAGTTTTTATAGATACCTTTTCTGGCTGGA 5640
 TCGGGCCTAACATAACCGATATTTATAGAAGATCAAAAATATCTATGGAAAAGACCGACCT

5641 TAGAAGCCTTCCCAACCAAGAAAGAAACCGCCAAGGTCGTAACCAAGAAGCTACTAGAGG 5700
 ATCTTCGGAAGGGTTGGTTCTTTCTTTGGCGGTTCCAGCATTGGTTCTTCGATGATCTCC

PaeI
 ↓
 BbuI
 ↓
 SpaHI
 ↓
 SphI
 ↓

5701 AGATCTTCCCCAGGTTCCGCATGCCTCAGGTATTGGGAACTGACAATGGGCCTGCCTTCG 5760
 TCTAGAAGGGGTCCAAGCCGTACGGAGTCCATAACCCCTGACTGTTACCCGGACGGAAGC

6901 CTTCCAAGGGGCTACTCGAGGGGGCAGATGCAACCCCTCTAGTCCTAGAATTCACTGATGC 6960
 GAAGGTTCCCCGATGAGCTCCCCCGTCTACGTTGGGAGATCAGGATCTTAAGTGACTACG

6961 AGGAAAAAAGGCTAACTGGGACGGGCCCCAAATCGTGGGGACTGAGACTGTACCGGACAGG 7020
 TCCTTTTTCCGATTGACCCTGCCCGGGTTTAGCACCCCTGACTCTGACATGGCCTGTCC

7021 AACAGATCCTATTACCATGTTCTCCCTGACCCGGCAGGTCCTTAATGTGGGACCCCGAGT 7080
 TTGTCTAGGATAATGGTACAAGAGGGACTGGGCCGTCCAGGAATTACACCCCTGGGGCTCA

7081 CCCCATAGGGCCCCAACCCAGTATTACCCGACCAAAGACTCCCTTCCTCACC AATAGAGAT 7140
 GGGSTATCCCCGGTTGGGTCATAATGGGCTCGTTTCTGAGGGAAGGAGTGGTTATCTCTA

7141 TGTACCGGCTCCACAGCCACCTAGCCCCCTCAATAACAGTTACCCCCCTTCCACTACCAG 7200
 ACATGGCCGAGGTGTCGGTGGATCGGGGGAGTTATGGTCAATGGGGGAAGGTGATGGTC

7201 TACACCCCTCAACCTCCCCTACAAGTCCAAGTGTCCCACAGCCACCCCCAGGAACTGGAGA 7260
 ATGTGGGAGTTGGAGGGGATGTTCAAGGTTACAGGGTGTCCGTGGGGGTCCTTGACCTCT

7261 TAGACTACTAGCTCTAGTCAAAGGAGCCTATCAGGCGCTTAACCTCACCAATCCCGACAA 7320
 ATCTGATGATCGAGATCAGTTTCCTCGGATAGTCCGCGAATTGGAGTGGTTAGGCCTGTT

7321 GACCCAAGAATGTTGGCTGTGCTTAGTGTCCGGACCTCCTTATTACGAAGGAGTAGCGGT 7380
 CTGGGTTCTTACAACCGACACGAATCACAGCCCTGGAGGAATAATGCTTCCTCATCGCCA

7381 CGTGGGCACTTATACCAATCAFTCCACCGCTCCGGCCAACTGTACGGCCACTTCCCAACA 7440
 GCACCCGTCAATATGGTTAGTAAGGTGGCGAGCCCGGTTGACATGCCGTTGAAGGCTTGT

FIGURE 3E (cont'd)

17/36

```

                                EcoT22I
                                ||
                                NsiI
                                ||
                                Mph1103I
                                ||
                                Zsp2I
                                ||
                                BfrBI
                                ||
                                ||

7441 TAAGCTTACCOCTATCTGAAGTGACAGGACAGGGCCTATGTCATGGGGGCAGTACCTAAAAC 7500
     ATTGGAATGGGATAGACTTCACCTGTCCTGTCCCGGATACGTACCCCGTCATGGATTTC

                                NaeI
                                ||
                                PdiI
                                ||
                                MroNI
                                ||
                                NgoMIV
                                ||
                                ||

7501 TCACCAGGCCTTATGTAACACCACCCAAAGCGCGCGGCTCAGGATCCTACTACCTTGCAGC 7560
     AGTGGTCCGGAATACATTGTGGTGGGTTTCGCGCGCGAGTCCTAGGATGATGGAACGTGC

                                AleI
                                ||
                                OliI
                                ||

7561 ACCCGCCGGAACAATGTGGGCTTGCAGCACTGGATTGACTCCCTGCTTGTCCACCACGGT 7620
     TGGGCGGCCTTGTACACCCGAACGTGCTGACCTAACTGAGGGACGAACAGGTGGTGCCA

7621 GCTCAATCTAACCACAGATTATTGTGTATTAGTTGAACTCTGGCCCAGAGTAATTTACCA 7680
     CGAGTTAGATTGGTGTCTAATAACACATAATCAACTTGAGACCGGGTCTCATTAAATGGT

6901 CTTCCAAGGGGCTACTCGAGGGGGCAGATGCAACCCCTCTAGTCCTAGAATTCACCTGATGC 6960
     GAAGGTTCCTCGATGAGCTCCCCCGTCTACCTTGGCAGATCAGGATCTTAAGTGACTACG

6961 AGCAAAAAAGCCTAACTGGGACGGGGCCAAATCGTGGGGACTGAGACTGTACCGGACAGG 7020
     TCCTTTTTTCCGATTGACCCTGCCCGGGTTTAGCACCCCTGACTCTGACATGGCCTGTCC

7021 AACAGATCCTATTACCATGTTCTCCCTGACCCGGCAGGTCCTTAATGTGGGACCCCGAGT 7080
     TTGCTTAGGATAATGGTACAAGAGGGACTGGGCGCTCCAGGAATTACACCCTGGGGCTCA

```

FIGURE 3E (cont'd)

18/36

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7081  CCCCATAGGGCCCAACCCAGTATTACCCGACCAAAGACTCCCTTCCTCACCAATAGAGAT 7140
      GGGGTATCCCGGGTTGGGTCAATGGGCTGCTTCTGAGGGAAGGAGTGGTTATCTCTA

7141  TGTACCGGCTCCACAGCCACCTAGCCCCCTCAATACCAGTTACCCCCCTCCACTACCAG 7200
      ACATGGCCGAGGTGTGGGTGGATCGGGGAGTTATGGTCAATGGGGGAAGGTGATGGTC

7201  TACACCCCTCAACCTCCCCTACAAGTCCAAAGTGTCCCACAGCCACCCCCAGGAACTGGAGA 7260
      ATGTGGGAGTTGGAGGGGATGTTCAAGGTTACAGGGTGTGGGTGGGGGTCCCTTGACCTCT

7261  TAGACTACTAGCTCTAGTCAAAGGAGCCTATCAGGCGCTTAACCTCACCNAATCCCGACAA 7320
      ATCTGATGATCGAGATCAGTTTCCTCGGATAGTCCGCGAATTGGAGTGGTTAGGGCTGTT

7321  GACCCAAGAATGTTGGCTGTGCTTAGTGTGGGACCTCCTTATTACGAAGGAGTAGCGGT 7380
      CTGGGTTCTTACAACCGACACGAATCACAGCCCTGGAGGAATAATGCTTCCTCATCGCCA

7381  CGTGGGCACTTATACCAATCATTCCACCGTTCGGGCCAACTGTACGGGCACTTCCCAACA 7440
      GCACCCGTGAATATGGTTAGTAAGGTGGCGAGCCCGGTTGACATGCCGGTGAAGGGTTGT

                                     EcoT22I
                                     |
                                     NsiI
                                     |
                                     Mph1103I
                                     |
                                     Zsp2I
                                     |
                                     BfrBI
                                     ||

7441  TAAGCTTACCCCTATCTGAAGTGACAGGACAGGGCCTATGCATGGGGSCAGTACCTAAAAC 7500
      ATTCGAATGGGATAGACTTCAGTGTCTGTCCCGGATACGTACCCCGTCATGGATTTTG

                                     NaeI
                                     |
                                     PdiI
                                     |
                                     MroNI
                                     ||
                                     NgoMIV
                                     ||

7501  TCACCAGGCCTTATGTAACACCACCCAAAGCGCGGCTCAGGATCCTACTACCTTGCAGC 7560
      AGTGGTCCGGAATACATTGTGGTGGGTTTCGGGGCCGAGTCCTAGGATGATGGAACGTGC

```

FIGURE 3E (cont'd)

19/36

AlaI
|
OIII
|

7561 ACCCGCCGGAACAATGTGGGCTTGCAGCACTGGATTGACTCCCTGCTTGTCCACCACGGT 7620
TGGGCGGCGCTTGTACACCCGAACGTCGTGACCTAACTGAGGGACGAACAGGTGGTGCCA

7621 GCTCAATCTAACCACAGATTATTGTGTATTAGTTGAACTCTGGCCCAGAGTAATTTACCA 7680
CCAGTTAGATTGGTGTCTAATAACACATAATCAACTTGAGACCGGGTCTCATTAAATGGT

7681 CTCCCCCGATTATATGTATGCTCAGCTTGAACAGCGTACCAAATATAAAAGAGAGCCAGT 7740
GAGGGGGCTAATATACATACCAGTCGAACCTGTGGCATGGTTTATATTTTCTCTCGGTCA

7741 ATCATTGACCCCTGGCCCTTCTACTAGGAGGATTAACCATGGGAGGGATTGCAGCTGGAAT 7800
TAGTAACTGGGACCGGGAAGATGATCCTCCTAATTGGTACCCCTCCCTAACGTCGACCTTA

7801 AGGGACGGGGACCACTGCCTTAATTAACCCAGCACTTTGAGCAGCTTCATGCCGCTAT 7860
TCCCTGCCCCCTGGTGAAGGAATTAATTTTGGGTGGTCAAACTCGTCCAAGTACGGCGATA

7861 CCAGACAGACCTCAACGAAGTCGAAAAGTCAATTACCAACCTAGAAAAGTCACTGACCTC 7920
GGTCTGTCTGGAGTTGCTTCAGCTTTTCAGTTAATGGTTGGATCTTTTCAGTCACTGGAG

7921 GTTGTCTGAAGTAGTCTACAGAACCGCAGAGGCCTAGATTTGCTATTCTTAAAGGAGGG 7980
CAACAGACTTCATCAGGATGTCTTGGCGTCTCCGGATCTAAACGATAAGGATTTCCCTCCC

7981 AGGTCTCTGCCAGCCCTAAAAGAAGAATGTTGTTTTATGCAGACCACACGGGCTAGT 8040
TCCAGACAGCGTCGGGATTTTCTTCTTACAACAAAAATACGTCTGGTGTGCCCCGATCA

8041 GAGAGACAGCATGGCCAAATTAAGAGAAAGGCTTAATCAGAGACAAAACTATTTGAGAC 8100
CTCTCTGTCTGCTACCGGTTTAATTTCTCTTTCCGAATTAGTCTCTGTTTTTGATAAACTCTG

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

8101 AGGCCAAGGATGGTTCGAAGGCTGTTTAATAGATCCCCCTGGTTTACCACCTTAATCTC 8160
TCCGGTTCCTACCAAGCTTCCCGACAAATTATCTAGGGGGACCAAAATGGTGAATTAGAG

FIGURE 3E (cont'd)

20/36

```

8161 CACCATCATGGGACCTCTAATAGTACTCTTACTGATCTTACTCTTTGGACCTTGCATTCT 8220
      GTGGTAGTACCCTGGAGATTATCATGAGAATGACTAGAATGAGAAACCTGGAACGTAAGA

8221 CAATCGATTGGTCCAATTTGTAAAGACAGGATCTCAGTGGTCCAGGCTCTGGTTTTGAC 8280
      GTTAGCTAACCAGGTAAACAATTTCTGTCCCTAGAGTCACCAGGTCCGAGACCAAACTG

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

                                     ires_emcv reg(8378,8876)>>>
                                     |
8341 GCCGCTTGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACCATATTGCCGT 8400
      CGGCGAACCTTATTCGGGCCACACGCAACAGATATACAATAAAAGGTGCTATAACGGCA

8401 CTTTTGGCAATGTGAGGGCCCCGAAACCTGGCCCTGTCTTCTTGACGAGCATTTCCTAGGG 8460
      GAAAACCGTTACACTCCCGGCCCTTTGGACCGGGACAGAAGAACTGCTCGTAAGGATCCC

8461 GTCTTTCCCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTC 8520
      CAGAAAGGGGAGAGCGGTTTCTTACGTTCCAGACAACTTACAGCACTTCTCTCGTCAAG

8521 CTCTGGAAGCTTCTTGAAGACAAACAACGTCTGTAGCGACCCCTTTCAGGCAGCGGAACC 8580
      GAGACCTTCGAAGAACTTCTGTTTGTGTCAGACATCGCTGGGAAACGTCGCTCGCCTTGG

8581 CCCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAA 8640
      GGGGTGGACCGCTGTCCACGGAGACGCGGTTTTTCGGTGCACATATTCTATGTGGACGTT

8641 AGCGGGCACAACCCCAAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGC 8700
      TCCGCGGTGTTGGGGTCACGGTGCAACACTCACCCTATCAACACCTTTCTCAGTTTACCG

8701 TCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAGAAGGTACCCCATTTGTATGG 8760
      AGAGGAGTTCCGATAAGTTGTTCCCCGACTTCCTACGGGTCTTCCATGGGGTAACATACC

8761 GATCTGATCTGGGGCCTCGGTGCACATGCTTTACATGTGTTTAGTCCAGGTTAAAAAAC 8820
      CTAGACTAGACCCCGGAGCCACGTGTACGAAATGTACACAAATCAGCTCCAATTTTTTTG

```

FIGURE 3E (Cont'd)

21/36

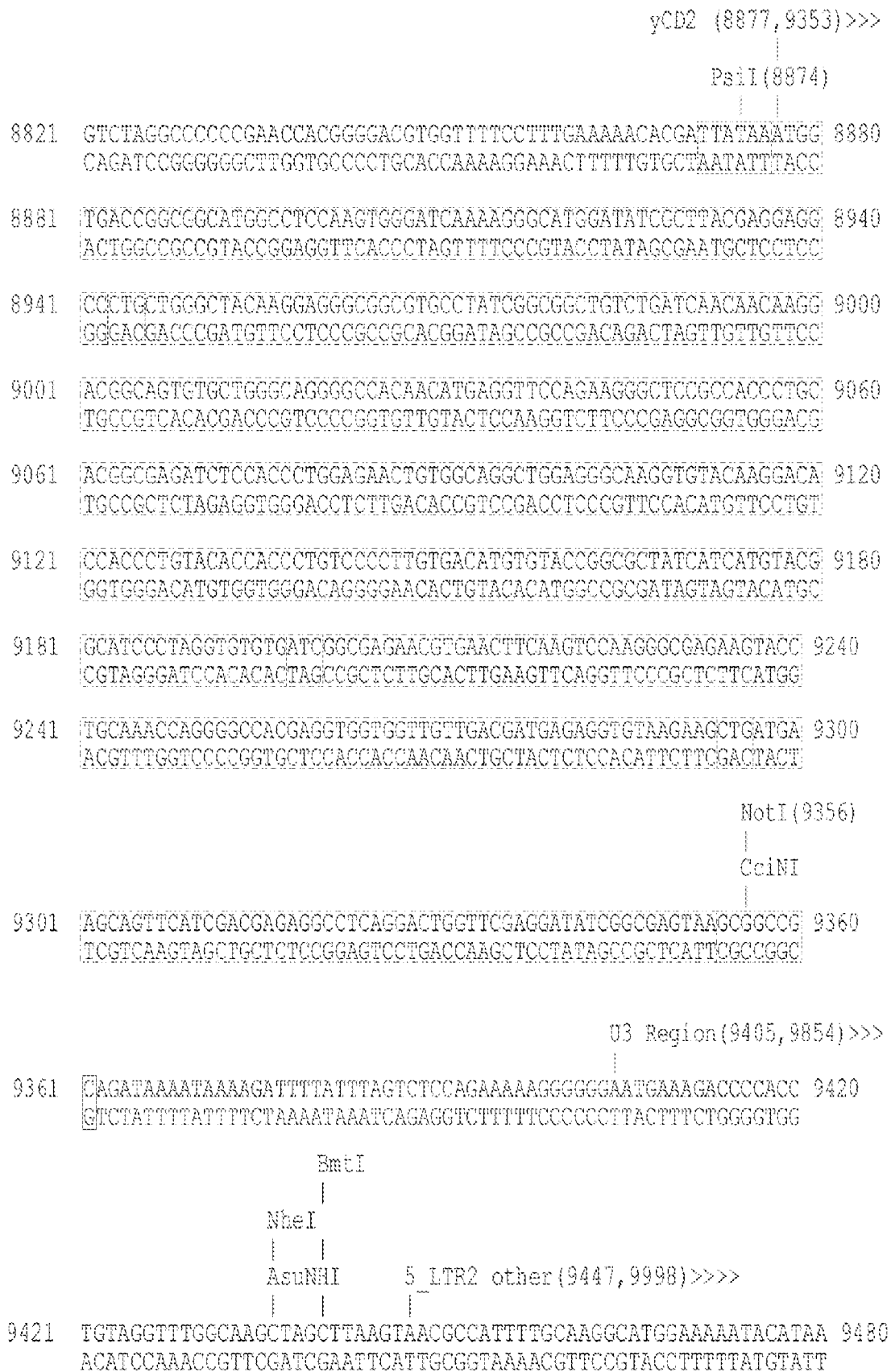


FIGURE 3E (cont'd)

22/36

```

9481 CTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCA 9540
    GACTCTTATCTCTTCAAGTCTAGTTCAGTCCCTTGCTACCTTGTCGACTTATACCCGGT

9541 AACAGGATATCTGTGGTAAGCAGTTCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACA 9600
    TTGTCTATAGACACCATTCTGTCAGGACGGGGCCGAGTCCCGGTTCTTGTCTACCTTGT

9601 GCTGAATATGGGCCAAGCAGGATATCTGTGGTAAGCAGTTCTGCCCCGGCTCAGGGCCA 9660
    CGACTTATACCCGGTTTGTCTATAGACACCATTCTGTCAGGACGGGGCCGAGTCCCGGT

9661 AGAACAGATGGTCCCGAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATG 9720
    TCTTGTCTACCAGGGGTCTACGCCAGGTGCGGAGTCTCTCAAAGATCTCTTGCTAGTCTAC

9721 TTTCCAGGGTGGCCCCAAGGACCTGAAATGACCCTGTCCCTTATTTGAACTAACCAATCAG 9780
    AAAGTCCCACGGGGTTCTGGACTTTACTGGGACACGGAATAAACTTGATTGGTTAGTC

                                     SacI
                                     |
                                     SstI
                                     |
                                PvuI   Psp124BI
                                |       |
                                BsePI   EcoICRI
                                |       |
                                BssHII   Ecl136II
                                |       |
9781 TTCGCTTCTCGCTTCTGTTCCGCGCTTCTGCTCCCGAGCTCAATAAAAGAGCCACAA 9840
    AAGCGAAGAGCGAAGACAAGCCTCCGAAGACGAGGGGCTCGAGTTATTTTCTCGGGTGT

                                R Region(9855,9921)>>>>
                                |
9841 CCCCTCACTCGGGGGCCAGTCTCTCCGATTTGACTGAGTCGCCCCGGGTACCCGTGTATCCA 9900
    GGGGAGTGAGCCCCCGCGTCAGGAGGCTAACTGACTCAGCGGGCCCATGGGCACATAGGT

                                U5 Region(9922,9998)>>>>
                                |
9901 ATAAACCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCTTGGGAGGGTCTCCT 9960
    TATTTGGGAGAACGTCAACGTAGCCTGAACACCAGACGACAAAGGAACCTCCACAGGA

9961 CTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTTCATTACATGTGAGCAAAAGGCCAGCA 10020
    GACTCACTAACTGATGGGCACTCCCCCCCCAGAAAGTAATGTACACTCGTTTTCGGTCTGT

                                pBR322 origin(10045,10664)<<<
                                |
10021 AAAGGCCAGGAACCGTAAAAAGGCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCC 10080
    TTTCGGTCTCTGGCATTTTTTCCGGCGCAACGACCGCAAAAGGTATCCGAGGCGGGGGG

10081 TGACGAGCATCACAATAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATA 10140
    ACTGCTCGTAGTGTTTTTAGCTGCGAGTTCAGTCTCCACCGCTTTGGGCTGTCTGATAT

10141 AAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGGGCTCTCCTGTTCCGACCTGCC 10200
    TTCTATGGTCCGCAAGGGGGACCTTCGAGGGAGCACGGGAGAGGACAAGGCTGGGACGG

```

FIGURE 3E (cont'd)

23/36

10201 GCTTACCGGATACCTGTCCGCCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTC 10260
CGAATGGCCTATGGACAGGCGGAAAGAGGGAAGUCCTTCGCACCGCGAAAGAGTTACGAG

10261 ACCGTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCAAGA 10320
TGCGACATCCATAGAGTCAAGCCACATCCAGCAAGCGAGGTTCCACCCGACACACGTGCT

10321 ACCCCCCCGTTACGCCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAAACCC 10380
TGGGGGGCAAGTCGGGCTGGCGACGCGGAATAGGCCATTGATAGCAGAACTCAGGTTGGG

10381 GGTAAACACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAG 10440
CCATTCTGTGTCTGAATAGCGGTGACCGTCTGTCGGTGACCATTGTCTAATCGTCTCGCTC

10441 GTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAG 10500
CATACATCCGCCACGATCTCTCAAGAACTTCACCACCGGATTGATGCCGATGTGATCTTC

10501 GACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAG 10560
CTGTTCATAAACCATAGACGCGAGACGACTTCGGTCAATGGAAGCCTTTTTCTCAACCATC

10561 CTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGCAAGCAGCA 10620
GAGAACTAGGCCGTTTTGTTGGTGGCGACCATCGCCACCAAAAAAACAACGTTCTGTCT

10621 GATTACGGCGCAGAAAAAAGGATCTCAAGAAGATCCCTTTGATCTTTTCTACGGGGTCTGA 10680
CTAATGCGCGTCTTTTTTTTCTAGAGTTCTTCTAGGAACTAGAAAAGATGCCCCAGACT

10681 CGCTCAGTGGAAACGAAACTCAGCTTAAGGCAFTTTGGTCAATGAGATTATCAAAAAGGAT 10740
GCCAGTCACCTTGCTTTTGAGTGCAATTCCTFAAAACCAGTACTCTAATAGTTTTTCTTA

10741 CTTACCTAGATCCTTTTAAATTA AAAATGAAGTTTTAAATCAATCTAAAGTATATATGA 10800
GAAGTGGATCTAGGAAAATTTAATTTTTTACTTCAAAATTTAGTTAGATTTTCATATATACT

amp marker(10819,11679)<<<
|

10801 GTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAAGGCACCTATCTCAGCGATCTG 10860
CATTTGAACCAGACTGTCAATGGTTACGAATTAGTCACTCCGTGGATAGAGTCGCTAGAC

10861 TCTATTTCTGTTTCATCCATAGTTGCCTGACTCCCCGTGCTGTAGATAACTACGATACGGGA 10920
AGATAAAGCAAGTAGGTATCAACGGACTGAGGGGCAGCACATCTATTGATGCTATGCCCT

10921 GGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACC GGCTCC 10980
CCCGAATGGTAGACCGGGGTCACGACGTTACTATGGCGCTCTGGGTGCGAGTGGCCGAGG

10981 AGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCTCTGCAAC 11040
TCTAAATAGTCGTTATTTGGTCTGGTCGGCCTTCCCGGCTCGCGTCTTCACCAGGACGTTG

FIGURE 3E (cont'd)

24/36

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11041 TTTATCCGCCTCCATCCAGTCTATTAAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCCGCC 11100
      AAATAGGCGGAGGTAGGTCAGATAATTAACAACGGCCCTTCGATCTCATTTCATCAAGCGG

11101 AGTTAATAGTTTGGCGCAACGTTGTTGCCATTGCTGCAGGCATCGTGGTGTACGGCTCGTC 11160
      TCAATTATCAAACGCGTTGCAACAACGGTAACGACGTCGGTAGCACCCACAGTGGGAGCAG

11161 GTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCC 11220
      CAAACCATAACCGAAGTAAGTCGAGGCCAAGGGTTGCTAGTTCCGCTCAATGTACTAGGGG

11221 CATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCCTCCGATCGTTGTCAGAAGTAAGTT 11280
      GTACAACACGTTTTTTTCCGCAATCGAGGAAGCCAGGAGGCTAGCAACAGTCTTCATTCAA

11281 GGCCGCAGTGTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCTATGCC 11340
      CCGCGCTCACAATAGTGAGTACCAATACCGTCTGTGACGTATTAAGAGAATGACAGTACCG

11341 ATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTG 11400
      TAGGCATTCTACGAAAAGACACTGACCCTCATGAGTTGGTTCAGTAAGACTCTTATCAC

11401 TATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAACACGGGATAATACCGCGCCACATAG 11460
      ATACGCGCGCTGGCTCAACGAGAACGGGCCGCACTTGTGCCCTATTATGGCGCGGTGTATC

11461 CAGAACTTTAAAAGTGCTCATCATTGGAAAAACGTTCTTCGGGGCGAAAACTCTCAAGGAT 11520
      GTCTTGAAATTTTCACGAGTAGTAACCTTTTGCAAGAAGCCCCGCTTTTGAGAGTTCTTA

11521 CTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGC 11580
      GAATGGCGACAACTCTAGGTCAAGCTACATTGGGTGAGCACGTGGGTGACTAGAAGTCC

11581 ATCTTTTACTTTTACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAA 11640
      TAGAAAAATGAAAGTGGTCGCAAGACCCACTCGTTTTTGTCTCTCCGTTTTACGGCGTTT

11641 AAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTA 11700
      TTTCCCTTATTCCCGCTGTGCCTTTACAACCTATGAGTATGAGAAGGAAAAAGTTATAAT

      amp prom(11721,11749)<<<
      |
11701 TTGAAGCATTTATCAGGGTTATTGTCTCATGACGGGATACATATTTGAATGTATTTAGAA 11760
      AACTTCGTAAATAGTCCAATAACAGAGTACTCGCTATGTATAAACTTACATAAATCTT

11761 AAATAAACAAATAGGGGTTCCGCGCACATTTCCCGAAAAAGTGCCACCTGACGTCTAAGA 11820
      TTTATTTGTTTATCCCAAGGCGCGTGTAAAGGGGCTTTTCACGGTGCAGTGCAGATTCT

11821 AACCATTATTATCATGACATTAACCTATAAAAAATAGGCGTATCAGGAGGCCCTTTCTGTCT 11880
      TTGGTAATAATAGTACTGTAATTGGATATTTTATCCGCATAGTCTCCGGGAAAGCAGA

11881 TCAAGAATTCAT 11892
      AGTTCTTAAGTA

```

FIGURE 3E (cont'd)

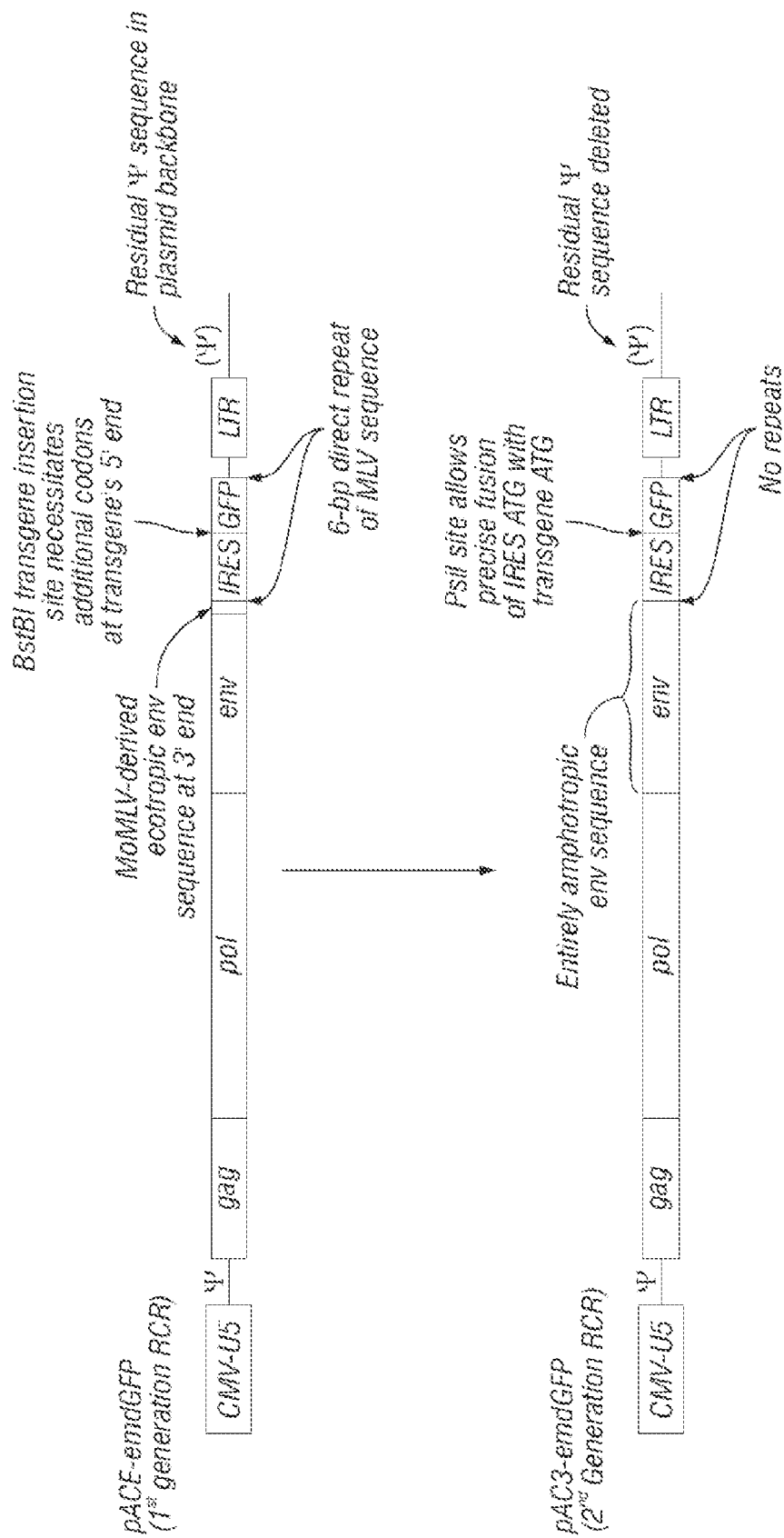


FIGURE 3F

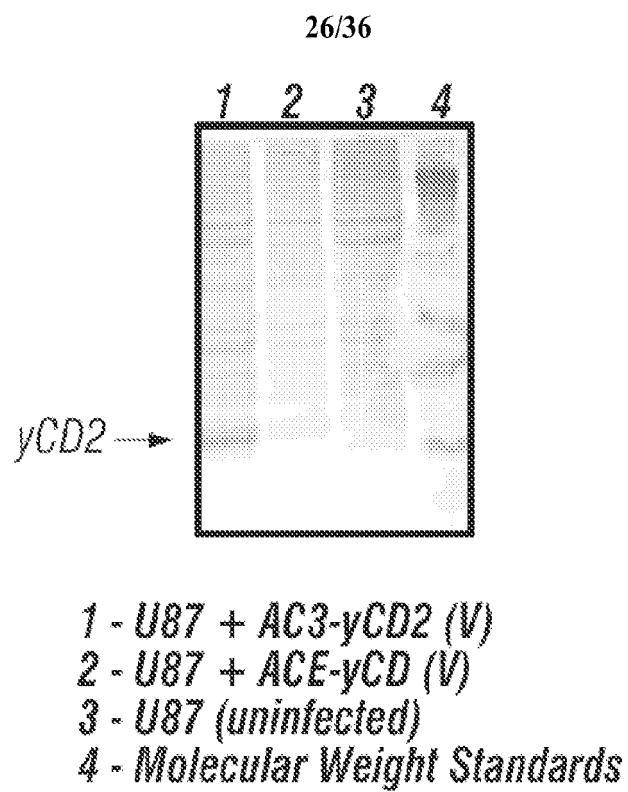


FIGURE 4

27/36

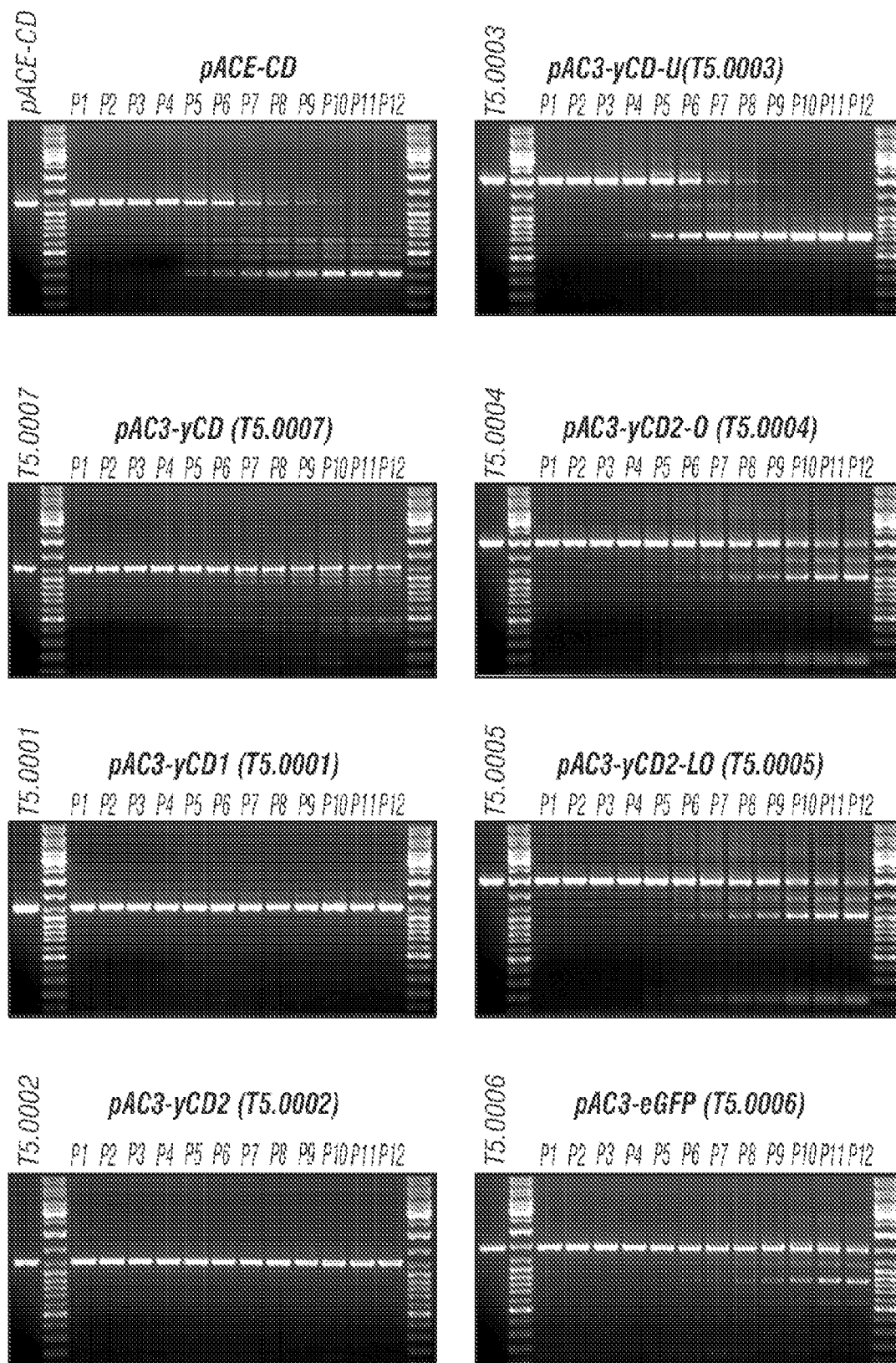


FIGURE 5

28/36

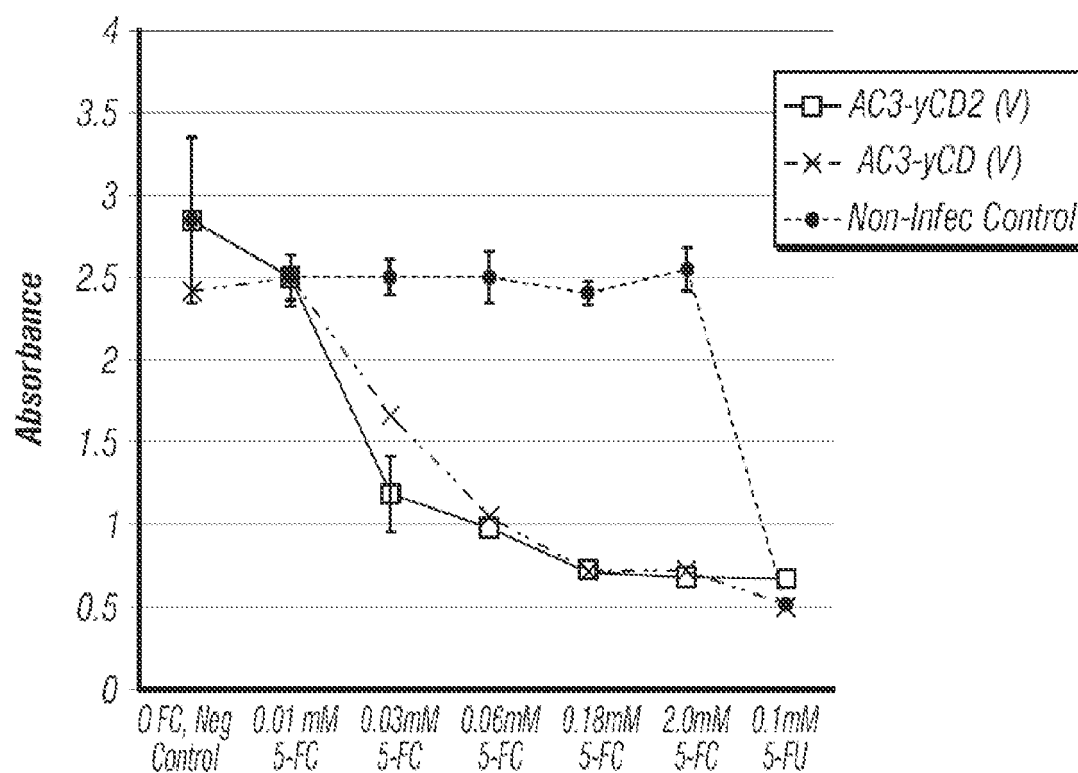


FIGURE 6A

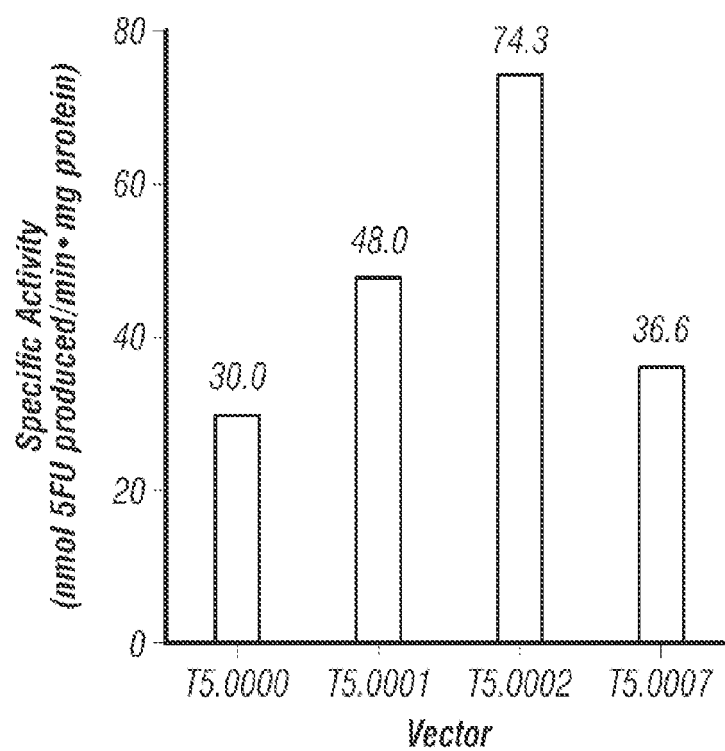


FIGURE 6B

29/36

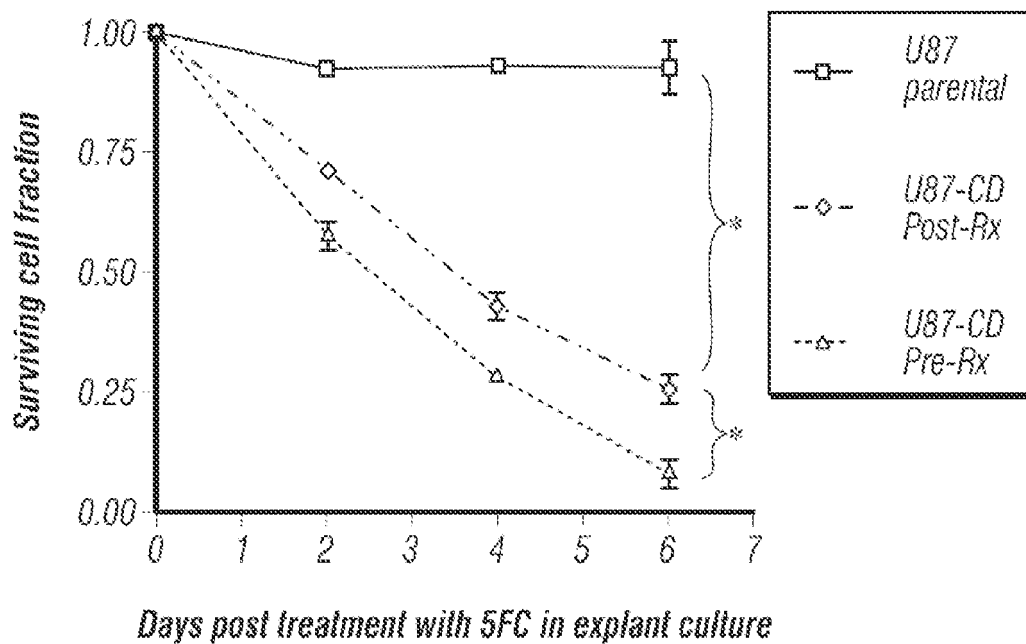


FIGURE 7

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

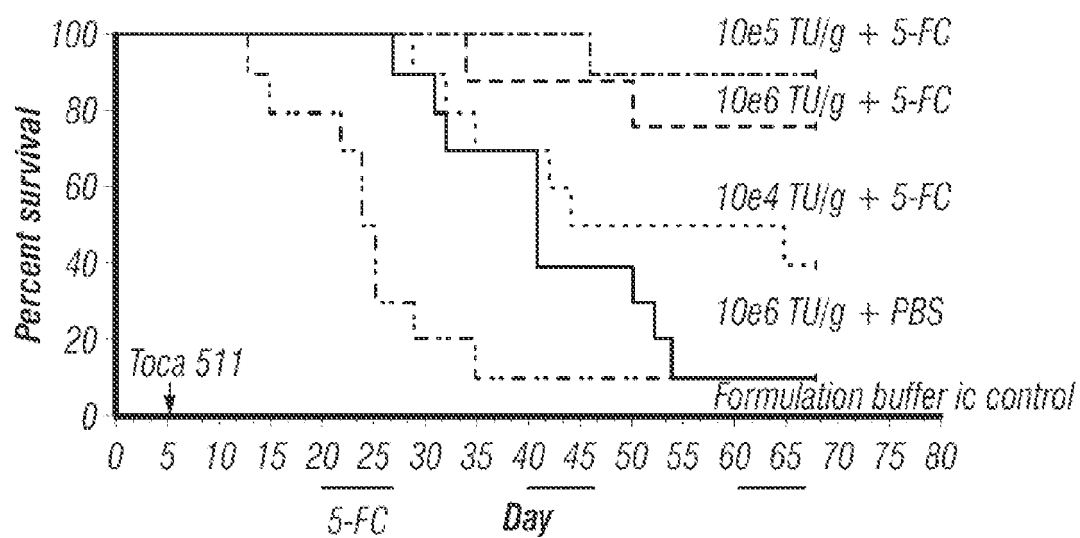


FIGURE 8

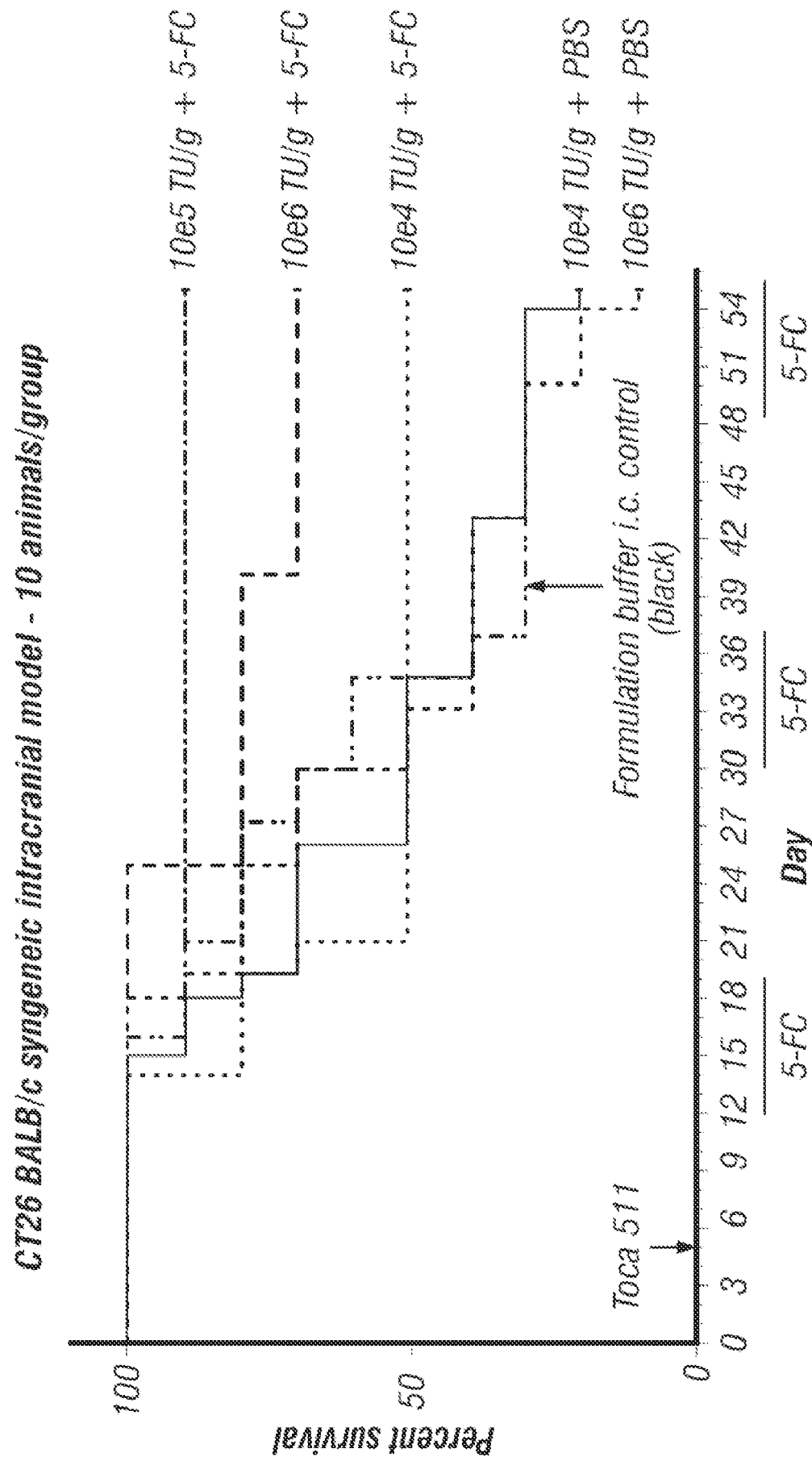


FIGURE 9

31/36

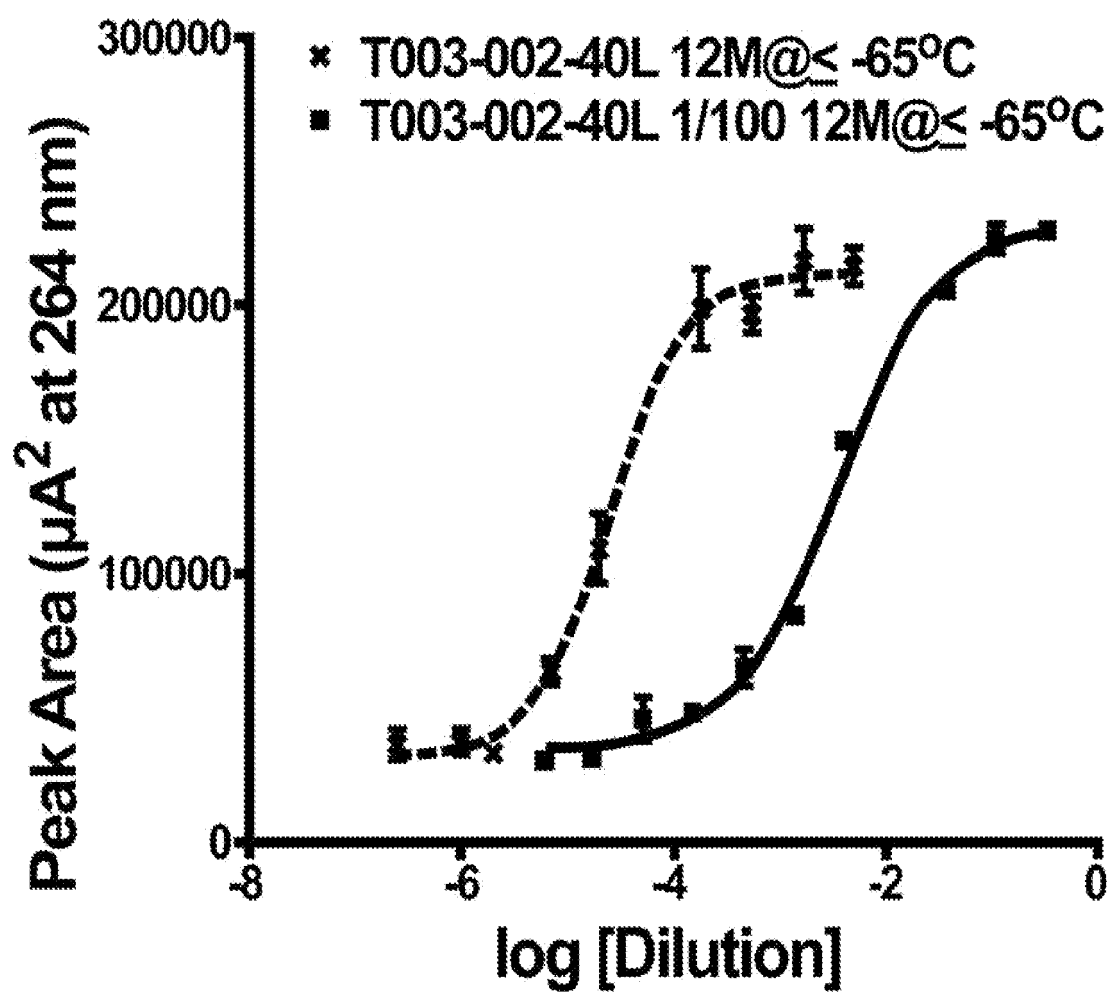


FIGURE 10

32/36

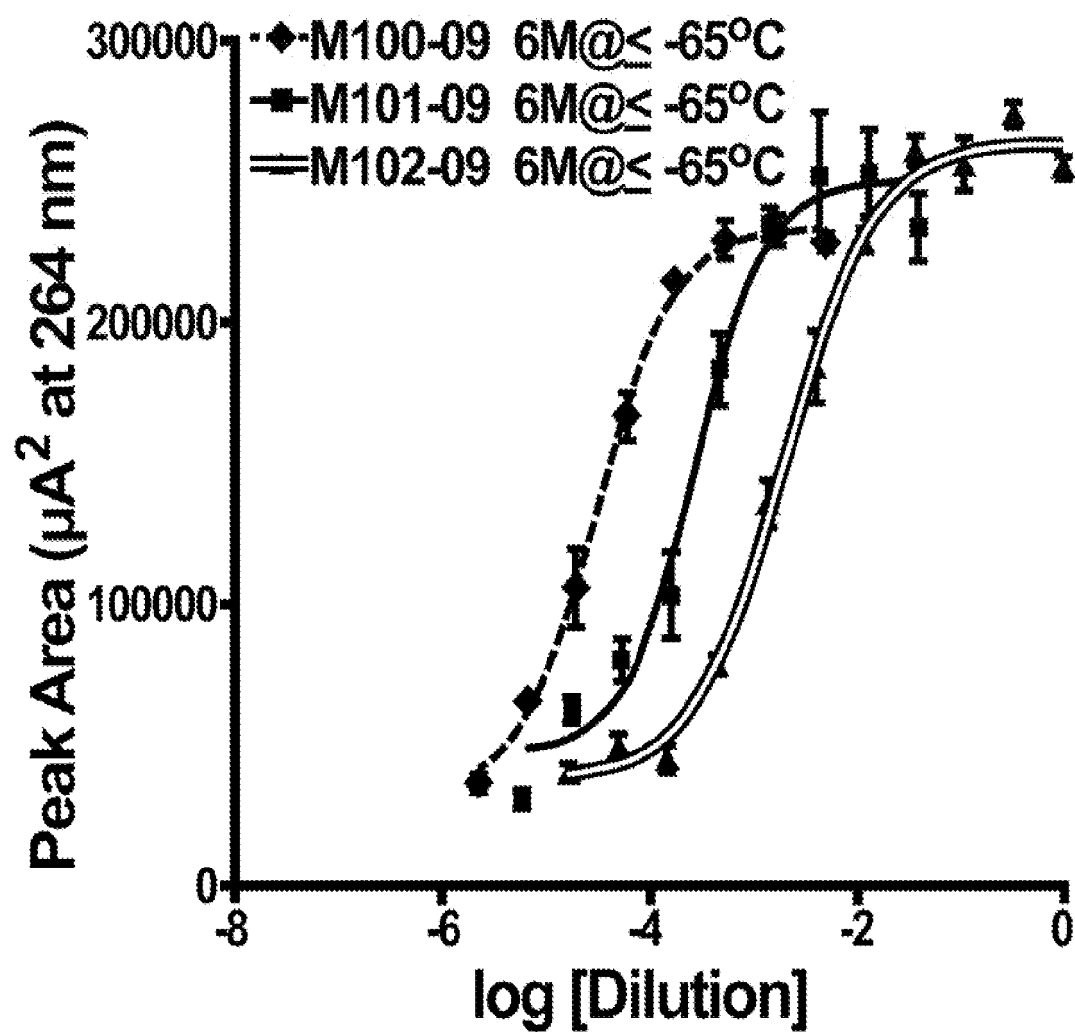


FIGURE 11

Direct Comparison of HT1080+ T5.0002 Adherent Clones for Titer Production from Confluent Cultures

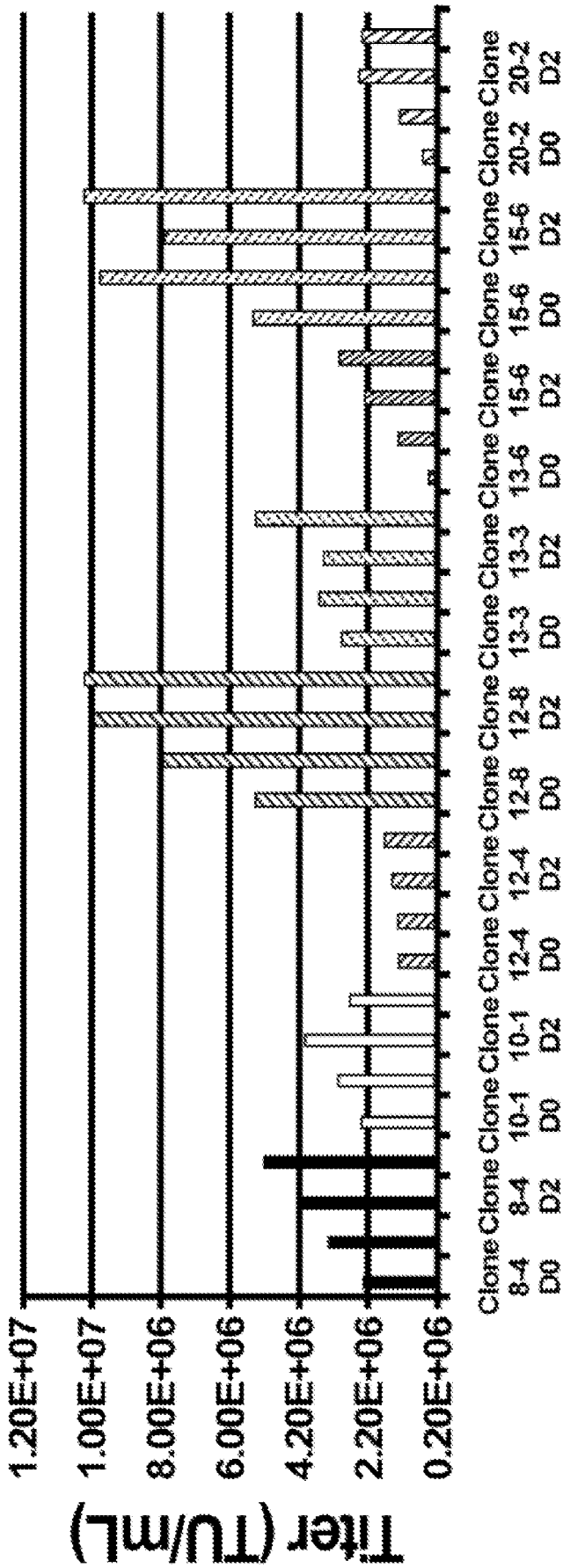


FIGURE 12

34/36

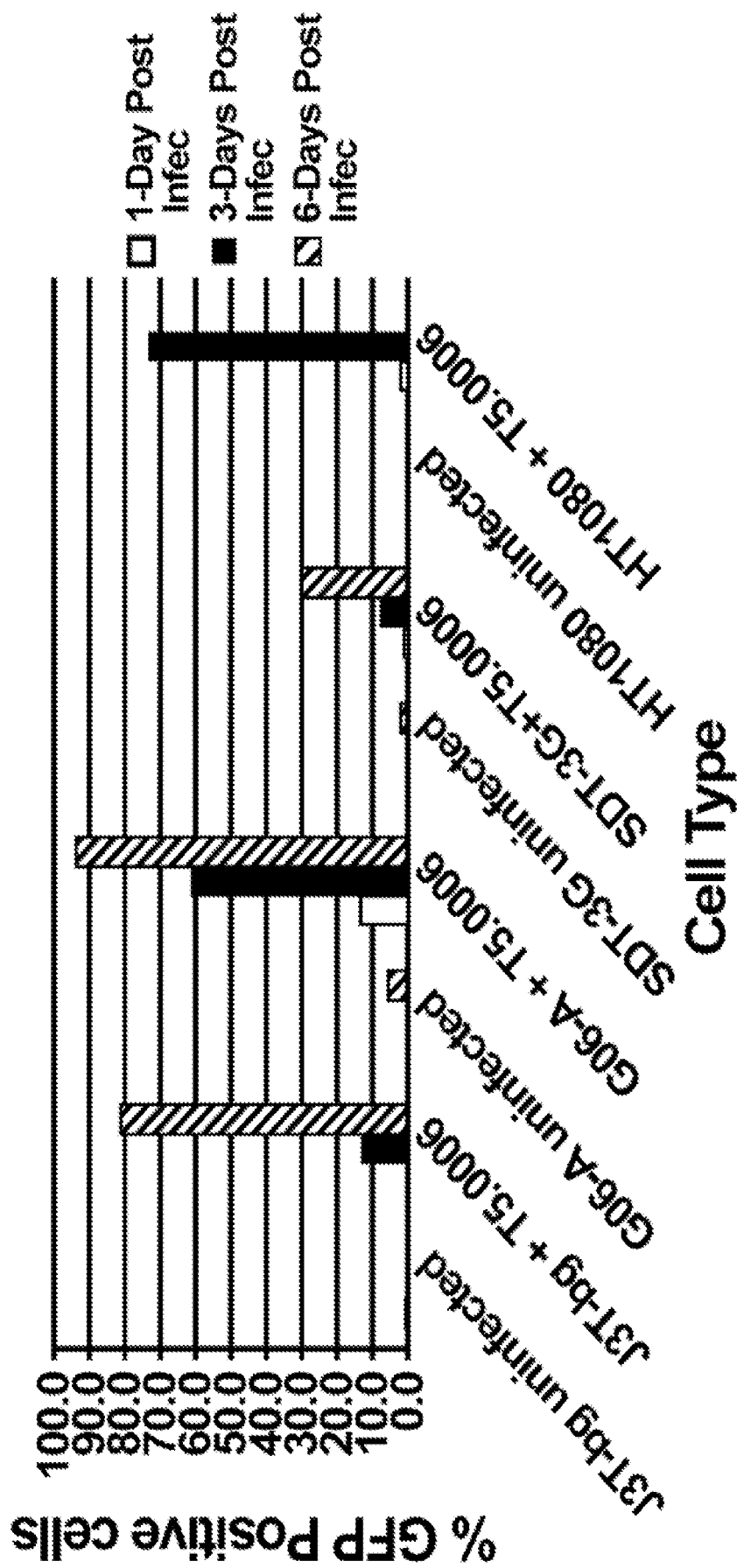


FIGURE 13

35/36

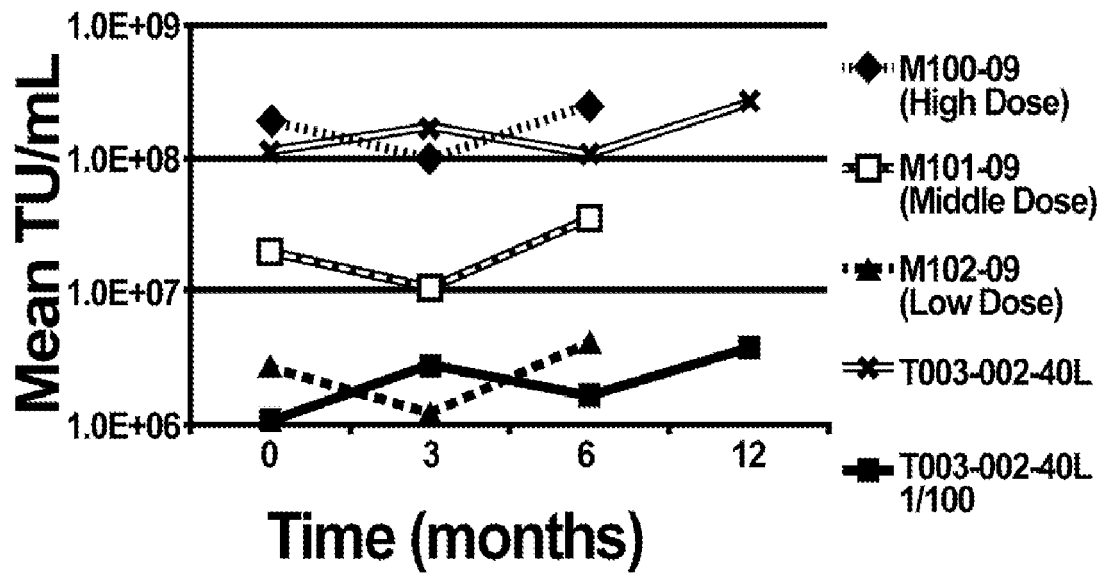


FIGURE 14

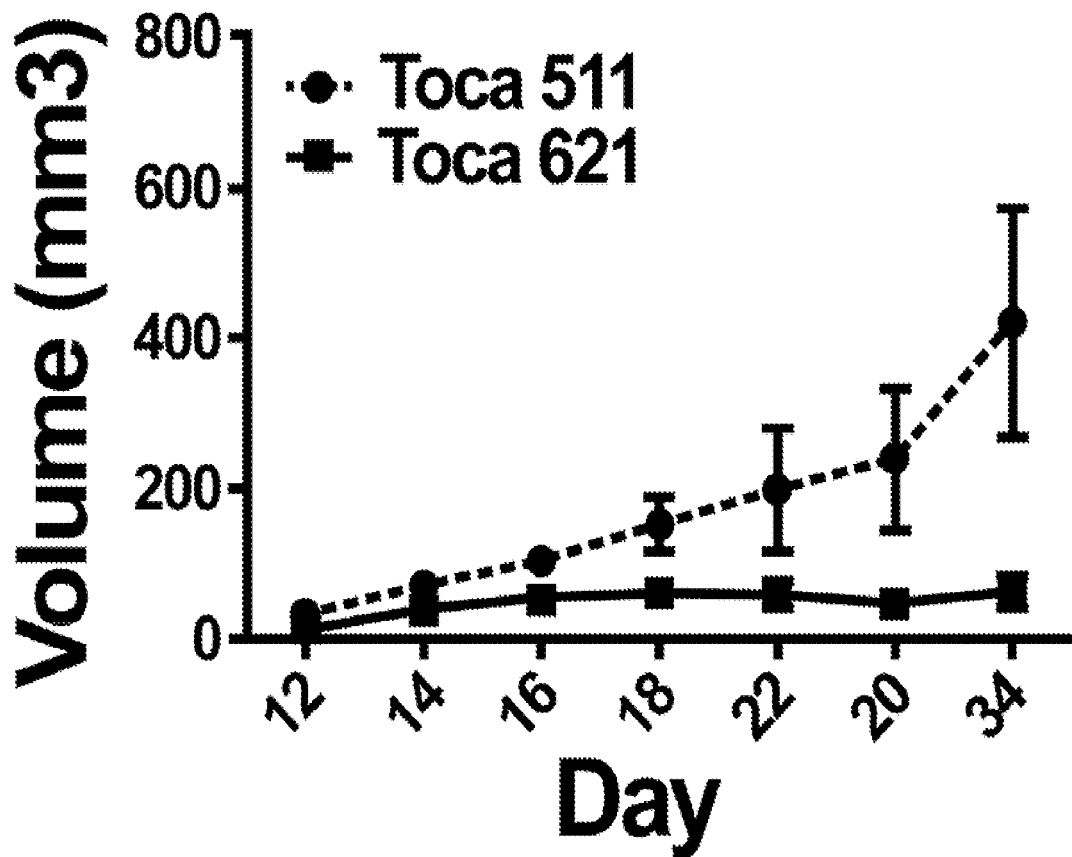


FIGURE 15

36/36

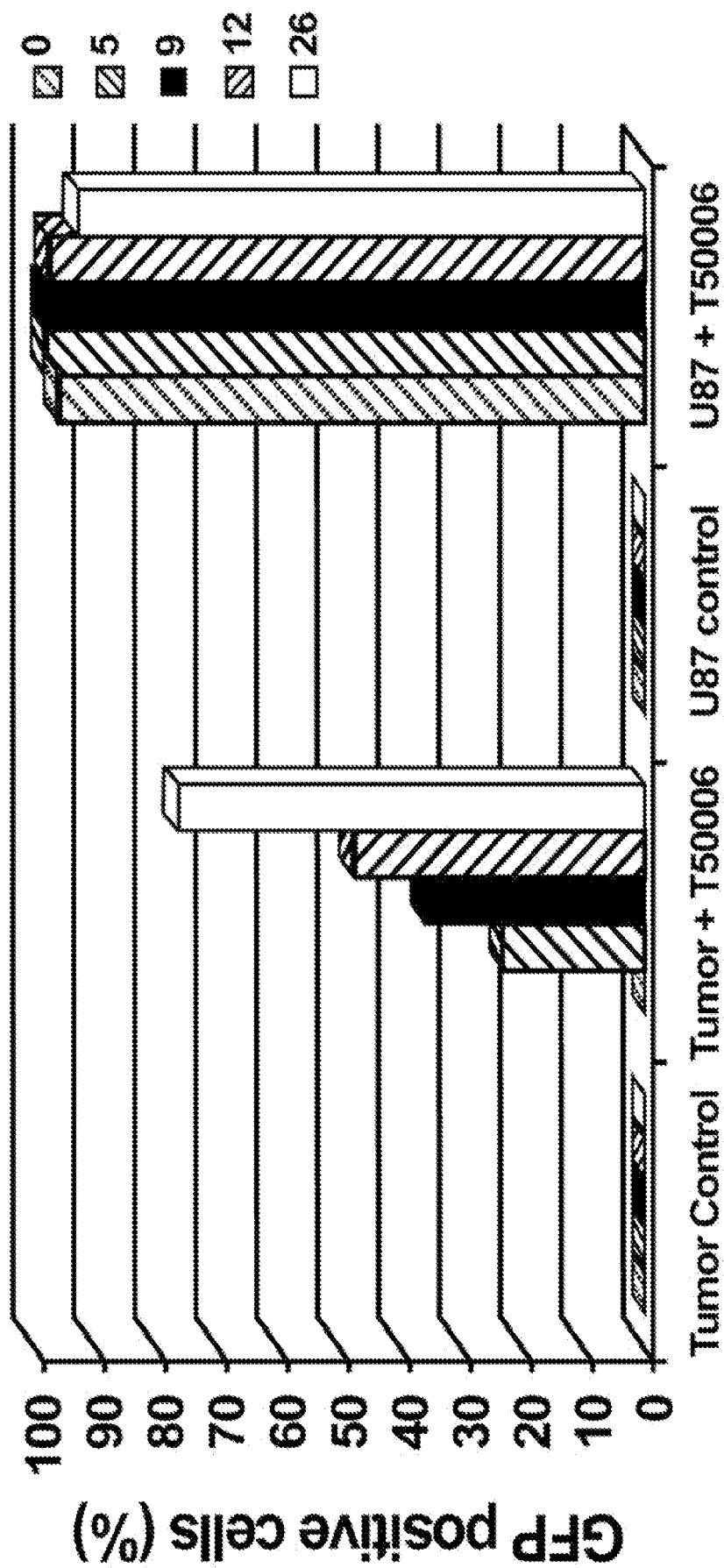


FIGURE 16