

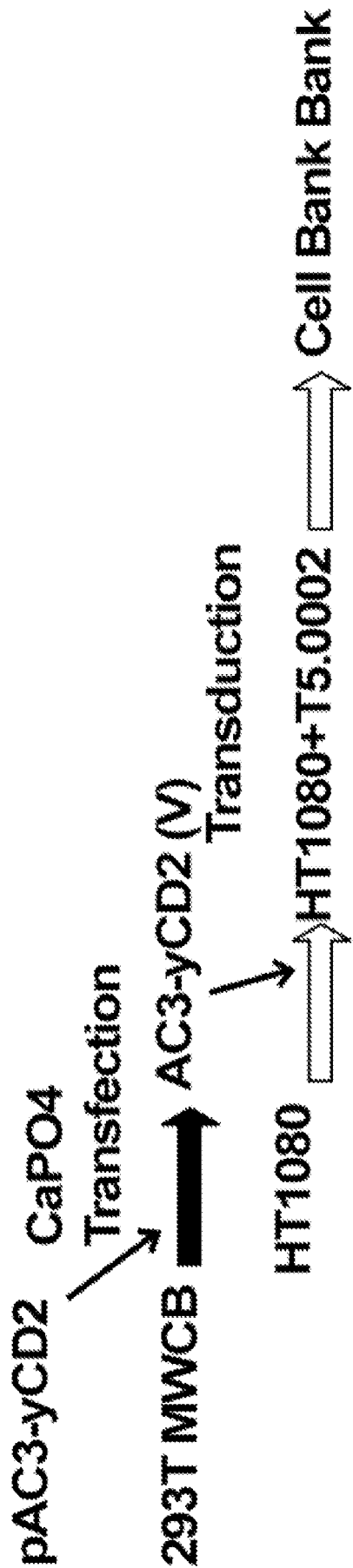


FIGURE 1

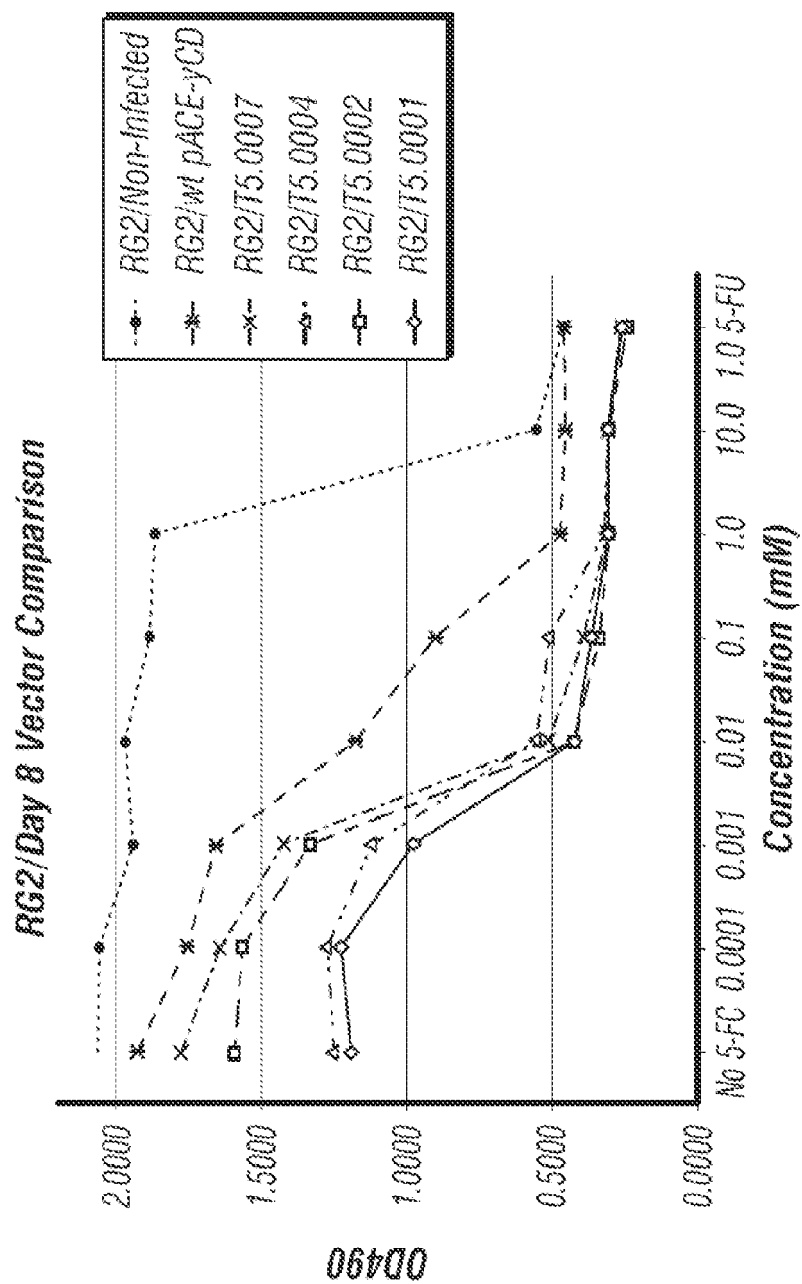


FIG. 2

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

FIG. 2 (Cont'd)

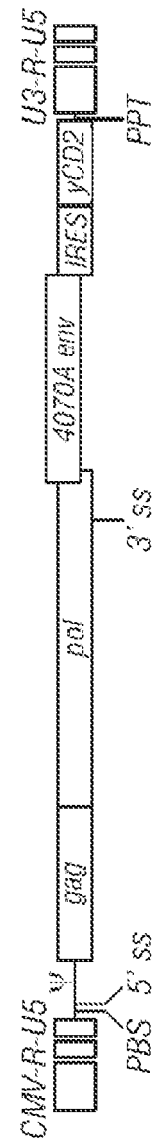


FIG. 3A

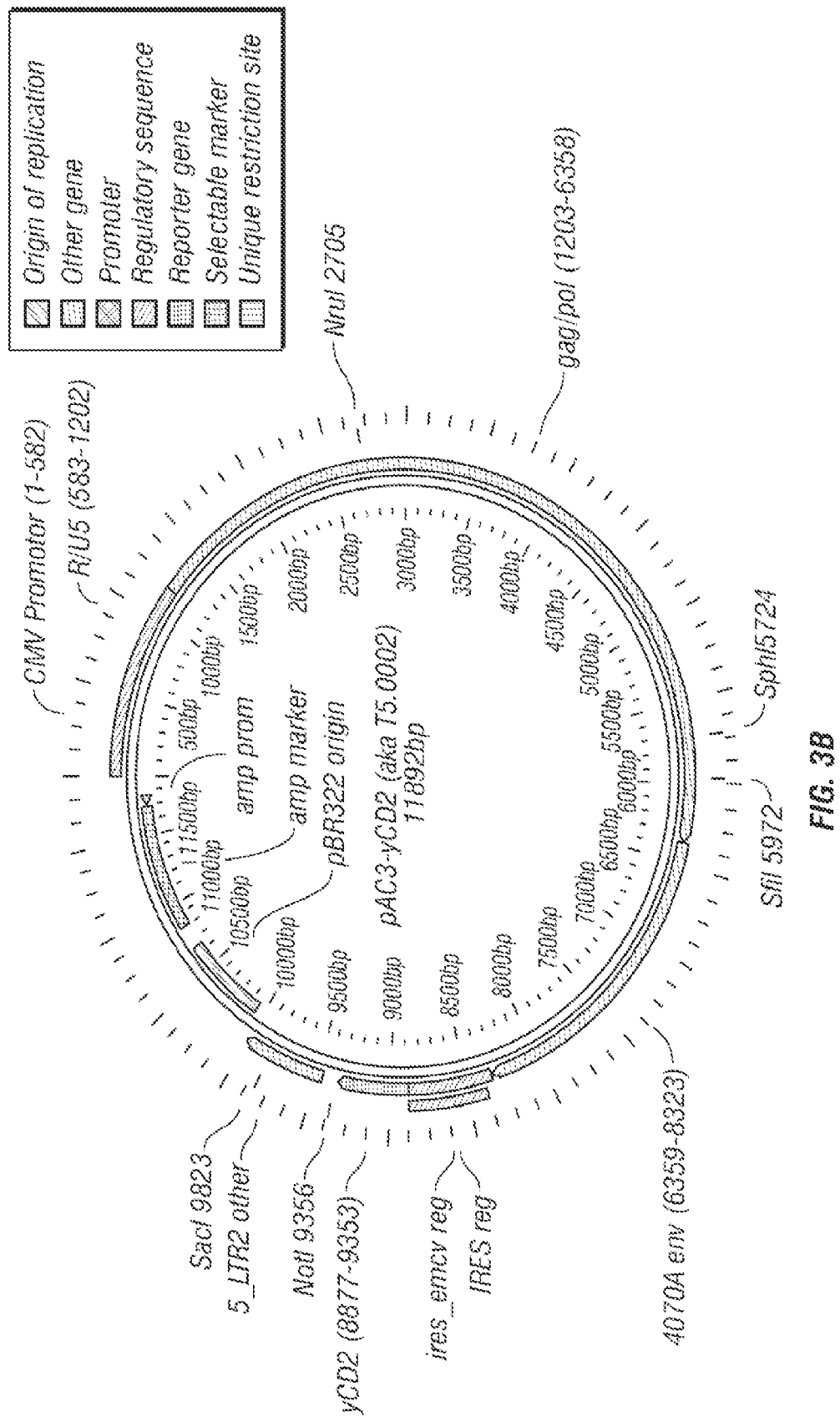


FIG. 3B

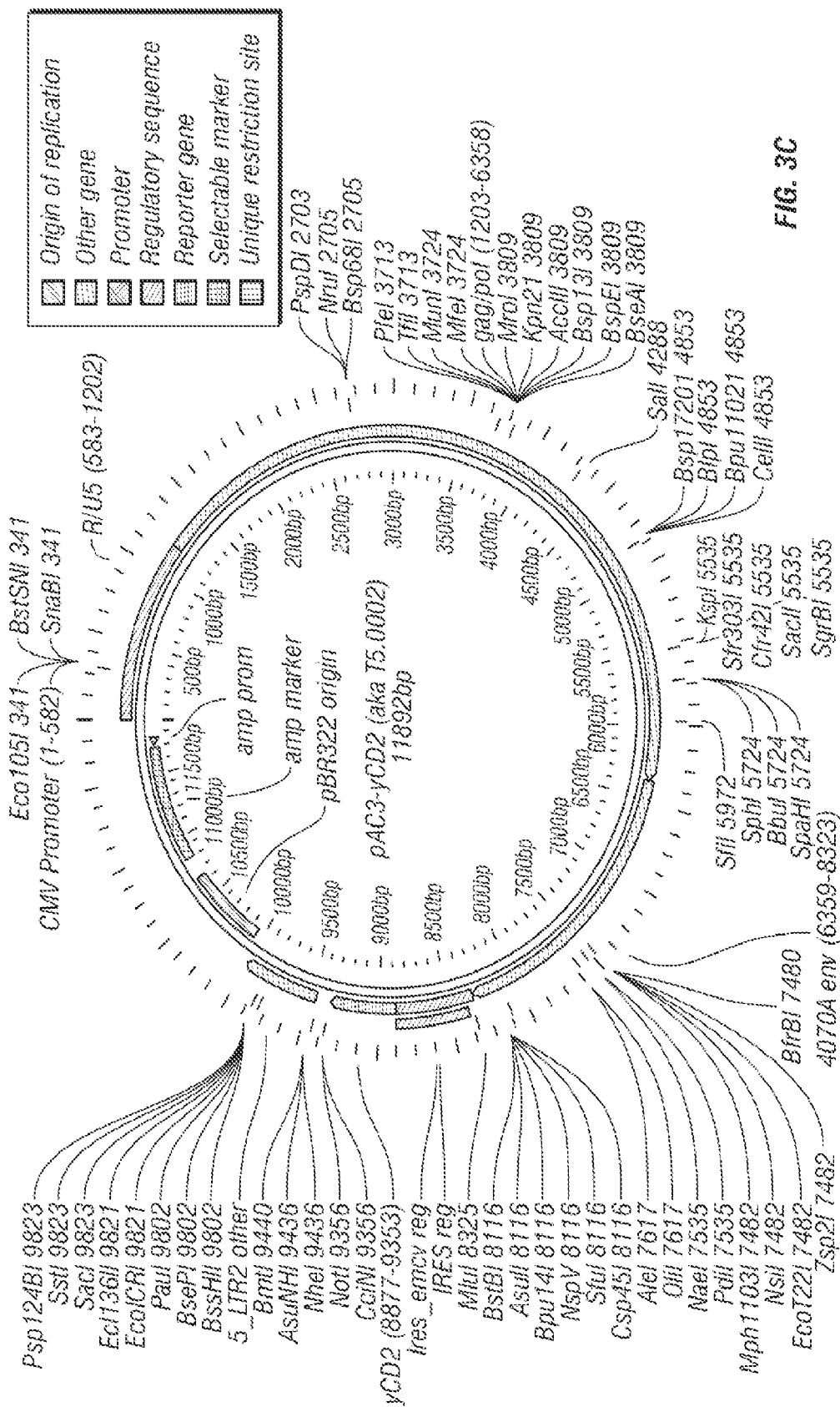


FIG. 3C

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TACTTATTAACTAATCAATTAAGGGTTCATTAGTTCTAGGCCATATATGGAGTTCCGCTTACTAACTTACGGTAAAT
 GGCCCGCTTGGCTGACGGCCCAACGACCCCGCCCTTGGAGTCAATAATGACGTATGTTCCUATAGTAAGCCCAATAGGGA
 CTTTCCATTGACGTCATAGGGTGGASTATTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTAC
 GCCCCTATTTGACGTCATGACGCTAAATGGCCCGCTTGGCATTATGCCAGTACATGACCTTATGGGACTTTCTACTTGG
 CAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGTATGGGTTTGGCAGTACATCAATGGGCTGGATAGCGGTTTG
 ACTCAGCGGGATTTCAGGTCTCCACCCCATTTGACGTCATGAGGTTTGTTTTGGUACCAAAATCAACGGGACTTTCCAAA
 ATGTCGTAAACAATCCGCCCATTTGACGCAATGGGCGTAGGCGTGTACGGTGGGAGGTCATATTAAGCAGAGCTGGTTTA
 GTGAACCGCGCGAGTCCCTCGATTGACTGAGTGGCCGGTACCCGTGTATCCAAATAAACCTCTTGCAGTTGCATCCGAC
 TTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCTCTGAGTGTATGACTACCCGTGAGGGGGTCTTTTCATTTGGGGGCTCGT
 CCGGGATCGGGAGACCCCTGCCCAGGGACCCAGACCCACACCGGGAGCTTACCTGGCCAGCACTTATCTGTGTCTGTCC
 GATTGCTTACTGTCTATGACTGATTTTATCGCCCTGGCTCGGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCGGTG
 GTGGAAGTGAAGACTTCGGAACACCCGGCCGCAACCTCGGAGAGCTCCAGGGACTTCGGGGCCGTTTGTGTGGCCGAC
 CTGAGTCCAAAATCCCGATCTTTTGGACTCTTTGGTGCACCCCTTAGAGGAGGATATGTGGTTCTGGTAGGAGACGA
 GAACCTAAACAGTTCCCGCCTCCGTCTGAATTTTGGCTTGGCTTGGGACCGAAGCCCGCCGCGCTCTGTCTGCTGC
 AGCATCGTTCTGTGTGTCTCTGTGACTGTGTTTCTGTATTTGTCTGAGAAATAGGGCCAGACTGTACCACTCCCTTAA
 GTTTGACCTTAGGTCAGTGGAAAGATGTCGAGCGGATCGCTCACAACCACTCGGTAGATGTCAGAAGAGAGCTTGGGTAC
 CTTCTGCTCTGCAGAAATGGCCAACTTTTACGTGGGATGGCCGCGAGACGGCACTTTAACCGAGAGCTCATCACCCAGGTT
 AAGATCAAGGCTCTTTTCACTTGGCCGCTATGACACCCGACCAAGGTCCCTACATCGTGACCTGGGAAGCTTGGCTTTTG
 ACCCCCTCCCTGGGTCAAGCCCTTTGTACACCTTAGGCTCCGCTCCCTCTTCTCCATCCGCCCCGTCTCTCCCTTGA
 AACTCTCGTTCGACCCCGCTCGATCTCTCTTTATCCAGCCCTCACTCTCTCTAGCGGCCAAACCTAAACCTCAAGTT
 CTTTCTGACAGTGGGGGGCTCTATCGACCTACTTACAGAGAGCCCCCGCTTATAGGAGCCCAAGACACCCCTTCCG
 ACAGGAGCGGAAATGCTGGAGAAAGCCCTCGGGAGAGGCAACCGACCCCTCCCAATGGATCTCGCTACGTTGGGAG
 ACGGGAGCCCTGTGGCGACTCCACTACCTCGCAGGCAATCCCTCCGCGAGGAGGAAACGGACAGCTTCAATACTGG
 CCGTCTCTCTCTCTGACCTTTACAACTGGAAAAATAATAACCTCTCTTTTCTGAGATCCAGGTAACTGACAGCTCTGA
 TCGAGTCTGTTCTCATCACCCTCAGCCCACTGGGAGGACTGTCAGCAGCTGTGGGAGCTGTGCTGACCGGAGAGAAAA
 ACACCGGGTCTCTTAGAGGCTAGAAAGCGGTGCGGGGCTATGATGGGCGCCCACTCAACTGCCCAATGAAGTCGATGCC
 GCTTTTCCCTCGAGCGCCAGACTGGGATTACACCAACCCAGGAGTAGGAACCACTAGTCCACTATCGCCAGTCTCTCC
 TAGCGGCTCTCCAAACCGCGGAGAGCCCAACCAATTTGGCCAGAGTAAAGGAATAACACAGGGGCCAANTGAGTCTCC
 CTGCGCTCTCTAGAGAGACTTAAAGGAGCTATCGCAGGTACACTCTTATGACCTGAGGACCCAGGGCAAGAACTAAT
 GTGTCTATGTCTTTCATTTGGCAGTCTGCCCCAGACATTGGGAGAAAGTTAGAGAGGTTAGAAAGATTAAAAACAAGAGCC
 TTGAGATTTGGTTAGAGAGCGCAGAAAGATCTTTAATAAACGAGAAACCCGGAAGAAAGAGAGGAGCTATCAGGAGAGA
 AACAGAGGAAAAAGAGAACCCCTAGGACAGAGGATGAGCAGAGAGAGAAAGAGAGATCTTAGGAGACATAGAGAGTGC
 AGCAGGCTATTGGCCACTGTCTTGTAGTGGACAGAAACAGGATAGACAGGGAGGAGACGAGAGGAGGTCCCACTCGATCGCG
 ACCAGTGTGCTACTGCCAAGAAAAGGGCACTGGGCTAAAGATTGTCCCAAGAAACAGAGGAGCTCGGGGACCAAGACC

CMV promoter

R
 U5
 GT = 5' ss

gag

FIGURE 3D

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CCAGACCTCCCTCTGACCTAGATGACTAGGGAGGTCAGGGTCAGGAGCCCCCTGAAACCCAGGATAACCCCTCAAAGTC
 GGGGGGCAACCCGTCACCTTCCTGCTAGATAGTGGGGCCACACACTCCGTGCTGACCCAAAATCCTGGACCCCTAAGTGATA
 AGTCTGCTGGGTCCAAAGGGCTACTGGAGGAAAGCGGTATCCTGGACCTACGATCGCAAAGTACATCTAGCTACCGGTAA
 GGTACCCACTCTTTCTCCATGTACAGACTCTCCCTATCCTCTGTTAGGAAGAGATTTCCTGACTAAACTAAAAGGCCAA
 ATCCACTTTGAGGGATCAGGAGCCAGGTTATGGGACCAATGGGGCAGCCCTGCAAGTGTGACCCCTAAATATAGACATG
 AGCATCGCTACATGAGACCTCAAAGAGCCACATGTTCTCTAGGGTCCACATGGGTGCTGATTTCCTCAGGCCCTGGGC
 GGAACCCGGGGCATGGGACTGCGAGTTCCGCAAGCTCCTCTGATCATACCTCTGAAAGCAACCTCTACCCCGTGTCCATA
 AAACATATACCCCATCTCACAAGCAACCCAGACTGGGGTCAAGGCCACATACAGAGACTGTTGGACAGGGGAATCTGGTAC
 CCTGCCAGTCCCCCTGGAAACCGCCCTGCTACCCGTTAAGAAAACAGGGACTAATGATTATAGCCCTGTCCAGGATCTGAG
 AGAAGTCACACAGCCGGTGGAAACATCCACCCACCGTGCCACCCCTTACACCTCTTGAGCGGGCTCCACCGTCCAC
 CAGTGGTACACTGTGCTTGATTAAAGGATGCTTTTCTGCTGAGACTCCACCCACAGTCCAGCCTCTCTGGCCTTTG
 AGTGGAGAGATCCAGAGATGGGAATCTCAGGACAAATGACCTGGACAGACTCCACAGGGTTTCAAAAACAGTCCACCT
 GTTTGATGAGGCACTGCACAGACCTAGCAGACTTCGGATCCAGCACCCAGACTTGATCCTGCTACAGTAGGTGGATGAC
 TTACTGCTGGCCGCACTTCTGAGCTAGACTGCCAACAGGTAAGTCTGGGCCCTGTTACAAACCTAGGGAACCTCGGGTATC
 GGGCTCGGGCAAGAAAGCCCAATTTGCCAGAACAGGTCAAGTATCTGGGTAATCTTCTAAAGAGGGTCAGAGATGGCT
 GACTGAGGCCAGAAAAGAGACTGTGATGGGGCGCTACTCCGAGACCCCTCGACAACTAAGGGATTCCTAGGGAAGGCA
 GGGTTCTGTGCCCTCTGATCCCTGGGTTTGCAAAATGGCAGCCCCCTGTACCCCTCTACCCAAAACGGGGACTCTGTTA
 ATTTGGGGCCAGACCAACAAAGGCCTATCAACAAATCAAGCAAGCTCTTCTAACTGCCCCAGCCCTGGGGTTGCCAGATT
 GACTAAGCCCTTTGAACTCTTTGTGACGAGAGGAGGGCTACGCCAAAGGTGTCTAACGCCAAAACCTGGGACCTTGGCGT
 CGGCGGTGGCTACCTGTCCAAAAGCTAGACCCAGTAGCACTGGGTGGCCCTTGCCTACGGATGGTAGCAGCCATTG
 CCGTACTGACAAAGGATGCAGGCAAGCTAACCATGGGACAGCCACTAGTCATTCTGGCCCCCATGCASTAGAGCCACTAGT
 CAAACAAACCCCGACCCGCTGCTTTCCACCCCGGATGACTCACTATCAGGCTTGCTTTGGACACGGACCCGGTCCAG
 TTGGACCCGTTGGTAGCCCTGAAACCGGCTACCTGCTCCCACTGCTGAGGAGGGCTGCAACACACTGCTTCAATATCC
 TGGCGAAGCCACGGAAACCGACCCGACCTAACGGACAGCCGCTCCAGAGCCGAACACACCTGCTACAGGATGGAAG
 CAGTCTCTTACAGAGGGACAGCCTAAGCGGGCAGCTGCGGTGAACCAAGAGACCGAGGTAATCTGGGCTAAAGCCCTGCCA
 GCCGGGACATCCGCTCAGCGGGCTGAAGTATAGCACTCAGCCAGGCCCTAAAGATGGCAGAGGTAAGAAGCTAAATGTTT
 ATACTGATAGCCCTATGCTTTTGTACTGCCCCATATCCATGCAGAAATATACAGAAGCCCTGGGTGCTCACATCAGAAGG
 CRAAGAGATCAAAAATAAAGACGAGATCTTGGCCCTACTAAAGCCCTCTTTCTGCCAAAAGACTTAGCATATCCATTGT
 CCAGGACATCAAAAGGGACACAGGCCGAGGCTAGAGGCCAACCGGATGGCTGACCAAGGGGCCGAAAGGAGGCATCACAG
 AGACTCCAGACACCTCTACCTCTCTATAGAAAATTCATCACCCTACCTCAGAACATTTTCAATTACAGTGAATGAT

pol

FIGURE 3D (cont'd)

AAAGGACCTAACCAAGTTGGGGGCCATTATGTATAAACAAGAAGATATTTGGGTCTACCACAGGAAAACCTTGATGCCTGCAC
CAGTTTACTTTTGAATFATAGACTTTTCCTCATCAGCTGACTCACCTCAGCTTCTCAAAAAATGAGGCTCTCCTAGAGAGAA
GCCACAGTCCCTACTACATGCTGAAOCCGGATCGAACTCAAAAAATACCTGAGAGCTTGCAGAGCTTGTGCACAAGTCAA
CGCCASCAAGTCTGCTGTAAACACCGGAAGCTAGGCTTCCCGGSCATCGGCTCGGCTACTTATGGAGATCGAATTCACOGAG
ATAAAGCCCCGATGTATAGCTATAAATATCTTCTAGTTTTTAATAGATACCTTTCTGGCTGGATAGAAGCTTCCCAAACA
ACAAGCAAAACCCCAGGTCGTAAACACAGAGCTACTACAGSAGATCTTCCCGAGCTTGGCATGCTCTACGTAATGGGAC
TGACATATGGGCTGCTCTCCAAGGTGAGTCAGACAGTGGCGGATCTGTGTGGGGTTGATTGGAAATTTACATTTGTGCA
TACAGACCCCAAAGCTCAGGCTAGGATAGAAGATGAATAGAACCATCAGGAGACTTTAACTAAATTAACGCTTGCACCTG
GCTCTAGAGACTGGGTGCTCTACTCTCCCTTAGCTCTGTACCGAGGCTGCAACAGCTTGGGCCCCATGGCTTCACCCCAT
TGACATCTTATATGGGCAACCCCGGCCCTTGTAACTTCCCTGAACCTGCATGCAAGAGTTACTTAACAGCCCTCTCTC
CAGCTCTCACTTACAGGCTCTCTACTTTACTTCAGCACGAGTCTGGGAGACCTTGTGGCGGAGCTTACCAAGAACCTTGGACC
GACCGGTGCTAOTCAACCTTTACGAGTGGGCGACACAGTGTGGGTGCGCGACACAGACTAAGAACCCTAGAACCTTGCTG
GAAAGGACCTTACACAGTCTCTGCTGAACACCCCTCACGCTCTCAAGTAGACGGCTATCGGAGCTTGGATACACGCGGCCAC
GTGAAGGCTGCGACCCCGGGGGTGGACCATCTCTAGACTGACCTGGCGGCTTCAACGCTCTCAAACCCCTCAAGATAA
GATTAAACCCCTGGAGGCCCTTAATAGTCTATGGGAGTCTCTGTAGGAGTAGGATGGCAGAGAGACCCCATCAGGCTCTTAAT
GTAACCTGGAGAGTCAACCAACCTGATGACTGGGCTTACGCGCAATGCCACCTCTCTCTGGGAGCTGTACAAAGATGCTCTC
CAAAATTTATATTTTGTATCTATPSTGATCTGGTTCGGAGAGGAGTGGGACCTTTCAGACACAGGAACCGTATGTGGGTATGGCTG
CAAGTCCCTCGCAGGAGAGACAGCGGACCCGAGCTTTTGACTTTTAAGTGTGCTCTGGGCATACCGTAAAGTCCGGGTGTGGG
GCACACAGAGAGGCGCTACTCTGTAAATGGGCTGTCAAACCATGCGACAGGCTTACTGCAAGCCCATCTATCTGGGACC
TAATCTCTTTAAGGCGCTAAACACCCCTGGGACACGGGATGCTCTAAAGTGTGCTCTGGCTCTGCTACGCTCTCTCA
AGTATCCAAATTCCTTCAAGGCGCTACTCTGAGCGGCGAGATGCAACCTCTAGTCTTACAAATTCATGATGCAAGAAAAAG
GCTAACTGGGACGGGCAAACTCTGGGAGCTGAGACTGTACCGGACAGGAACAGATCTTATTACCTGTTCTCTCTGACCC
GGCAGGCTCTTAATGTGGGACCCCGAGTCTCCCATAGGCGCCACACCGAGTATTACCGGACCAAGATCTCTCTCTCACCAT
AGAGATTTGATCGGCTCCACAGCAAOCTAGCCCTCTCAATACAGTTAACTCTCTTCCATACAGGATACCCCTCAACCTCT
CTTACAAGTCCAAGTGTCTTCAAGTCACTCCAGGAAGTGGAGATAGACTACTAGTCTTACTCAAAGGAGCTTATCAGGCG
TTAACTCTCAAAATCTCGACAGACCCCAAGAGTGTGGCTGTGCTTACTGTGCGGACCTCTTATTACAGGAGTACGCGT
CTGGGCACTTATACCAATCATCTCCAGCGCTCCCGGCACTGTACGGGCTCTTCCCAACATAGCTTACCTATCTGAGG
ACAGGACAGGCGCTATGCTATGGGCGGCTACTTAAACTCACCAGGCTTATGTAAACACCAACCAAGGCGCTGCTCAGAT
CTACTACTCTTGCAGCACCCCGCGCAACAACTGGGCTTGCAGCACTGATTTGACTCTCTGCTTGTTCACACGGGCTCTAA
TCTAACCAACAGATTATTTGTATTTAGTTCAACTCTGCGCCACAGTAAATTTACCCTCTCCCGATTAATGTATGGTCACTT
GAACAGGCTACCAAAATATAAAGAGAGCCASTATCTTAGACCTTGGCTCTTCTACTAGGAGGATTAACCATGGAGGCTATC
CAGCTGGAATAGGACGCGGACCACTGCTTAAATTAAGCCAGAGTTTGAAGCAGCTTATGAGCAGCTTATGCGGCTATCCAGACAGCT
CAACGAAGTCCAAAAGTCAATTACCAACTAGAAAAGTCTACTGACCTCTGTTGTCTGAAGTAGCTTACAGAACCGCAGAGGC
CTAGATTTGCTATTCTTAAAGAGGAGGAGCTCTTCCGCGACCCCTAAAGAGAGATTTGTTTATTTATGACAGCACACGGGCT
TAGTACAGAGACAGCATGGCTAAATTAAGAGAAAGGCTTAACTAGAGACAAAATATTGAGACAGGCTAAGGATGGTTCG
AGGCTCTTTAATAGATCCCTCTGCTTACACCTTATCTCCACCATCATGGGACCTCTAATAGTACTCTTACTGATCTTA
CTCTTGGACCTTGCATTCTCAATGCAATGCTCAATTTGTAAAGACAGSATCTTACTGGTCCAGCTCTGCTTTTGAATC
AGCAATATCACAGCTAAACCCCATAGACTACGAGCCATGACCGCTTACTGGCGAGGCGCTTGAATTAAGGCGGCTGTG
CGTTTGTCTATATGTTATTTTCACCATATGGCGCTTTTGGCAATGTGAGGCGCGGCAAACTTGGCTCTCTTCTTGTGAC
GAGCATCTCTAGGCTCTTTCTCTCTCGCCAAAGCAATGCAAGCTCTGTTGAATGTCTGAAGGAAGCACTCTCTCTGGA
GTTCTTGAAGACAAACACCTCTGTAGCGACCTTTTCCAGGACAGCGGAACCTTCCACTGGGACAGGCTCTCTCTGCGGC
AAAAGCCACGTTGATATAGATACCTGCAAGAGGCGGACAAACCCAGTGGCAGCTTGTGAGTTGATAGTTGTGGAAGAGT
CAATGCTCTCTCAAGGCTATTCAACAAAGGCGCTGAAGGATGGCCAGAGCTACCCATTTGATGGGATCTGATCTGGGG
CTCTGGTGCACATGCTTTACATGTGTTTGTGAGGTTTAAAAAACGCTTAGGCGCCCGGCAACCGGGGACGTTGTTTCC
TTTCAAAAACACCTTATAAATGCTGACCTGGCGGATGGGCTTCAAGTGGATCAAAAAGGCTATGATATCGCTTACCAAGA
GGCTCTCTGGGCTACAGGAGGCTGGCTGCTCTCTGCGGCTTCTCTATCAACAAAGGCTGGGCTGTCTGGGCTGG
GCGCACACATGAGGTTCCAGAGGCTCTGGGCTCTCTGACGCGGAGATCTTCAACCTGGGACAGCTTGGGCTGGGCTGG
GCAAGGCTGACAGGACACACCTCTGTACCTACCTCTGCTCTCTGTGACATGTGTACGGGCTATCAATCATGTATCGGCT
CCCTAGGCTGTGATCTGGCGGACAGCTGAACTTCAAGTCCAAAGGCTGAGAGTACCTGCAAAACAGGCGGACAGGCTGTG
GTGTTGACGATGAGAGGCTTAAGAACTGATGAAGAGTTCACTGACGAGAGGCTTACGAGCTTGTGAGATATACGCT

[AG] = 3'ss

4070A envI

MblI

EMCV IRES

PstI

yCD2

FIGURE 3D (cont'd)

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

61 CGTTACATAACTTACGGTAAATGGCCCCGCTGGCTGACCGCCCAACGACCCCCGCCCCATT 120
GCAATGTATTGAATGCCATTTACCGGGCGGACCGACTGGCGGGTTGCTGGGGGCGGGTAA

121 GACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCATTGACGTCA 180
CTGCAGTTATTACTGCATACAAGGGTATCATTGCGGTATCCCTGAAAGGTAAGTGCAGT

181 ATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCC 240
TACCCACCTCATAAATGCCATTTGACGGGTGAACCGTCATGTAGTTCACATAGTATACGG

241 AAGTACGCCCCCTATTCACGTCAATGACGGTAAATGGCCCCGCTGGCTATTATGCCAGTA 300
TTCATGCGGGGGATAACTGCAGTTACTGCCATTTACCGGGCGGACCGTAATACGGGTCAAT

Eco105I
|
SnaBI
|
BstSNI
|
301 CATGACCTTATGGGACTTTTCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTAC 360
GTACTGGAATACCCTGAAAGGATGAACCGTCATGTAGATGCATAATCAGTAGCGGATAATG

361 CATGGTGATGCGGTTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGG 420
GTACCACTACGCCAAAACCGTCATGTAGTTACCCGACCTATCGCCAAACTGAGTGCCCC

421 ATTTCCAAGTCTCCACCCCATTCACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACG 480
TAAAGGTTCCAGAGGTGGGGTAACTGCAGTTACCCCTCAAACAAAACCTGCGTTTATGTTGC

481 GGACTTTCCAAAATGTCGTAACAACCTCCGCCCCATTGACGCAATGGGCGGTAGGCGTGT 540
CCTGAAAGGTTTTACAGCATTGTTGAGCGGGGTAAGTGCCTTTACCGCCATCCGCACA

R region (583-650)>>>
|
541 ACGGTGGCAGGTCTATATAAGCAGAGCTCGTTTTAGTGAACCGCGCGGCACTCCTCCGATTG 600
TGCCACCCCTCCAGTATATTCGTCTCGACCAATCACTTGGCGCGGTCAGGAGGCTAAC

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FIGURE 3E

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05 region (651-1202)>>>

|

601 ACTGASTCGCCCGGGTACCCGTGTATCCAAATAAACCCCTCTTGCAGTTGCATCCGACTTGT 660
TGACTCAGCGGGCCCATGGGCACATAGGTTATTTGGGAGAACGTCAACGTAGGCTGAACA

661 GGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTC 720
CCAGAGCGACAAAGGAACCCCTCCAGAGGAGACTCACTRACTGATGGGCAGTCGCCCCCAG

721 TTTCATTTGGGGCTCGTCCGGGATCGGGAGACCCCTGCCAGGGACACCGACCCACCA 780
AAAGTAAACCCCGAGCAGGCCCTTAGCCCTCTGGGGACGGGTCCCTGGTGGCTGGGTGGT

5'SS (788)

|

781 CCGGGAGGTAAGCTGGCCAGCAACTTATCTGTCTGTCCGATTGCTAGTGTCTATGAC 840
GGCCCTCCATTCCAGCCGGTCGTTGAATAGACACAGACAGGCTAACAGATCACAGATACTG

841 TGATTTTATGCGCCTGCGTCGGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCG 900
ACTAAAATAAGCGGACCCAGCCATGATCAATCGATTGATCGAGACATAGACCGCCTGGGC

901 TGGTGGAACTGACGAGTTCCGAACACCCGGCCGCAACCCCTGGGAGACGTCCAGGGACTT 960
ACCACCTTGACTGTCTCAAGCTTTGTGGCCGGCGTTGGGACCCCTCTGCAGGGTCCCTGAA

961 CCGGGGCCCTTTTGTGGCCCGACCTGAGTCCAAAATCCCGATCGTTTGGACTCTTTG 1020
GCCCCCGGCAAAACACCGGGCTGGACTCAGGTTTITAGGGCTAGCBAACCTGAGAAAC

1021 GTGCACCCCTTTAGAGGAGCGATATCTGGTTCTGGTAGGAGACGAGAACCTAAAACAGT 1080
CACCTGGGGGGAATCTCTCCCTATACACCAAGACCATCTCTGCTCTTGGATTTTGTCA

1081 TCCCGCCTCCGTCTGAATTTTGTCTTTCGGTTTGGGACCGAAGCCGCGCGCGGCTCTTG 1140
AGGGCGGAGGCAGACTTAAAACCAAAAGCCAAACCCCTGGCTTCGGCGCGGCGGCGAGAAC

1141 TCTGCTGAGCATCGTTCTGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTGTAGA 1200
AGACGACGTCTGTAGCAAGACACAAACAGACAGACTGACACAAAGACATRAACAGACTCT

gag (1203, 2819)>>>

|

1201 ATATGGGUCAGACTGTTACCACTCCCTTAAGTTTGGACCTTAGGTCACTGGAAAGAGTTCG 1260
TATACCCGGTCTGACAATGGTGAGGGAAATTCAAACTGCAATCCAGTGAACCTTTCTACAGC

1261 AGCGGATCGCTCACAACCACTCGGTAGNTGTCAAGAAGAGAGCTTGGGTTACCTTCTGCT 1320
TCGCTTAGCGAGTGTGGTCAAGCCATCTACAGTTCTTCTCTGCAACCCATGGAAGACGA

1321 CTGCAGAAATGGCCACCTTTAAGCTCGGATGGCCGCGAGACCGCACCTTTAACCAGAGAC 1380
GACGTCTTACCGGTTGGAAATTCAGGCTACCGGGCGCTCTGCCGTGGAAATTGGGTCTGTG

1381 TCATCACCCAGGTTAAGATCAAGGTCTTTTCACTCGCCCGCCTGGACACCCAGAACAGG 1440
AGTAGTGGGTCCAAATTCATATTCCAGAAAGTGGACUGGGCGTACCTGTGGGTCTGGTCC

1441 TCCCCTACATCGTGACCTGGGAAGCCTTGGCTTTTGACCCGCCCTCCCTGGGTCAAGCCCT 1500
AGGGGATGTAGCACTGGACCCCTTCGGAACCGAAACTGGGGGAGGGACCCAGTTCCGGGA

FIGURE 3E (cont'd)

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1501 TTGTACACCCCTAAGCCTCCGCCTCCTCTTCCATCCGCCCCGTCTCTCCCCCTTGAAC 1560
 AACATGTGGGATTCCGAGGGCGAGGAGAAGGAGGTAGCGGGGCAGAGAGGGGGAACCTG
 1561 CTCCTCGTTTCGACCCCCCTCGATCCTCCCTTTATCCAGCCCTCACTCCTTCTCTAGGCG 1620
 GAGGAGCAAGCTGGGGCGGAGCTAGGAGGGAAATAGGTCCGGAGTGAGGAAGAGATCCGC
 1621 CCAAACCTAAACCTCAAGTTCTTTCTGACAGTGGGGGGCCGCTCATCGACCTACTTACAG 1680
 GGTTTGGATTTCGAGTTCAAGAAAGACTGTCACCCCCCGCGAGTAGCTGGATGAATGTC
 1681 AAGACCCCCCGCCTTATAGGGACCCAAGACCACCCCTTCCGACAGGGACGGAAATGGTG 1740
 TTCTGGGGGGCGGAATATCCCTGGGTTCTGGTGGGGGAAGGCTGTCCCTGCCTTTACCA
 1741 GAGAAGCGACCCCTGCGGGAGAGGCCACCGACCCCTCCCCAATGGCATCTCGCTACGTG 1800
 CTCTTCGCTGGGGACGCCCTCTCCGTGGCTGGGGAGGGGTACCGTAGAGCGGATGCAC
 1801 GGAGACGGGAGCCCCCTGTGGCCGACTCCAATACTCGCAGGCATTCCCCCTCCGCGCAG 1860
 CCTCTGCCCTCGGGGACACCGGCTGAGGTGATGGAGCGTCCGTAAGGGGAGCGCGCTC
 1861 GAGGAAACGGACAGCTTCAATACTGGCCCTTCTCCTCTTCTGACCTTTACAATGGAAAA 1920
 CTCCTTTGCCTTETCGAAGTTATGACCGGCAAGAGGAGAAGACTGGAAATGTTGACCTTTT
 1921 ATAATAACCCCTTCTTTTTCTGAAGATCCAGGTAAACTGACAGCTCTGATCGAGTCTGTC 1980
 TATTATTGGGAAGAAAAAGACTTCTAGGTCCATTTCAGTGTGAGACTAGCTCAGACAAG
 1981 TCATCACCACATCAGCCACCTGGGACGACTGTCAGCAGCTGTTGGGGACTCTGCTGACCG 2040
 AGTAGTGGGTAGTCGGGTGGACCTGCTGACAGTCCGTCGACAACCCCTGAGACGACTGGC
 3121 ACTTTGAGGGATCAGGAGCCCAGGTTATGGGACCAATGGGGCAGCCCTGCAAGTGTGTA 3180
 TGAAACTCCCTACTCCTCGGGTCCAATACCCTGGTTACCCCGTCGGGGACGTTACACACT
 3181 CCCTAAATATAGAAGATGAGCATCGGCTACATGAGACCTCAAAAGAGCCAGATGTTTCTC 3240
 GGGATTTATATCTTCTACTCGTAGCCGATGTACTCTGGAGTTTTCTCGGTCTACAAAGAG
 3241 TAGGGTCCACATGGCTGTCTGATTTTTCTCAGGCCTGGGCGGAAACCGGGGGCATGGGAC 3300
 ATCCCAGGTGTACCGACAGACTAAAAGGAGTCCGGACCCCGCTTTGGCCCCCGTACCCCTG
 3' SS (3314)
 3301 TGGCAGTTCGCCAAGCTCCTCTGATCATACCTCTGAAAGCAACCTCTACCCCCGTGTCCA 3360
 ACCGTCAAGCGGTTCCAGGAGACTAGTATGGAGACTTTCGTTGGAGATGGGGGCACAGGT
 3361 TAAACAATAACCCATGTCACAAGAAGCCAGACTGGGGATCAAGCCCCACATACAGAGAC 3420
 ATTTTGTATGGGGTACACTGTTCTTCGGTCTGACCCCTAGTTCCGGGTGTATGTCTCTG
 3421 TGTTGGACAGGGAATACTGGTACCCTGCCAGTCCCCCTGGAACACGCCCCCTGCTACCCG 3480
 ACAACCTGGTCCCTTATGACCATGGGACGGTCAGGGGGACCTTGTGCGGGGACGATGGGC
 3481 TTAAGAAACCAGGGACTAATGATTATAGGCCTGTCCAGGATCTGAGAGAAGTCAACAAGC 3540
 AATTCCTTGGTCCCTGATTACTAATATCCGCACAGGTCCCTAGACTCTCTTCAGTTGTTCC

FIGURE 3E (cont'd)

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3541  GGGTGGGAAGACATCCACCCACCGTGCCCAACCCCTTACAACCTCTTGAGCGGGCTCCCAC 3600
      CCCACCTTCTGTAGGTGGGGTGGCACGGGTGGGAATGTTGGAGAACTCGCCCGAGGGTG

3601  CGTCCCACCACTGGGTACACTGTGCTTGATTTAAAGCATGCCCTTTTCTGCCGTGAGACTCC 3660
      GCAGGGTGGTCACCATCTGACACGAACATAAATTTCTACCGAAAAGACGGACTCTCAGG

                                     PfeI
                                     |
                                     TfiI
                                     |
3661  ACCCCACCACTCAGCCTCTCTTCGCCCTTTGAGTGGAGAGATCCAGAGATGGGAATCTCAG 3720
      TGGGGTGGTCAGTCGGAGAGAAGCGGAAACTCACCTCTCTAGGTCTCTACCCCTTAGAGTC

      MfeI
      |
      MunI
      |

3721  GACAATTGACCTGGACCAGACTCCCACAGGGTTTCAAAAACAGTCCCACCTGTTTGATG 3780
      CTGTTAACTGGACCTGGTCTGAGGGTGTCCCAAAGTTTTGTGAGGGTGGGACAAACTAC

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

3781  AGGCACTGCACAGAGACCTAGCAGACTTCGGGATCCAGCACCCAGACTTGATCCTGCTAC 3840
      TCCGTGACGTGTCTCTGGATCGTCTGAAGGCCTAGGTCTGTTGGTCTGAAGTACGACCATG

3841  AGTACGTGGATGACTTACTGCTGGCCGCCACTTCTGAGCTAGACTGCCAACAAGGTACTC 3900
      TCATGCACCTACTGAATGACGACCGGCGGTGAAGACTCGATCTGACGGTGTTCATGAG

3121  ACTTTGAGGGATCAGGAGCCCAGGTTATGGGACCAATGGGGCAGCCCTGCAAGTGTGA 3180
      TGAAACTCCCTAGTCCTCGGGTCCAATACCTGGTTACCCCGTCGGGGACGTTACAACT

3181  CCCTAAATATAGAAGATGAGCATCGGCTACATGAGACCTCAAAAGAGCCAGATGTTTCTC 3240
      GGCATTTATATCTTCTACTCGTAGCCGATGTAATCTGGAGTTTTCTCGGTCTACAAAGAG

3241  TAGGGTCCACATGGCTGTCTGATTTTCTCAGGCCTGGGCGGAAACCGGGGGCATGGGAC 3300
      ATCCCAGGTGTACCGACAGACTAAAAGGAGTCCCGACCCGCCCTTTGGCCCCCGTACCCCTG

```

FIGURE 3E (cont'd)

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FIGURE 3E (cont'd)

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3841 AGTACGTGGATGACTTACTGCTGGCCGCCACTTCTGAGCTAGACTGCCAACAAGGTACTC 3900
 TCATGCACCTACTGAATGACGACCGGCGGTGAAGACTCGATCTGACGGTGTGTCATGAG

3901 GGGCCCTGTTACAAACCCTAGGGAACCTCGGGTATCGGGCCTCGGCCAAGAAAGCCCCAA 3960
 CCGGGACAATGTTTGGGATCCCTTGGAGCCCATAGCCCGGAGCCGGTTCCTTCGGGTTT

3961 TTTGCCAGAAACAGGTCAAGTATCTGGGSTATCTTCTAAAAGAGGGTCAGAGATGGCTGA 4020
 AAACGGTCTTTGTCCAGTTCATAGACCCCATAGAAGATTTTCTCCAGTCTCTACCGACT

4021 CTGAGGCCAGAAAAGAGACTGTGATGGGSCAGCCTACTCCGAAGACCCCTCGACAATAA 4080
 GACTCCGGTCTTTTCTCTGACACTACCCCGTCGGATGAGGCTTCTGGGGAGCTCTTGATT

4081 GGGAGTTCTAGGGACGGCAGGCTTCTGTGCCTCTGGATCCCTGGGTTTGCAGAAATGG 4140
 CCTCAAGGATCCCTGCCGTCCGAAGACAGCGGAGACCTAGGGACCCAAACGTCCTTACC

4141 CAGCCCCCTTGTACCCTCTCACCAAAACGGGGACTCTGTTTAAATTGGGGCCCAGACCAAC 4200
 GTCGGGGGAACATGGGAGAGTGGTTTTGCCCTGAGACAAATTAACCCCGGGTCTGGTTG

4201 AAAAGGCCTATCAAGAAATCAAGCAAGCTCTTCTAACTGCCCCAGCCCTGGGGTTGCCAG 4260
 TTTTCCGGATAGTTCTTTAGTTCGTTGAGAGAATTGACGGGGTCGGGACCCCAACGGTC

Salt
|

4261 ATTTGACTAAGCCCTTTGAACCTCTTTGTGACGAGAAGCAGGGCTACGCCAAAGGTGTCC 4320
 TAAACTGATTGCGGAAACTTGAGAAACAGCTGCTCTTCGTCCCGATGCGGTTTCCACAGG

4321 TAACGCCAAAACTGGGACCTTGGCGTCGSCCGGTGGCCTACCTGTCCAAAAGCTAGACC 4380
 AFTGCGTTTTTGCACCCTGGAACCCGAGCCGSCCACC GGATGGACAGGTTTTTGCATCTGG

4381 CAGTAGCAGCTGGGTGGCCCCCTTGCCCTACGATGGTAGCAGCCATTGCCGTACTGACAA 4440
 GTCATCGTCGACCCACCGGGGGAACGGATGCCTACCATCGTCGGTAACGGCATGACTGTT

4441 AGGATGCAGGCAAGCTAACCATGGGACAGCCACTAGTCATTCTGGCCCCCATGCAGTAG 4500
 TCCTACGTCCGTTGCGATTGGTACCCTGTGGGTGATCAGTAAGACCGGGGGGTACGTCATC

4501 AGGCACTAGTCAAAACAACCCCCGACCGCTGGCTTTCCAACGCCCGGATGACTCACTATC 4560
 TCCGTGATCAGTTTGTGTTGGGGGCTGGCGACCGAAAGGTTGCGGGCCTACTGAGTGATAG

4561 AGGCCTTGCTTTTGGACACGGACCGGTCAGTTGCGACCGGTGGTAGCCCTGAACCCGG 4620
 TCCGGAACGAAAACCTGTGCCTGGCCCAGGTCAAGCCTGGCCACCATCGGGACTTGGGCC

4621 CTACGCTGCTCCCACTGCCTGAGGAAGGGCTGCAACACAACCTGCCTTGATATCCTGGCCG 4680
 GATGCGACGAGGGTGACGGACTCCTTCCCGACGTTGTGTTGACGGAACATATAGGACCGGC

4681 AAGCCACCGGAACCCGACCCGACCTAACGGACAGCCGCTCCCGACCGCGACCCACACCT 4740
 TTCGGGTGCCTTGGGCTGGGCTGGATTGCCTGGTCGGCGAGGGTCTGCGGCTGGTGTGGA

4741 GGTACACGGATGGAAGCAGTCTCTTACAAGAGGGACAGCGTAAGGCGGGAGCTGCGGTGA 4800
 CCATGTGCCTACCTTCGTGAGAGAATGTTCTCCCTCTCGCATTCCGCCCTCGAGGCCACT

FIGURE 3E (cont'd)

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BspI
 |
 CclII
 |
 Bpu1102I
 |
 Bsp1720I
 |

4801 CCACCGAGACCGAGGTAATCTGGGCTAAAGCCCTGCCAGCCGGGACATCCGCTCAGCGGG 4860
 GGTGGCTCTGGCTCCATTAGALCCGATTCGGGGACGGTUGGCCCTGTAGGCGAGTCGCCC

4861 CTGAACTGATAGCACTCAGCCAGGCCCTAAAGATGGCAGAAGGTAAGAAGCTAAATGTTT 4920
 GACTTGACTATCGTGAGTGGGTCCGGGATTTCTACCGTCTTCCATTCTTCGATTTACAAA

4921 ATACTGATAGCGGTTATGCTTTTGGCTACTGCCCATATCCATGGAGAAATATACAGAAGGC 4980
 TATGACTATCGGCAATACGAAAACGATGACGGGTATAGGTACTTCTTTATATGTCTTCGG

4981 GTGGGTTGCTCACAECAGAAGGCCAAGAGATCAAAAATAAAGACGAGATCTTGGCCCTAC 5040
 CACCCAAACGAGTGTAGTCTTCCGTTTCTCTAGTTTTTATTTCTGCTGTAGAACCUGGATG

5041 TAAAGCCCTCTTTCTGCCCAAAAGACTTAGCATAATCCATTGTCCAGGACATCAAAAGG 5100
 ATTTTCGGGAGAAAGACGGGTTTTCTGAATCGTATTAGGTAAACAGCTCCTGTAGTTTTCC

5101 GACACAGCGCCCGAGGCTAGAGGCCAACCGGATGGCTGACCAAGCGGCCCGAAAGGCAGCCA 5160
 CTGTGTCCGGCTCCGATCTCCGTTGGCCTACCGACTGGTTCCGCCGGCTTTCCGTCGGT

5161 TCACAGAGACTCCAGACACCTCTACCCCTCTCATAGAAAATTCATCACCCCTACACCTCAG 5220
 AGTGTCTCTGAGGTCTGTGGAGATGGGACGAGTATCTTTAAGTAGTGGGATGTGCACTC

5221 AACATTTTCATTACACAGTCACTGATATAAAGGACCTAACCAAGTTGGGGGCCATTTATG 5280
 TTGTAAAAGTAATGTGTCACTGACTATATTTCCCTGGATTGGTTCAACCCCGGTAAATAC

5281 ATAAAACAAAGAAGTATTGGGCTTACCAAGCAAAACCTGTGATGCTTGACCACTTTACTT 5340
 TATTTTCTTTCTTCATAACCCAGATGGTTCTTTTGGACACTACGGACTGGTCAAATGAA

5341 TTGAATTATTAGACTTTCTTCATCAGGTCACTCACCTEAGCTTCTCAAAAATGAAGCTC 5400
 AACTTAATAATCTGAAGAAGTAGTGGACTGAGTGGAGTCCGAAGASTTTTTACTTCCGAG

5401 TCCTAGAGAGAAGCCACAGTCCCTACTACATGCTGAACCGGATCGAACACTCAAAAATA 5460
 AGGATCTCTCTTCTGTGTGAGGATGATGTACEACTTGGCCCTAGCTTGTGATTTTTAT

5461 TCACTGAGACCTGCCAAGCTTGTGCACAAETCAACGCCAGCAAGTCTGCCGTTAAACAGG 5520
 AGTGACTCTGGACGTTTCGAACACGTGTTCACTGGGGTCGTTCCAGACGGCAATTTGTCC

SacII
 |
 SgrBI
 |
 Cfr42I
 |
 Sfr303I
 |
 KspI
 |

FIGURE 3E (cont'd)

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5521 GAACTAGGGTCCGCGGGCATCGGCCCCGGCACTCATTGGGAGATCGATTTACCGAGATAA 5580
 CTTGATCCCAGGCGCCCCGTAGCCGGGCGGTGAGTAACCCCTCTAGCTAAAGTGGCTCTATT

5581 AGCCCCGATTGTATGGCTATAAATATCTTCTAGTTTTTATAGATAACCTTTTCTGGCTGGA 5640
 TCGGGCCTAACATACCGATATTTATAGAAGATCAAAAATATCTATGGAAAAGACCGACCT

5641 TAGAAGCCTTCCCAACCAAGAAAGAAACCGCCAAGGTCGTAACCAAGAAGCTACTAGAGG 5700
 ATCTTCGGAAGGGTTGGTTCTTCTTTGGCGGTTCCAGCATGGGTTCTTCGATGATCTCC

PaeI
 ...
 BbuI
 ...
 SpaHI
 ...
 SphI
 ...

5701 AGATCTTCCCCAGGTTCCGCATGCCTCAGGTATTGGGAAGTACAAATGGGCCTGCCTTCG 5760
 TCTAGAAGGGGTCCAAGCCGTACCGAGTCCATAACCCCTTGACTGTTACCCGGACGGAAGC

6901 CTTCCAAGGGGCTACTCGAGGGGGCAGATGCAACCCCTCTAGTCCTAGAATTCAGTGATGC 6960
 GAAGGTTCCCCGATGAGCTCCCCGCTCTACGTTCCGAGATCAGGATCTTAAGTGACTACG

6961 AGGAAAAAAGGCTAACTGGGACGGGCCCCAAATCGTGGGGACTGAGACTGTACCGGACAGG 7020
 TCCTTTTTCCGATTGACCCTGCCCGGGTTTAGCACCCCTGACTCTGACATGGCCTGTCC

7021 AACAGATCCTATTACCATGTTCTCCCTGACCCGGCAGGTCCTTAATGTGGGACCCCGAGT 7080
 TTGTCTAGGATAATGGTACAAGAGGGACTGGGCGGTCCAGGAATTACACCCTGGGGCTCA

7081 CCCCATAGGGCCCCAACCCAGTATTACCCGACCAAAGACTCCCTTCCTCACCAATAGAGAT 7140
 GGGGATCCCGGGTTGGGTCAATGSGGCTGGTTTCTGAGGGAAGGAGTGGTTATCTCTA

7141 TGTACCGGCTCCACAGCCACCTAGCCCCCTCAATACCAGTTACCCCCCTTCCACTACCAG 7200
 ACATGGCCGAGGTGTGCGGTGGATCGGGGGAGTTATGGTCAATGGGGGAAGGTGATGCTC

7201 TACACCCTCAACCTCCCTTACAAGTCCAAGTGTCCACAGCCACCCCAAGGAAGTGGAGA 7260
 ATGTGGGAGTTGGAGGGGATGTTGAGGTTACAGGGTGTGCGGTGGGGGTCCTTGACCTCT

7261 TAGACTACTAGCTCTAGTCAAAGGAGCCTATCAGGCGCTTAACCTCACCAATCCCGACAA 7320
 ATCTGATGATGAGATCAGTTTCCCTCGGATAGTCGCGCAATTGGAGTGGTTAGGGCTCTT

7321 GACCCAGAATGTTGGCTGTGCTTAGTGTCCGGGACCTTCCTTATTACGAAGGAGTAGCGGT 7380
 CTGGGTTCTTACAACCGACACGAATCACAGCCCTGGAGGAATAATGCTTCCTCATCGCCA

7381 CGTGGGCACTTATACCAATCAATCCACCGCTCCGGCCAACTGTACGGCCACTTCCCAACA 7440
 GCACCCGTCAATATGTTAGTAAGGTGGCGAGGCCGGTTGACATGCCGTTGAAGGTTGT

FIGURE 3E (cont'd)

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EcoT22I
 ||
 NsiI
 ||
 MphI103I
 ||
 Zsp2I
 ||
 BfrBI
 ||

7441 TAAGCTTACCCCTATCTGAAGTGACAGGACAGGGCCCTATGCATGGGGGCAGTACCTAAAAC 7500
 ATTCCGAATGGGATAGACTTCACCTGTCCTGTCCCGGATACGTACCCCGTCATGGATTTTC

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

7501 TCACCAGGCCCTTATGTAACACCACCCAAAGCGCGCGGCTCAGGATCCTACTACCTTGCAGC 7560
 AGTGGTCCCGAATACATTGTGGTGGGTTTCGCGGCCGAGTCCTAGGATGATGGAACGTCG

AleI
 |
 OhiI
 |

7561 ACCCGCCGGAACAATGTGGGCTTGCAGCACTGGATTGACTCCCTGCTTGTCCACCACGGT 7620
 TGGGCGGCCCTTGTTACACCCGAACGTCGTGACCTAACTGAGGGACGAACAGGTGGTGCCA

7621 GCTCAATCTAACCACAGATTATTGTGTATTAGTTGAACTCTGGCCCAGAGTAATTTACCA 7680
 CGAGTTAGATTGGTGTCTAATAACACATAATCAACTTGAGACCGGGTCTCATTAAATGGT

6901 CTTCCAAGGGGCTACTCGAGGGGGCAGATGCAACCCCTCTAGTCCTAGAATTCAGTGATGC 6960
 GAAGGTCCCCGATGAGCTCCCCCGTCTACGTTGGGAGATCAGGATCTTAAGTGACTACG

6961 AGGAAAAAAGGCTAACTGGGACGGGGCCAAATCGTGGGACTGAGACTGTACCGGACAGG 7020
 TCCTTTTTTCCGATTGACCCTGCCCGGGTTTAGCACCCCTGACTCTGACATGGCCTGTCC

7021 AACAGATCCTATTACCATGTTCTCCCTGACCCGGCAGGTCCTTAATGTGGGACCCCGAGT 7080
 TTGTCCTAGGATAATGGTACAAGAGGGACTGGGCGCTCCAGGAATTACACCCTGGGGCTCA

FIGURE 3E (cont'd)

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7081  CCCCATAGGGCCCAACCCAGTATTACCCGACCAAAAGACTCCCTTCCTCACCAATAGAGAT 7140
      GGGGTATCCCGGTTGGGTCATAATGGGCTGGTTTCTGAGGGAAGGAGTGGTTATCTCTA

7141  TGTACCGGCTCCACAGCCACCTAGCCCCCTCAATACCAGTTACCCCCCTCCACTACCAG 7200
      ACATGGCCGAGGTGTGGGTGGATCGGGGAGTTATGGTCAATGGGGGAAGGTGATGGTC

7201  TACACCCCTCAACCTCCCCTACAAGTCCAAGTGTCCACAGCCACCCCCAGGAAGTGGAGA 7260
      ATGTGGGAGTTGGAGGGGATGTTCAAGTTACAGGGTGTGGGTGGGGGTCTTGACCTCT

7261  TAGACTACTAGCTCTAGTCAAAGGAGCCTATCAGGGCGCTTAACCTCACCATCCCGACAA 7320
      ATCTGATGATCGAGATCAGTTTCCTCGGATAGTCCGCGAATTGGAGTGGTTAGGGCTGTT

7321  GACCCAAAGAATGTTGGCTGTGCTTAGTGTGGGACCTCCTTATTACGAAGGAGTAGGGT 7380
      CTGGGTTCTTACAACCGACACGAATCACAGCCCTGGAGGAATAATGCTTCCTCATCGCCA

7381  CGTGGGCACTTATACCAATCATTCCACCGGTCCGGCCAACTGTACGGCCACTTCCCAACA 7440
      GCACCCGTGAATATGCTTAGTAAGGTGGCGAGCCCGGTTGACATGCCGGTGAAGGCTTGT

                                     EcoT22I
                                     |
                                     NsiI
                                     |
                                     Mph1103I
                                     |
                                     Zsp2I
                                     |
                                     BfrBI
                                     ||

7441  TAAGCTTACCCCTATCTGAAGTGACAGGACAGGGCCTATGCATGGGGSCAGTACCTAAAAC 7500
      ATTGGAATGGGATAGACTTCAGTGTCTGTCCCGGATACGTACCCCGTCATGCATTTTG

                                     NaeI
                                     |
                                     PdiI
                                     |
                                     MroNI
                                     ||
                                     NgoMIV
                                     ||

7501  TCACCAGGCCTTATGTAACACCACCCAAAGCGCGGCTCAGGATCCTACTACCTTGCAGC 7560
      AGTGGTCCGGAATACATTGTGGTGGGTTTCGCGGCCGAGTCCTAGGATGATGGAACGTCG

```

FIGURE 3E (cont'd)

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A1e1
 |
 0111
 |

7561 ACCCGCCGGAACAATGTGGGCTTGCAGCACTGGATTGACTCCCTGCTTGTCCACCACGGT 7620
 TGGGGGGCCCTTGTTACACCCGAACGTCGTGACCTAACTGAGGGACGAACAGGTGGTGCCA

7621 GCTCAATCTAACCACAGATTATTGTGTATTAGTTGAACTCTGGCCCACAGTAATTTACCA 7680
 CCAGTTAGATTGGTGTCTAATAACACATAATCAACTTGAGACCGGGTCTCATTAAATGGT

7681 CTCCCCCGATTATATGTATGGTCAGCTTGAACAGCGTACCAAATATAAAAGAGAGCCAGT 7740
 GAGGGGGCTAATATACATACCAGTCGAACCTGTGCGCATGGTTTATATTTTCTCTCGGTCA

7741 ATCATTGACCCCTGGCCCTTCTACTAGGAGGATTAACCATGGGAGGGATTGCAGCTGGAAT 7800
 TAGTAACTGGGACCGGGAAGATGATCCTCCTAATTGGTACCCCTCCCTAACGTCGACCTTA

7801 AGGGACGGGGACCACTGCCTTAATTA AAAACCCAGCASTTTGAGCAGCTTCATGCCGCTAT 7860
 TCCCTGCCCCCTGGTGACGGAATTAATTTTGGGTGCTCAAACTCGTCGAAGTACGGCGATA

7861 CCAGACAGACCTCAACGAAGTCGAAAAGTCAATTACCAACCTAGAAAAGTCACTGACCTC 7920
 GGTCTGTCTGGAGTTGCTTCAGCTTTTTCAGTTAATGGTTGGATCTTTTCAGTGACTGGAG

7921 GTTGTCTGAAGTAGTCCTACAGAACCGCAGAGGCCTAGATTTGCTATTCCCTAAAGGAGGG 7980
 CAACAGACTTCATCAGGATGTCTTGGCGTCTCCGGATCTAAACGATAAGGATTTCTCTCC

7981 AGGTCTCTGCCAGCCCTAAAAGAAGAATGTTGTTTTATGCAGACCACACGGGGCTAGT 8040
 TCCAGACACGCGTCGGGATTTTCTTCTTACAACAAAAATACGTCTGGTGTGCCCCGATCA

8041 GAGAGACAGCATGGCCAAATTAAGAGAAAGGCTTAATCAGAGACAAAACTATTTGAGAC 8100
 CTCTCTGTCTGTACCGGTTTAATTCTCTTTCCGAATTAGTCTCTGTTTTTGATAAACTCTG

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

8101 AGGCCAAGGATGGTTCGAAGGCTGTTTAATAGATCCCCCTGGTTTACCACCTTAATCTC 8160
 TCCGGTTCCTACCAAGCTTCCCGACAAATTATCTAGGGGGACCAAATGGTGGAAATTAGAG

FIGURE 3E (cont'd)

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8161 CACCATCATGGGACCTCTAATAGTACTCTTACTGATCTTACTCTTTGGACCTTGCATTCT 8220
      GTGGTAGTACCCTGGAGATTATCATGAGAATGACTAGAATGAGAAACCTGGAACGTAAGA

8221 CAATCGATTGGTCCAATTTGTTAAAGACAGGATCTCAGTGGTCCAGGCTCTGGTTTTGAC 8280
      GTTAGCTAACCAGGTTAAACAATTTCTGTCCCTAGAGTCACCAGGTCGAGACCAAAACTG

                                     IRES reg(8327,8876)>>>
                                     |
                                     MluI(8325)
                                     | |
8281 TCAGCAATATCACCAGCTAAAACCCATAGAGTACGAGCCATGAACGCGTTACTGGCCGAA 8340
      AGTCGTTATAGTGGTCGATTTTGGGTATCTCATGCTCGGTACTTGGCCAATGACCGGCTT

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

8401 CTTTTGGCAATGTGAGGGCCCCGAAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGG 8460
      GAAAACCGTTACACTCCCGGGCCTTTGGACCCGGACAGAAGAACTGCTCGTAAGGATCCC

8461 GTCTTTCCCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTC 8520
      CAGAAAGGGGAGAGCGGTTTCTTACGTTCCAGACAACTTACAGCACTTCCTTCGTCAAG

8521 CTCTGGAAGCTTCTTGAAGACAAACAACGTCTGTAGCGACCCCTTTCAGGCAGCGGAACC 8580
      GACACCTTCGAAGAACTTCTGTTTGTTCAGACATCGCTGGGAAACCTCCGTCCGCTTGG

8581 CCCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAA 8640
      GGGGTGGACCGCTGTCCACGGAGACGCGGTTTTTCGGTGCACATATTCTATGTGGACGTT

8641 AGCGGGCACAACCCCAAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGC 8700
      TCCGCCGTGTTGGGGTCACGGTGCAACACTCAACCTATCAACACCTTTCTCAGTTTACCG

8701 TCTCCTCAAGCGTATTCAACAAGGGGCTGAGGGATGCCCAGAAGGTACCCCATTTGTATGG 8760
      AGAGGAGTTTCGCATAAGTTGTTCCCCGACTTCCTACGGGTCTCCATGGGGTAACATACC

8761 GATCTGATCTGGGGCCTCGGTGCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAAC 8820
      CTAGACTAGACCCCGGAGCCACGTGTACGAAATGTACACAAATCAGCTCCAATTTTTTTG

```

FIGURE 3E (Cont'd)

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yCD2 (8877, 9353)>>>

PstI (8874)

8821 GTCTAGGCCCCCGAACCACGGGGACGTGGTTTTCCTTTGAAAAACACGATTATAAATGG 8880
CACATCCGGGGGGCTTGGTGCCCTGCACCAAAAGGAAACITTTTGTGCTAATATTACC

8881 TGACCGGGCCGCATGGCCTCCAAGTGGGATCAAAAGGGCATGGATATCGCTTACGAGGAGG 8940
ACTGGCCCGCGTACCGGAGGTTACCCCTAGTITTTCCCGTACCTATAGCGAATGCTCCTCC

8941 CCGTGCTGGGCTACAAGGAGGGGGCGGTGCGCTATCGGGGGCTGTCTGATCAACAACAAGG 9000
GGCAGGACCCGATGTTCCCTCCCGCGCACGGATAGCCGCCGACAGACTAGTTGTTGTTCC

9001 ACCGCAGTGTGCTGGGCAGGGGCCACAACATGAGGTTCCAGAAGGGCTCCGCCACCCCTGC 9060
TGCCGTCACAAGACCCGTCCCCGGTGTGTACTCCAAGGTCTTCCCGAGGCGGTGGGAGC

9061 ACCGGGAGATCTCCACCCTGGAGAACTGTGGCAGGCTGGAGGGCAAGGTGTACAAGGACA 9120
TGCCGCTCTAGAGGTGGGACCTCTTGACACCGTCCGACCTCCCGTTCCACATGTTCTCTGT

9121 CCACCCTGTACACCACCCTGTCCCTTGTGACATGTGTACCGGCGCTATCATCATGTACG 9180
GGTGGGACATGTGGTGGGACAGGGGAACACTGTACACATGGCCGCGATAGTAGTACATGC

9181 GCATCCCTAGGTGTGTGATCGGCGAGAACTGAACTTCAAGTCCAAGGGCGAGAAGTACC 9240
CGTAGGGATCCACACACTAGCCGCTCTTGCACTTGAAGTTCAAGTTCCCGCTCTTCATGG

9241 TGCAAACCAGGGGCCACGAGGTGGTGGTGTGACGATGAGAGGTGTAAGAAGCTGATGA 9300
ACGTTTGGTCCCGGTGCTCCACCACCAACAACTGCTACTCTCCACATTCCTCGACTACT

NotI (9356)

CciNI

9301 AGCAGTTCATCGACGAGAGGCCCTCAGGACTGCTTCGAGGATATCGGGCAGTAAGCGGCCG 9360
TCGTCAAGTAGCTGCTCTCCGGAGTCTTGACCAAGCTCCTATAGCGCTCATTCCGCCGGC

U3 Region(9405, 9854)>>>

9361 CAGATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCACC 9420
CTCTATTTTATTTTCTAAATAAATCAGAGGTCCTTTTCCCCCTTACTTTCTGGGGTGG

BmtI

NheI

AsuNI

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

9421 TGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAA 9480
ACATCCAAACCGTTTCGATCGAATTCATTGCGGTAAAACGTTCCGTACCTTTTTATGTATT

FIGURE 3E (cont'd)

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```

9481 CTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGGCCA 9540
      GACTCTTATCTCTTCAAGTCTAGTTCAGTCCCTTGTCTACCTTGTCGACTTATACCCGGT

9541 AACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACA 9600
      TTGTCTATAGACACCATTCTGTCAAGGACGGGGCCGAGTCCCAGGTTCTTGTCTACCTTGT

9601 GCTGAATATGGGGCCAAACAGGATACTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCA 9660
      CGACTTATACCCGGTTTGTCTATAGACACCATTCTGTCAAGGACGGGGCCGAGTCCCAGT

9661 AGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATG 9720
      TCTTGTCTACCAGGGGTCTACGCCAGGTGCGGAGTCTCTCAAAGATCTCTTGCTAGTCTAC

9721 TTTCCAGGGTGGCCCCAAGGACCTGAAATGACCCCTGTGCCTTATTTGAACTAACCAATCAG 9780
      AAAGGTCCCACGGGGTTCTTGGACTTTACTGGGACACGGAATAAACTTGATTGGTTAGTC

                                     SacI
                                     |
                                     SstI
                                     |
                                PvuI   Psp124BI
                                |       |
                                BsePI   EcoICRI
                                |       |
                                BssHII  Ecl136II
                                |       |
9781 TTCGCTTCTCGCTTCTGTTCCGCGGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCACAA 9840
      AAGCGAAGAGCGAAGACAAGCGCCCGAAGACGAGGGGCTCGAGTTATTTTCTCGGGTGT

      R Region(9855, 9921)>>>>
      |
9841 CCCCTCACTCGGGGCGCCAGTCCCTCCGATTGACTGAGTGGCCCGGGTACCCGTGTATCCA 9900
      GGGGAGTGAGCCCCCGCGTCAGGAGGCTAACTGACTCAGCGGGGCCATGGGCACATAGGT

      U5 Region(9922, 9998)>>>>
      |
9901 ATAAACCCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCTTGGGAGGGTCTCCT 9960
      TATTTGGGAGAACGTCAACGTAGGCTGAACACCAGAGCGACAAGGAACCCCTCCAGAGGA

9961 CTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTTCATTACATGTGAGCAAAAGGCCAGCA 10020
      GACTCACTAACTGATGGGCAGTCCGCCCCAGAAAGTAATGTACACTCGTTTTCCGGTCTGT

      pBR322 origin(10045, 10664)<<<
      |
10021 AAAGGCCAGGAACCGTAAAAAGGCCGCGTGTCTGGCGTTTTTTCATAGGCTCCGCCCCC 10080
      TTTCGGTCTCTTGGCATTTTTCCGGCGCAACGACCGCAAAAGGTATCCGAGGCGGGGGG

10081 TGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATA 10140
      ACTGCTCGTAGTGTTTTTAGCTGCGAGTTCAGTCTCCACCGCTTTGGGCTGTCTGATAT

10141 AAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGGGCTCTCTGTTCCGACCCCTGCC 10200
      TTCTATGGTCCGCAAGGGGGACCTTCGAGGGAGCAGCGAGAGGACAAGGCTGGGACGG

```

FIGURE 3E (cont'd)

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10201 GCTTACCGGATACCTGTCCGCCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTC 10260
 CGAATGGCCTATGGACAGGCGGAAGAGGGGAAGCCTTCGCACCGCGAAAGAGTTACGAG

10261 ACGCTGTAGGTATCTCAGTTCCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGA 10320
 TGGGACATCCATAGAGTCAAGCCACATCCAGCAAGCGAGGTTCCACCCGACACACGTGCT

10321 ACCCCCCCGTTTCAGCCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCC 10380
 TGGGGGGCAAGTCGGGCTGGCGACGCGGAATAGGCCATTGATAGCAGAACTCAGGTTGGG

10381 GGTAAACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAG 10440
 CCAATTCTGTGCTGAATAGCGGTGACCGTCGTGGTGGTACCATTGTCTAATCGTCTCGCTC

10441 GTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAG 10500
 CATACATCCGCCACGATGTCCTCAAGAACTTCACCACCGGATTGATGCCGATGTGATCTTC

10501 GACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAG 10560
 CTGTCATAAAACCATAGACGCGAGACGACTTCGGTCAATGGAAGCCTTTTTCTCAACCATC

10561 CTCTTGATCCGGCAAACAAACACCGCTGGTAGCGGTGGTTTTTTTTGTTTGCAAGCAGCA 10620
 GAGAACTAGGCCGTTTGTFTTGGTGGCGACCATCGCCACCAAAAAACAAACGTTTCGTGCT

10621 GATTACGGCGAGAAAAAAGGATCTCAAGAAGATCCTTTTGATCTTTTCTACGGGGTCTGA 10680
 CTAATGCGCGTCTTTTTTTCCTAGAGTTCTTCTAGGAACTAGAAAAGATGCCCCAGACT

10681 CGCTCAGTGGAAACGAAAACTCACGTTAAGGGATTTTGGTCAATGAGATTATCAAAAAGGAT 10740
 GCGAGTCACCTTGGCTTTTGAGTGCAATTCCTTAAACCAGTACTCTAATAGTTTTCCTA

10741 CTTACCTAGATCCTTTTAAATTAAAAATGAAGTTTAAATCAATCTAAAGTATATATGA 10800
 GAAGTGGATCTAGGAAATTTAATTTTTTACTTCAAAATTTAGTTAGATTTTCATATATACT

amp marker(10819,11679)<<<
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10801 GTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTG 10860
 CATTTGAACCAGACTGTCAATGGTTACGAATTAGTCACTCCGTGGATAGAGTCGCTAGAC

10861 TCTATTTTCGTTTCATCCATAGTTGCCTGACTCCCCGTGGTGTAGATAACTACGATACGGGA 10920
 AGATAAAGCAAGTAGGTATCAACGSACTGAGGGGCAGCACATCTATTGATGCTATGCCCT

10921 GGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACC GGCTCC 10980
 CCCGAATGGTAGACCGGGGTCACGACGTTACTATGGCGCTCTGGGTGCGAGTGGCCGAGG

10981 AGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAAC 11040
 TCTAAATAGTCGTTATTTGGTCCGGTCGGCCTTCCCGGCTCGCGTCTTCACCAGGACGTTG

FIGURE 3E (cont'd)

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11041 TTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCC 11100
      AAATAGGCGGAGGTAGGTGAGATAATTAACAACGGCCCTTCGATCTCATTTCATCAAGCGG

11101 AGTTAATAGTTTGGCGAACGTTGTTGCCATTGCTGCAGGCAFCGTGGTGTACGCTCGTC 11160
      TCAATTATCAAACGCGTTGCAACAACGGTAACGACGTCCTAGCACACAGTGGCAGGAG

11161 GTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCC 11220
      CAAACCATAACCGAAGTAAGTCGAGGCCAAGGGTTGCTAGTTCCGGTCAATGTACTAGGGG

11221 CATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTT 11280
      GTACAACACGTTTTTTTCGCCAATCGAGGAAGCCAGGAGGCTAGCAACAGTCTTCATTCAA

11281 GGGCGCAGTGTATCACTCATGCTTATGGCAGCACTGCATANTTCTCTTACTGTGTCATGCC 11340
      CCGCGCTCACAATAGTGAGTACCAATACCGTCTGTGACGTATTAAGAGAATGACAGTACGG

11341 ATCCGTAAGATGCTTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTG 11400
      TAGGCATTCTACGAAAAGACACTGACCACCTCATGAGTTGGTTCAGTAAGACTCTTATCAC

11401 TATGCGGGGACCGAGTTGCTCTTGCCCGCGCTCAACACGGGATAATACCGCGCCACATAG 11460
      ATACGCCGCTGGCTCAACGAGAACGGGCGCAGTTGTGCCCTATTATGGCGCGGTGTATC

11461 CAGAACTTTAAAGTGCTCATCATTTGAAAAACGTTCTTCGGGGCGAAAACTCTCAAGGAT 11520
      GTCTTGAAATTTTCACGAGTAGTAACCTTTTGCAAGAAGCCCCGCTTTTGAGACTTCCTA

11521 CTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGC 11580
      GAATGGCGACAACCTCTAGGTCAAGCTACATTGGGTGAGCACGTTGGGTGACTAGAAGTCG

11581 ATCTTTTACTTTTACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAA 11640
      TAGAAAATGAAAGTGGTCGCAAGACCCACTCGTTTTTGTCCCTCCGTTTTACGGCGTTT

11641 AAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTA 11700
      TTTCCCTTATTCCCGCTGTGCCTTTACAACCTATGAGTATGAGAAGGAAAAAGTTATAAT

      amp prom(11721,11749)<<<
      |
11701 TTGAAGCATTATCAGGGTTATTTGTCTCATGACCGGATACATATTTGAATGTATTTAGAA 11760
      AACTTCGTAAATAGTCCCAATAACAGAGTACTCGCTATGTATAAACTTACATAAATCTT

11761 AAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGA 11820
      TTTATTTGTTTATCCCAAGGCGCGTCTAAAGGGGCTTTTCACGGTGCAGTGCAGATTCT

11821 AACCATTATTATCATGACATTAACTATAAAAAATAGGCGTATCAGAGGCCCTTTCGTCT 11880
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11881 TCAAGAATTCAT 11892
      AGTTCTTAAGTA

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FIGURE 3E (cont'd)

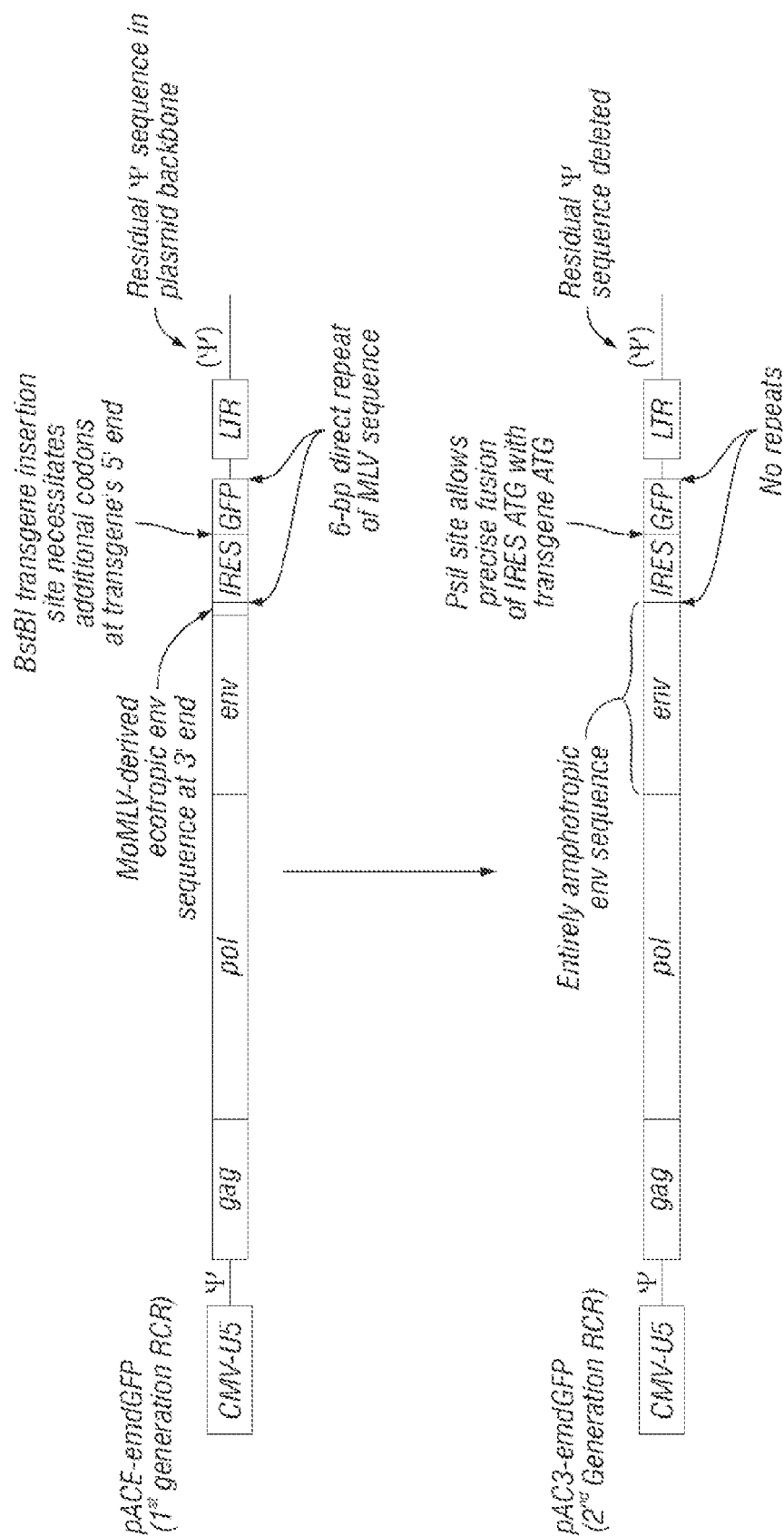


FIGURE 3F

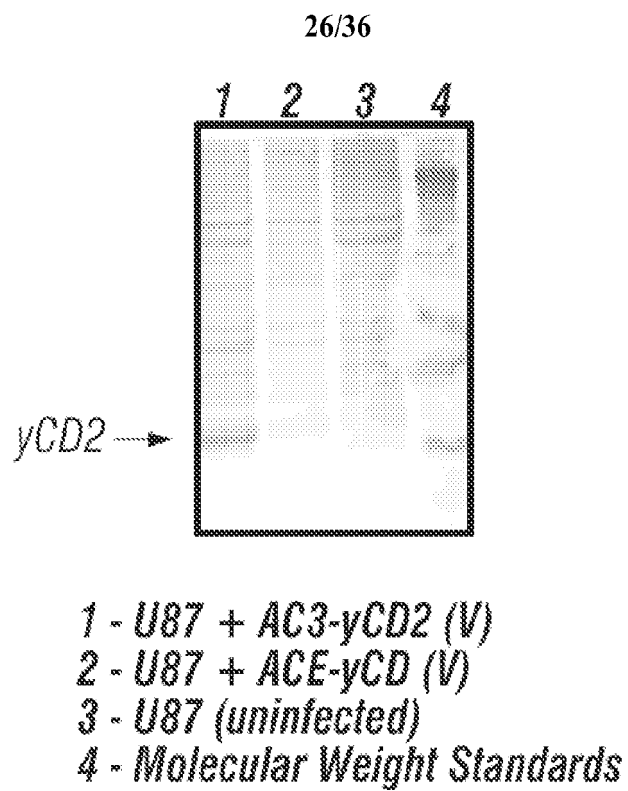


FIGURE 4

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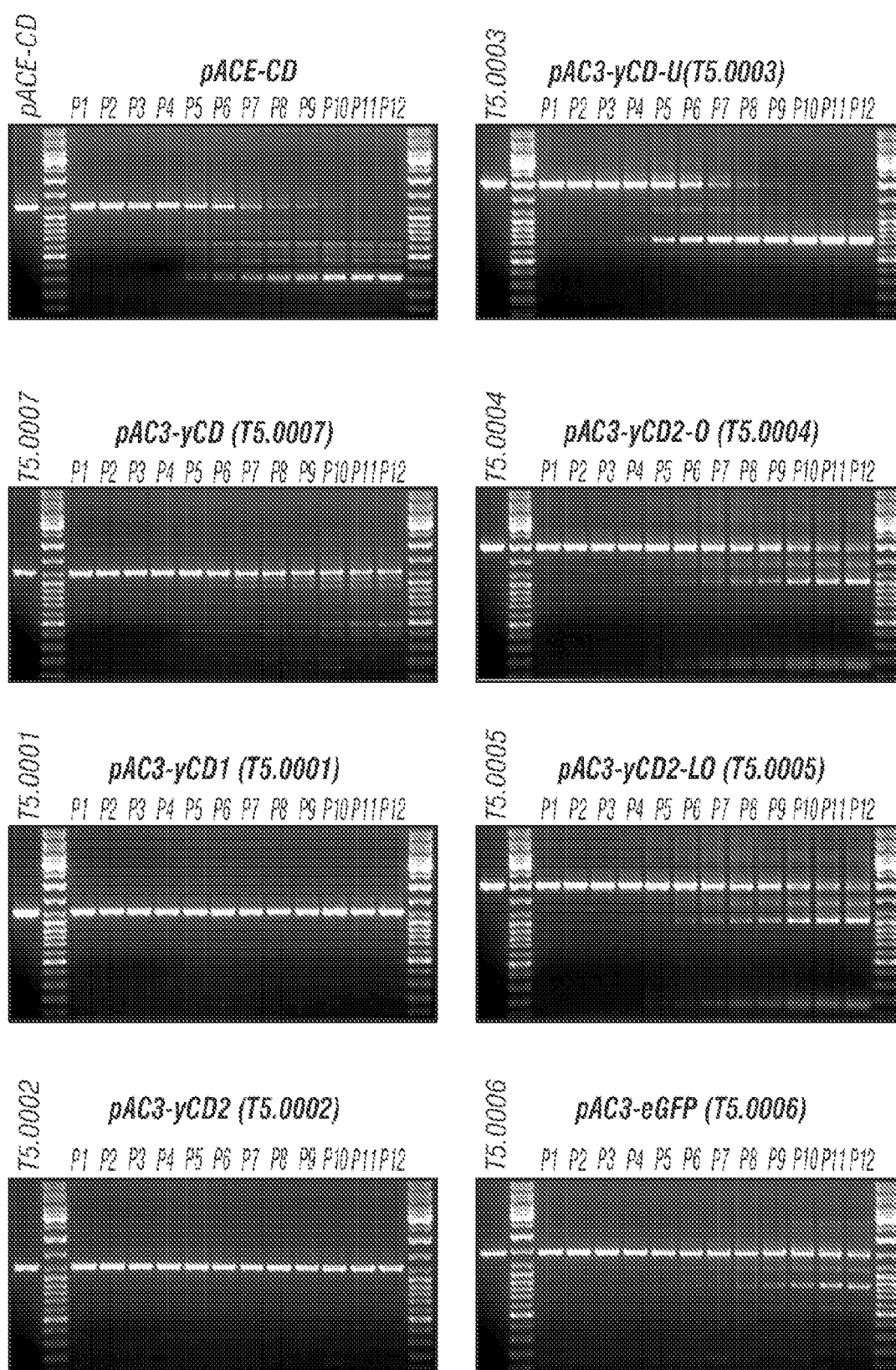


FIGURE 5

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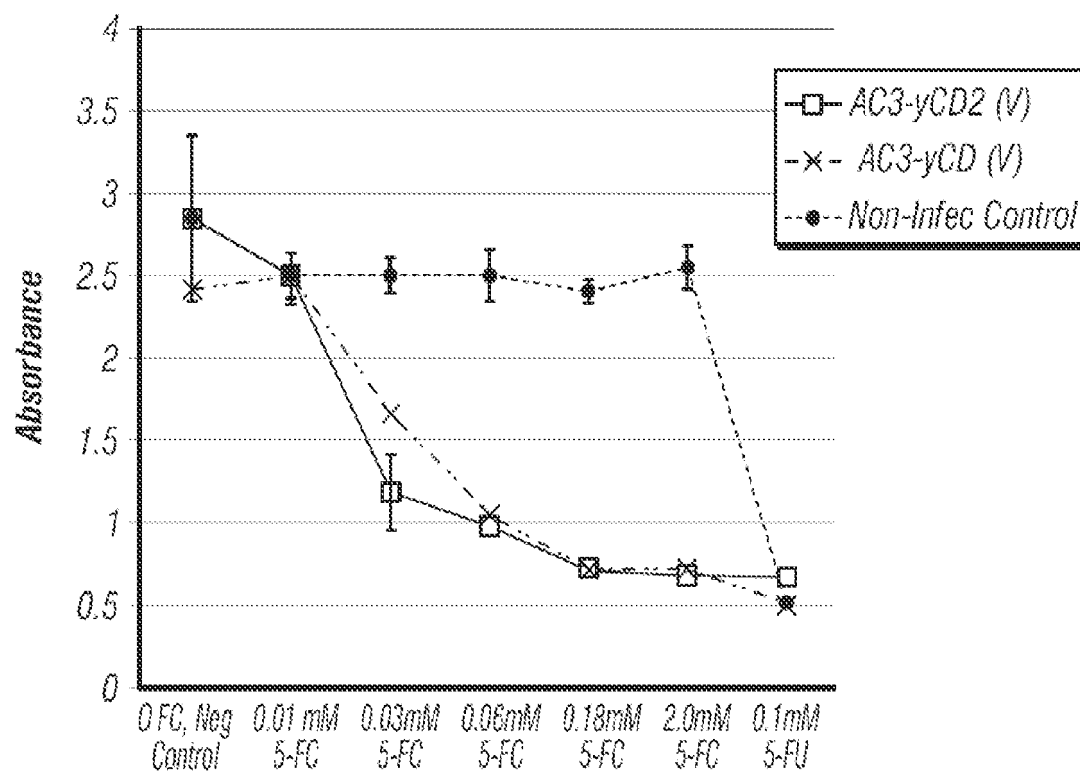


FIGURE 6A

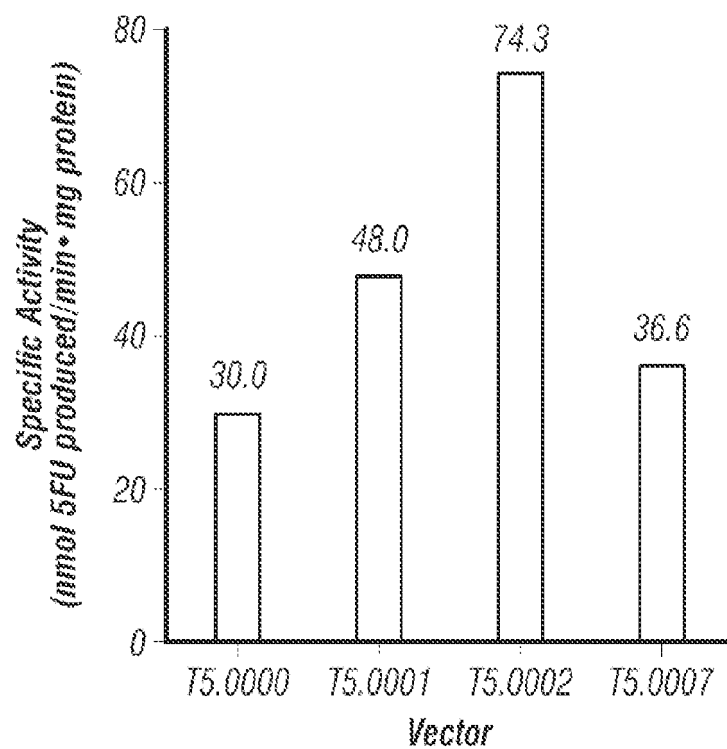


FIGURE 6B

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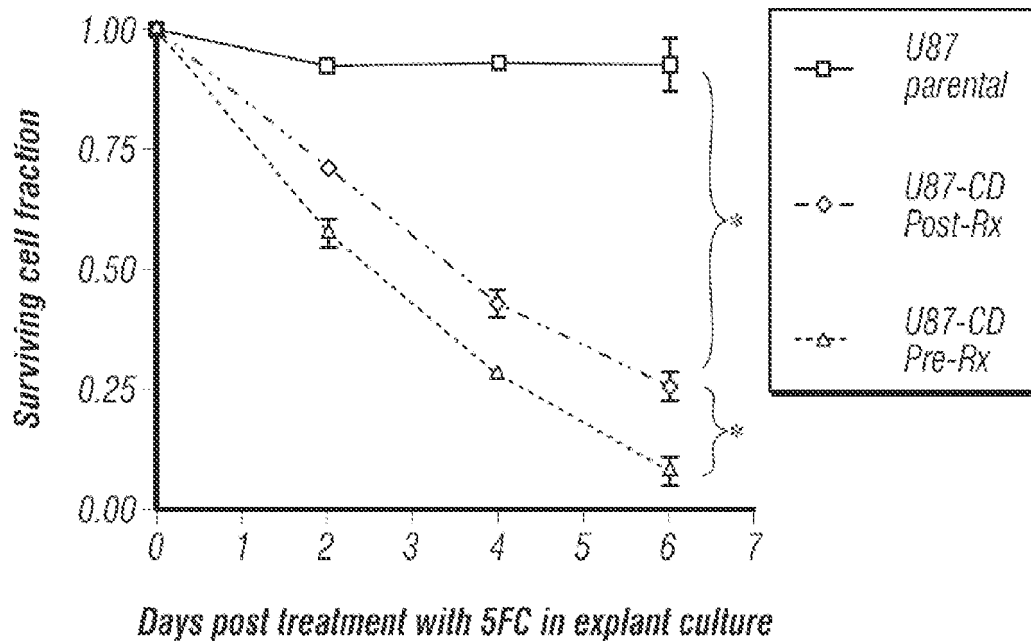


FIGURE 7

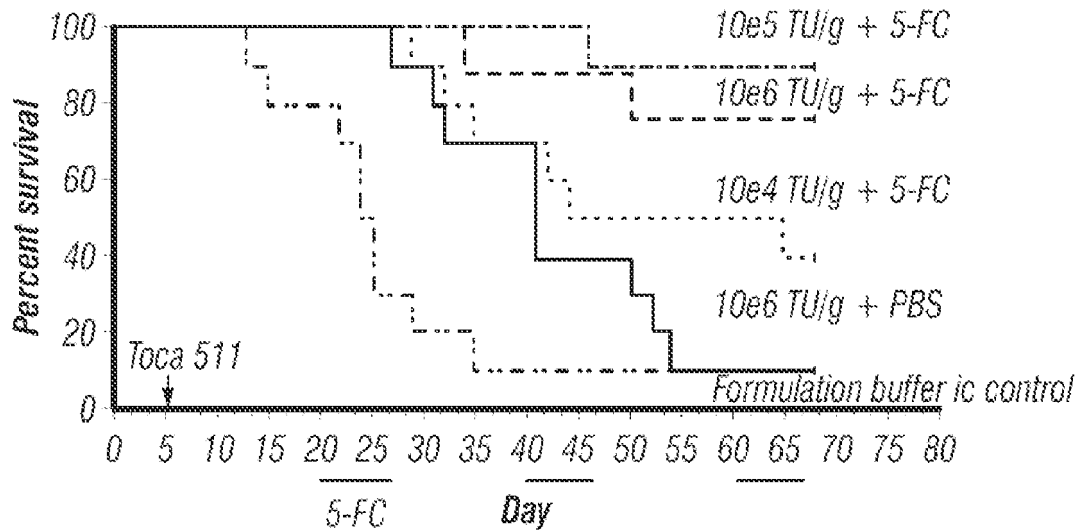
U-87 nude xenograft intracranial model-10 animals/group

FIGURE 8

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

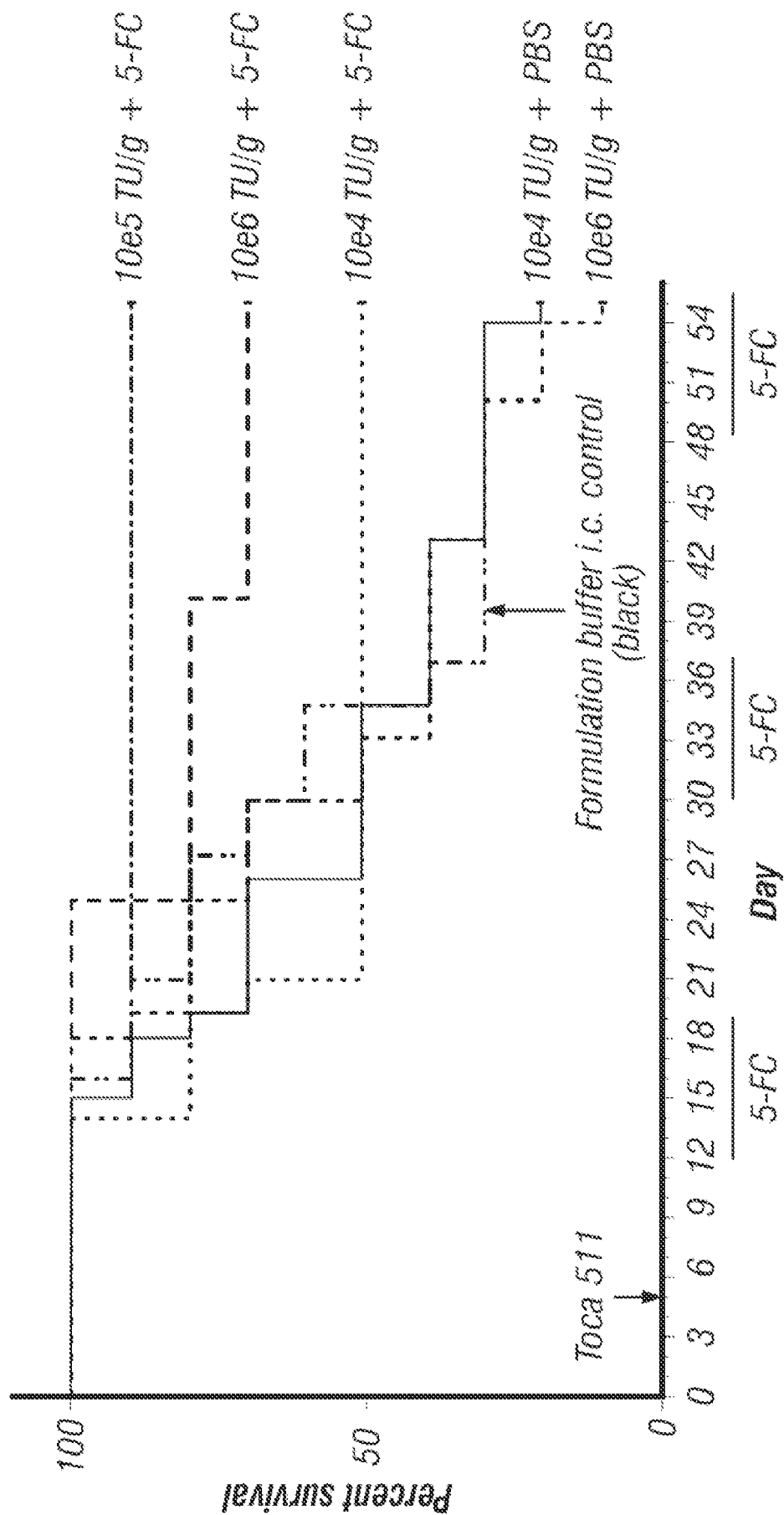


FIGURE 9

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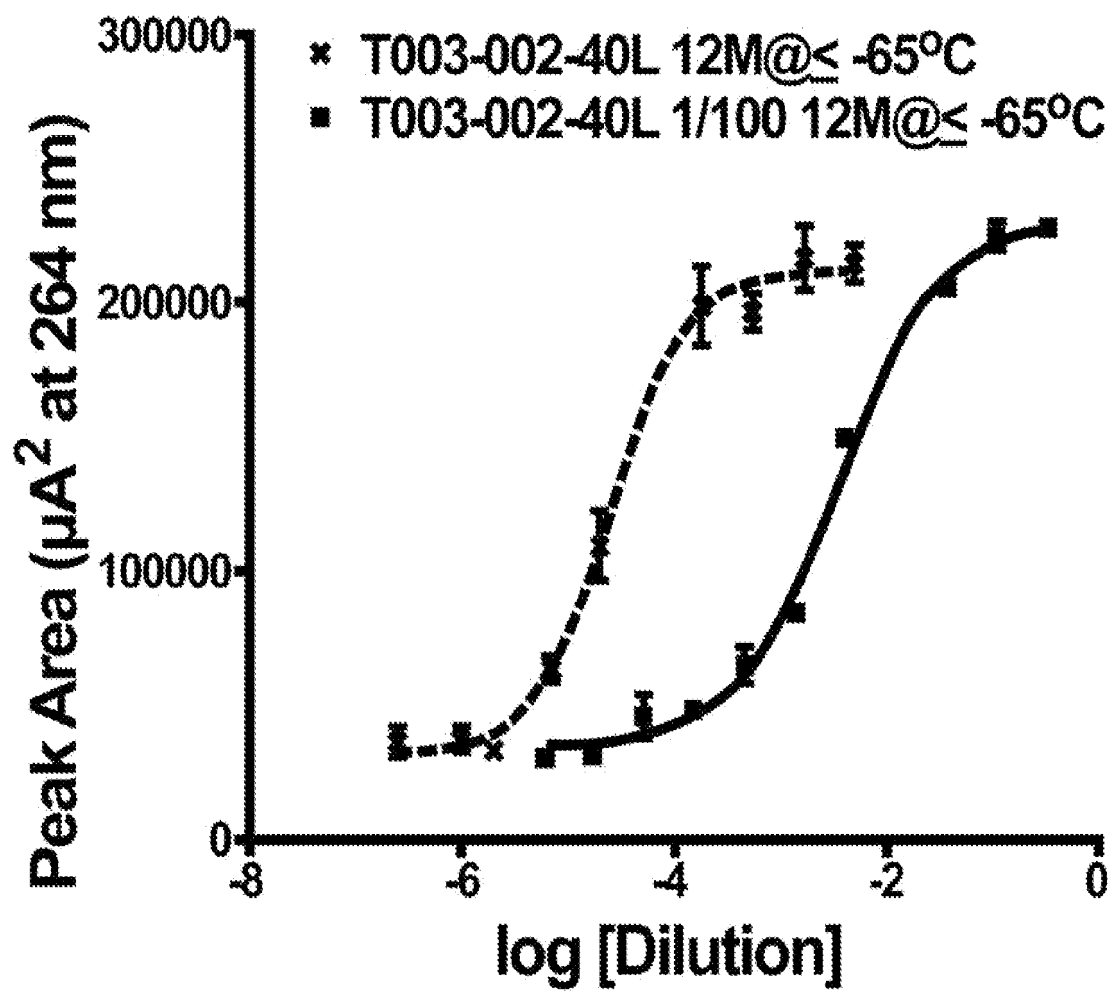


FIGURE 10

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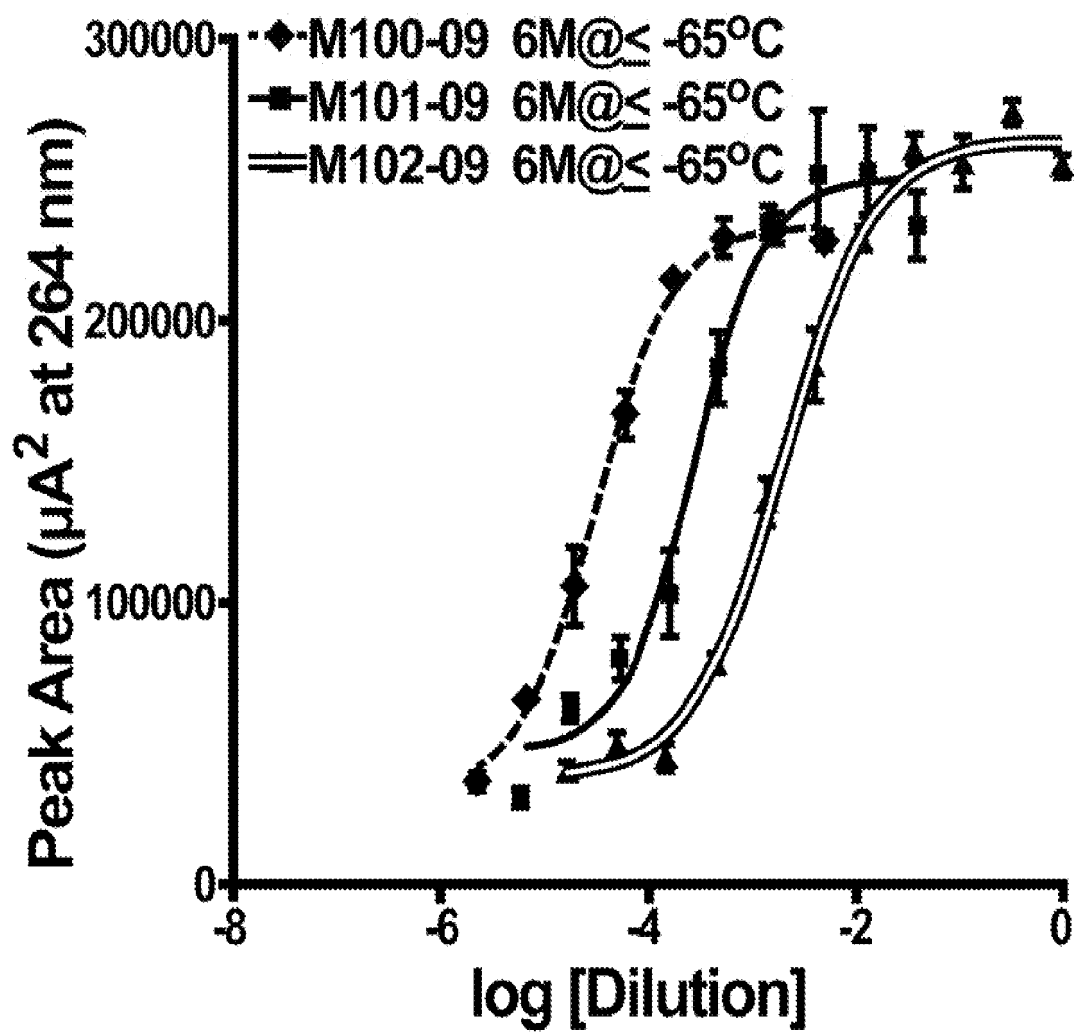


FIGURE 11

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

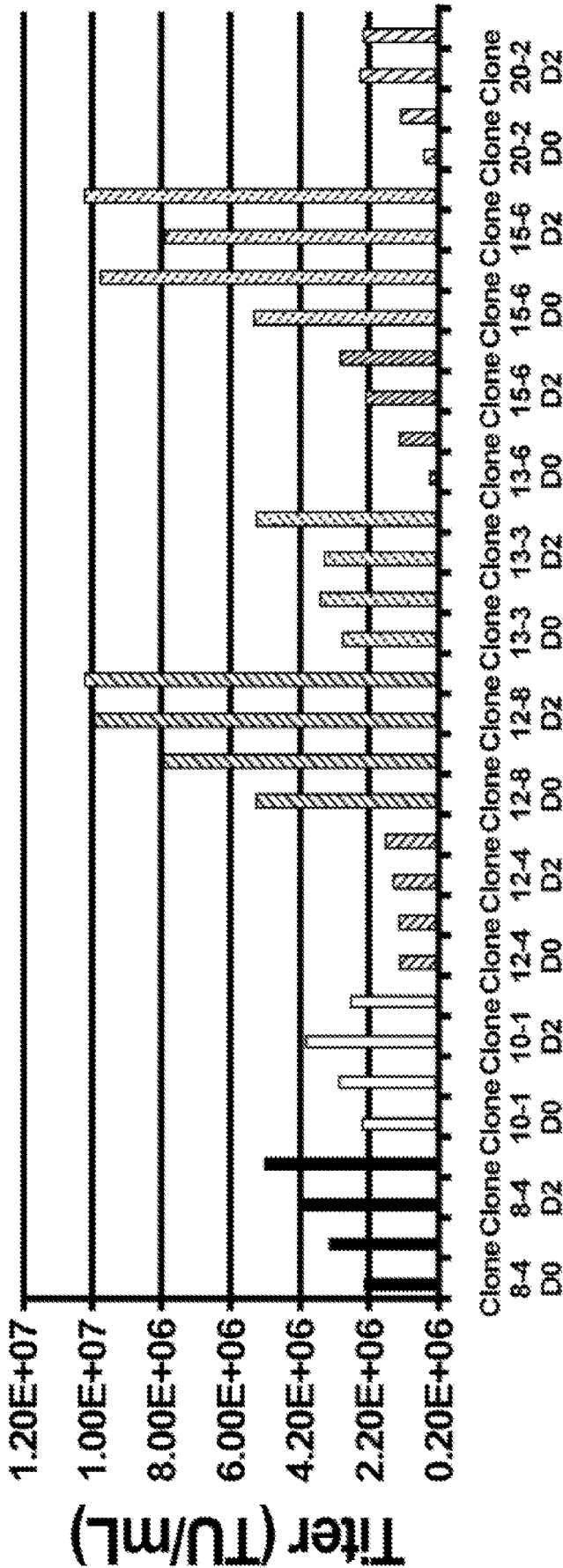


FIGURE 12

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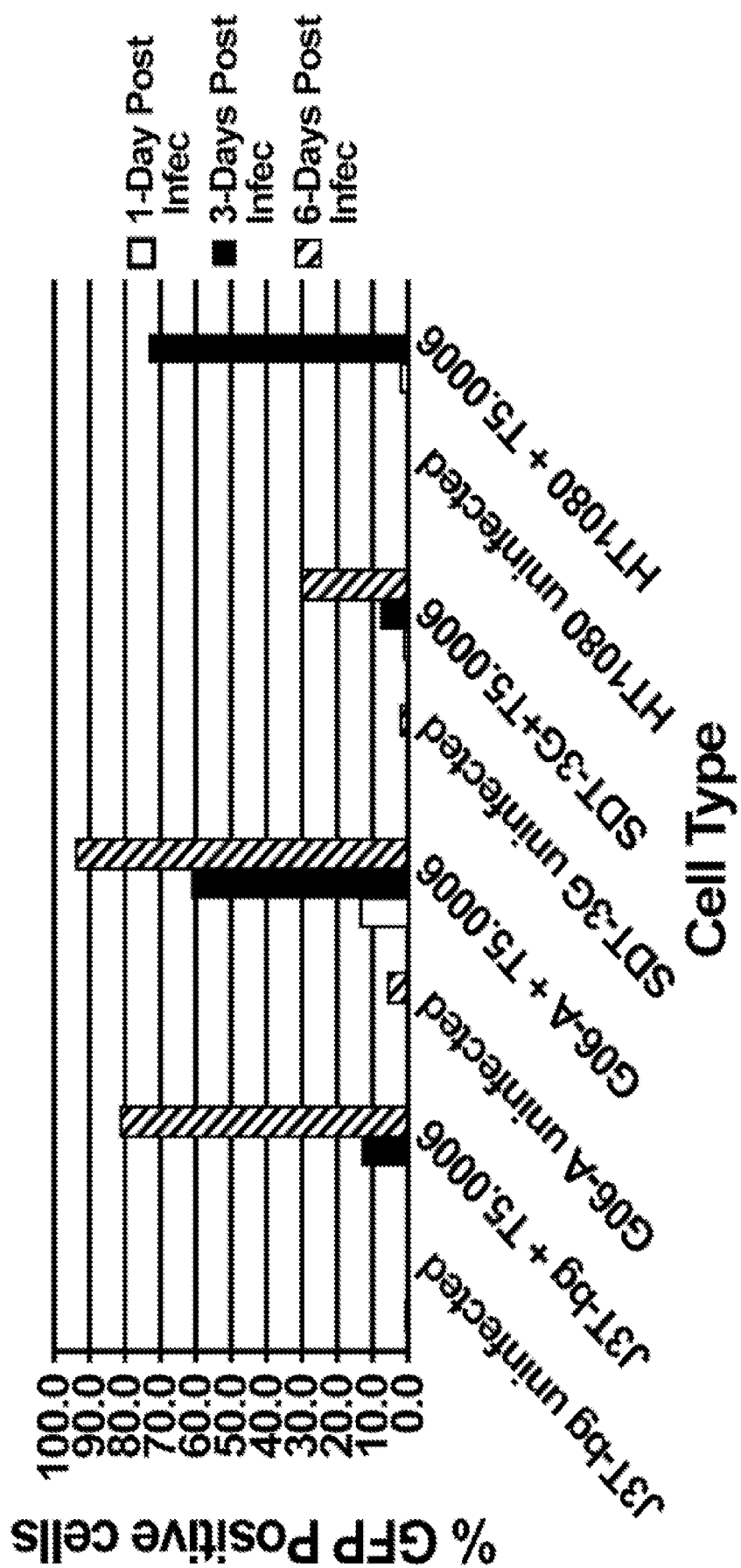


FIGURE 13

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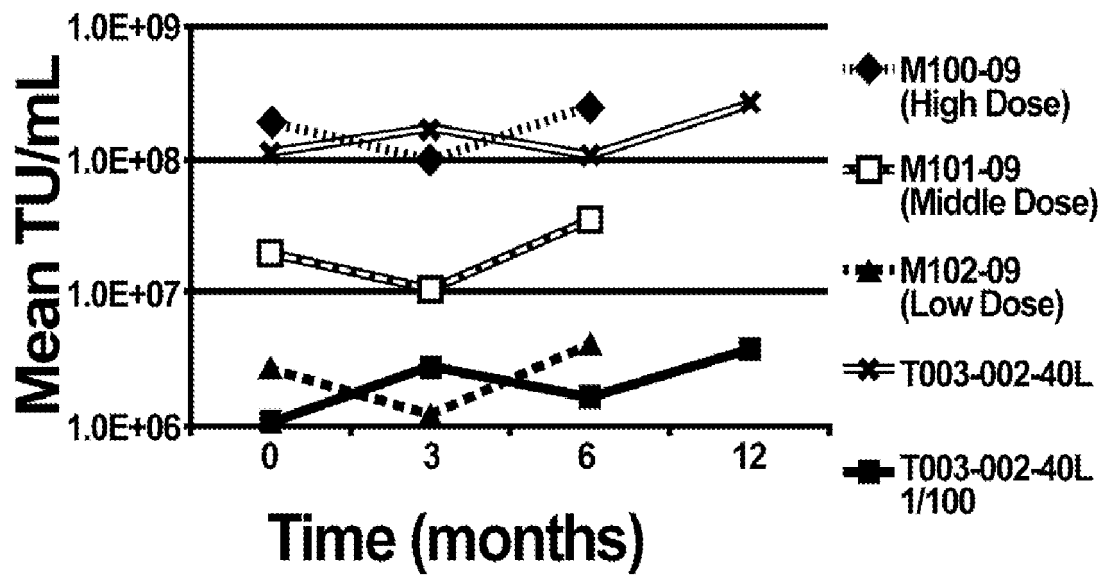


FIGURE 14

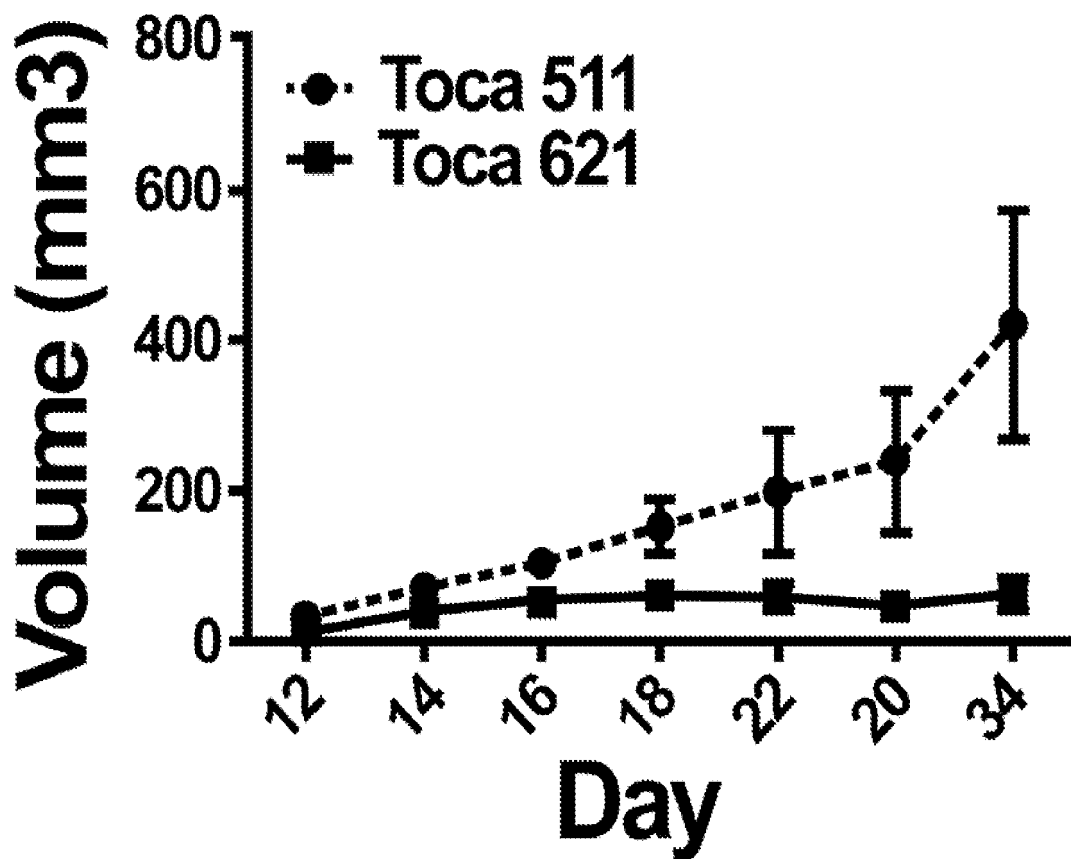


FIGURE 15

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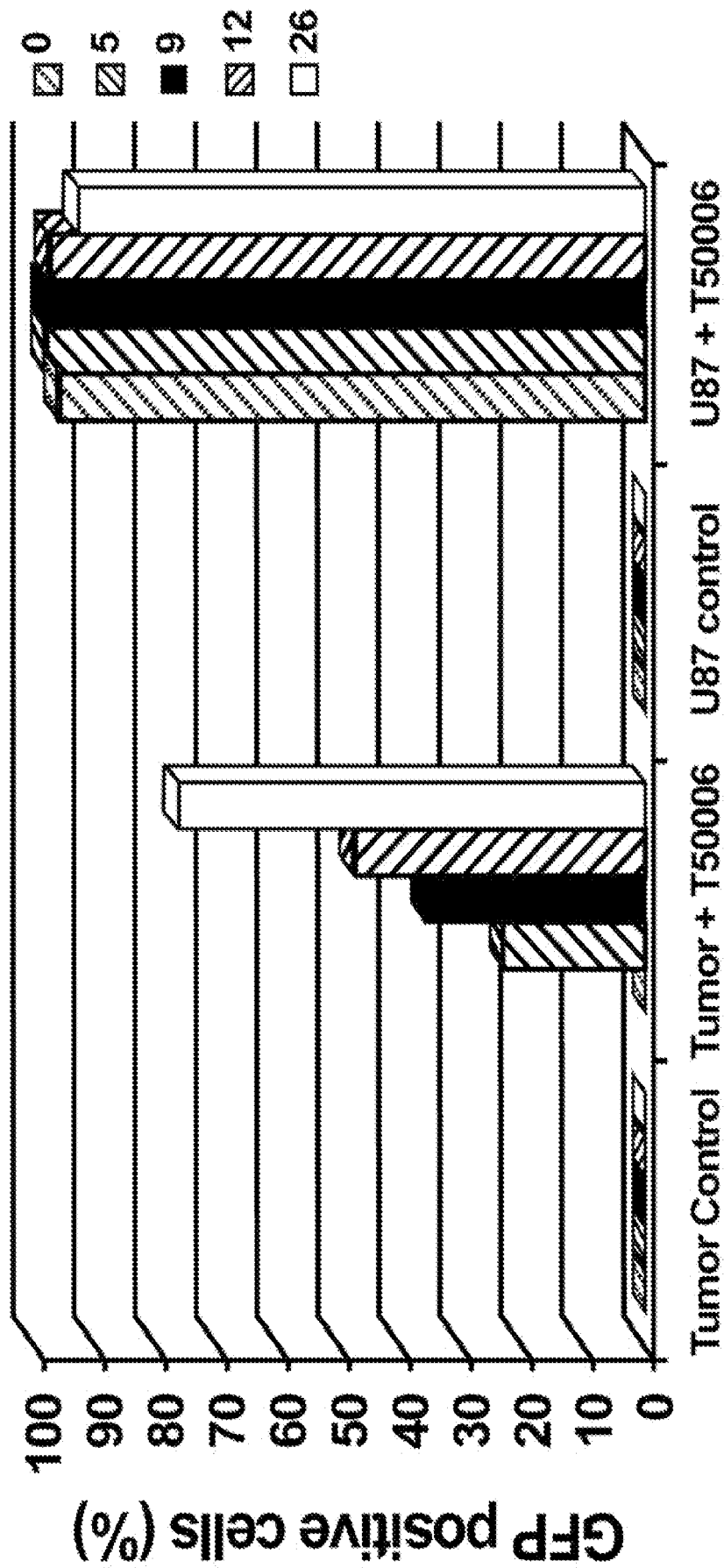


FIGURE 16