Fig. 1

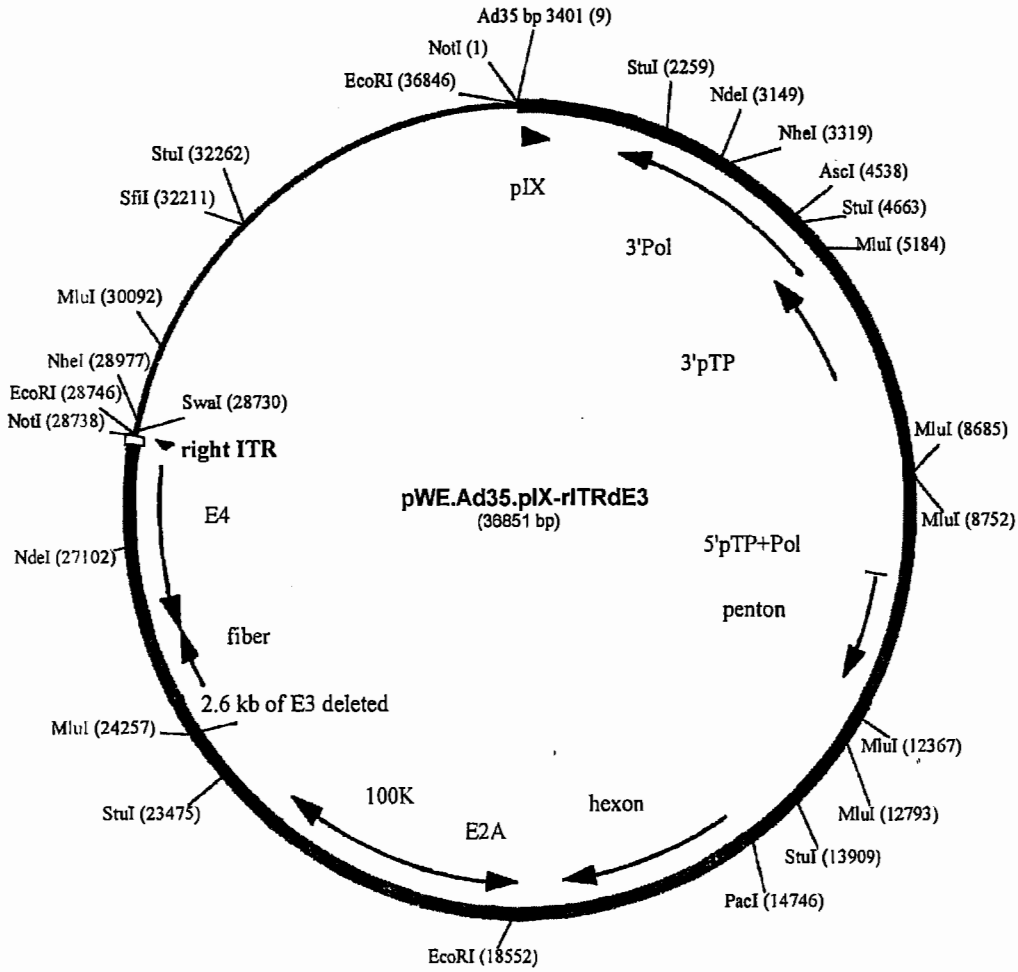

Ad35 bp 3401 (9)
NotI (1)
EcoRI (36846)
StuI (2259)
NdeI (3149)
NheI (3319)
AscI (4538)
StuI (4663)
MluI (5184)
pIX
3'Pol
3'pTP
MluI (8685)
MluI (8752)
5'pTP+Pol
penton
MluI (12367)
MluI (12793)
StuI (13909)
PacI (14746)
EcoRI (18552)
hexon
E2A
100K
StuI (23475)
MluI (24257)
2.6 kb of E3 deleted
fiber
NdeI (27102)
E4
right ITR
NotI (28738)
EcoRI (28746)
NheI (28977)
MluI (30092)
SfiI (32211)
StuI (32262)
SwaI (28730)
pWE.Ad35.pIX-rITRdE3
(36851 bp)

Fig. 2

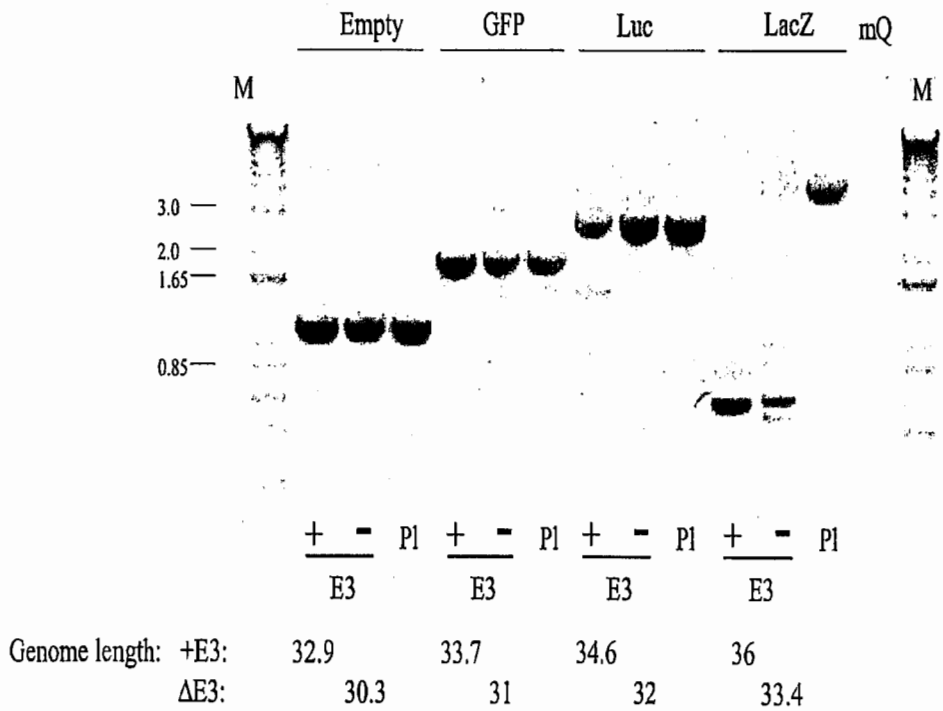

Transgene PCR on Ad35 E1- and E1/E3-deleted viruses
Empty
GFP
Luc
LacZ
mQ
M
M
3.0
2.0
1.65
0.85
+ - Pl + - Pl + - Pl + - Pl
E3 E3 E3 E3
Genome length: +E3: 32.9 33.7 34.6 36
ΔE3: 30.3 31 32 33.4

Fig. 3A

Alignment of pIX proximal regions

```
1  TGAGGTACTGAAATGTGTGGGCGTGGCTTAAGGGTGGGAAAGAATATATAAGGTGGGGGT Ad2.SEQ
1  TGAGGTACTGAAATGTGTGGGCGTGGCTTAAGGGTGGGAAAGAATATATAAGGTGGGGGT Ad5.SEQ
1  TGAGG---TAAGTGGGTGGAGCTA--------GGTGGGATTATAAAA--GGC-TGGAAGT Ad12.SEQ
1  TAGAGG--TAGGTCGAGTGAGTAGTGGGCGTGGCTAAGGT-GACTATA-AAGGCGGGTGT Ad9.SEQ
1  TAAGGG--TAAG------GGGCGGAGCCTATTAC--AGGTATAAAGGTTGGGGT-AGAGT Ad40.SEQ
1  TAGAG---TGAGTAGTG--------TTCTG-GGGCGGGGGA---GGACCTGCATGAGGGC Ad4.SEQ
1  TAGAG---TGAGTAGTG--------TTCTG-GGGCGGGGGA---GGACCTGCATGAGGGC S25.SEQ
1  TAAGG---TGAGTATTGGGA--AAACTTTG-GGGTGGGATTTTCAGAT---------GGA Ad35.SEQ
1  TAAGG---TGAGTATTGGGA--AAACTTTG-GGGTGGGATTTTCAGAT---------GGA Ad11.SEQ
1  TAAAG---TAAGTAGTGGGGGCAAAATGTG-GATGGGGACTTTCAGGTTGGTAAGGTGGA Ad7.SEQ

61 CTCATGTAGTTTTGTATCTGTTTTGCAGCA-GCCGCCGCC---ATG                Ad2.SEQ
61 CTTATGTAGTTTTGTATCTGTTTTGCAGCA-GCCGCCGCCGCCATG               Ad5.SEQ
47 CA-----ACTAAAAATTGT-TTTTGTTCT-TTTAACAGC-ACGATG              Ad12.SEQ
57 CTTACGAGGGTCTT--TTTGCTTTTCTGCA-GA------CATCATG               Ad9.SEQ
50 AAAAAAAAGGGAAG-------------------TTACAA----AATG             Ad40.SEQ
46 CAGAATAACTGAAATCTGTGCTTTTCTGTGTGTTGCAGCAG-CATG              Ad4.SEQ
46 CAGAATAACTGAAATCTGTGCTTTTCTGTGTGTTGCAGCAG-CATG              S25.SEQ
46 CAGATTGAGTAAAAATT-TGTTT-TTTCTGTCTTGCAGCTGACATG              Ad35.SEQ
46 CAGATTGAGTAAAAATT-TGTTT-TTTCTGTCTTGCAGCTGTCATG              Ad11.SEQ
57 CAAATTGGGTAAAT-TT-TGTTAATTTCTGTCTTGCAGCTGCCATG              Ad7.SEQ
```

Fig. 3B

: Comparison of putative pIX promoter regions

	stop 55k		Start pIX coding
Ad5:	3509	GGGCGT ..... 20 nucl..... TATATAA	3609
Ad12:	3295	GGGTGG .....11 nucl ..... ATTATAA	3374
Ad9:	3361	GGGCGT .....12 nucl ..... TATAAAG	3449
Ad40:	3149	GGGCGG ..... 13 nucl ..... TATAAAG	3217
Ad4:	3404	GGGCGG .....23 nucl ..... AATAACT	3489
		GGGAGG .....17 nucl ..... AATAACT	
Ad35:	3400	GGGTGG .....27 nucl ..... AATTTGT	3484
Ad11:	3399	GGGTGG ..... 27 nucl ..... AATTTGT	3483
Ad7:	3385	GGGACT ..... 30 nucl ..... AATTTTG	3480

Consensus SP1 site G/a G G C/t/a G/a G/t

Fig. 4

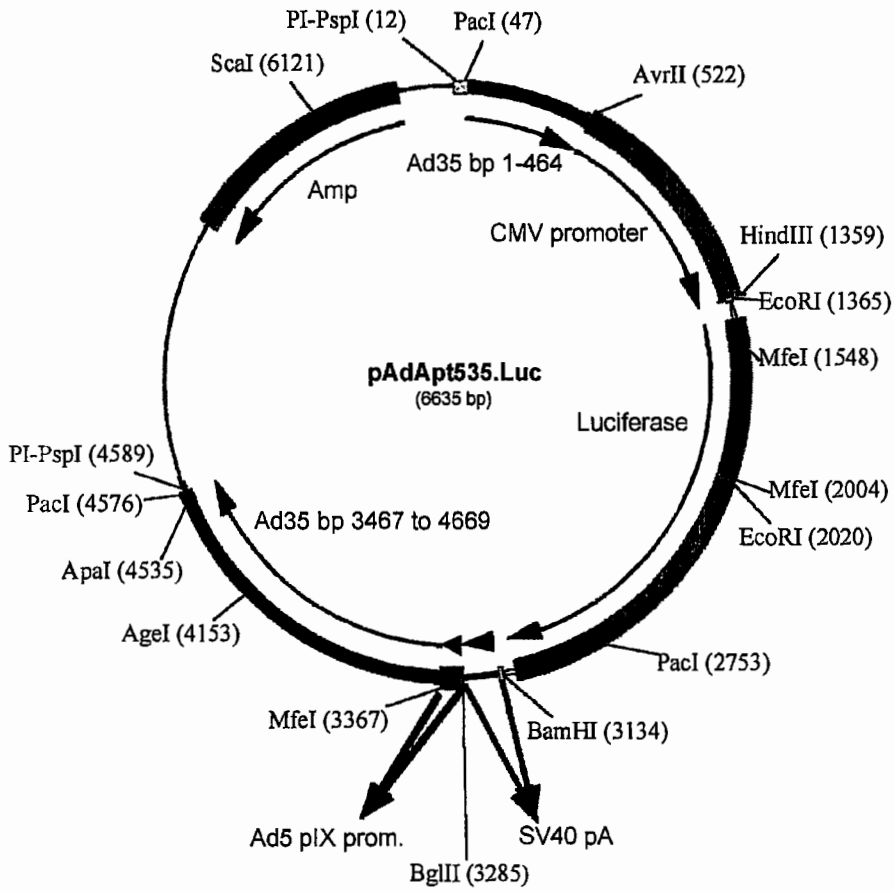

PI-PspI (12)
PacI (47)
ScaI (6121)
AvrII (522)
Ad35 bp 1-464
Amp
CMV promoter
HindIII (1359)
EcoRI (1365)
MfeI (1548)
pAdApt535.Luc
(6635 bp)
Luciferase
PI-PspI (4589)
PacI (4576)
Ad35 bp 3467 to 4669
MfeI (2004)
EcoRI (2020)
ApaI (4535)
AgeI (4153)
PacI (2753)
MfeI (3367)
BamHI (3134)
Ad5 pIX prom.
SV40 pA
BglII (3285)

Fig. 5

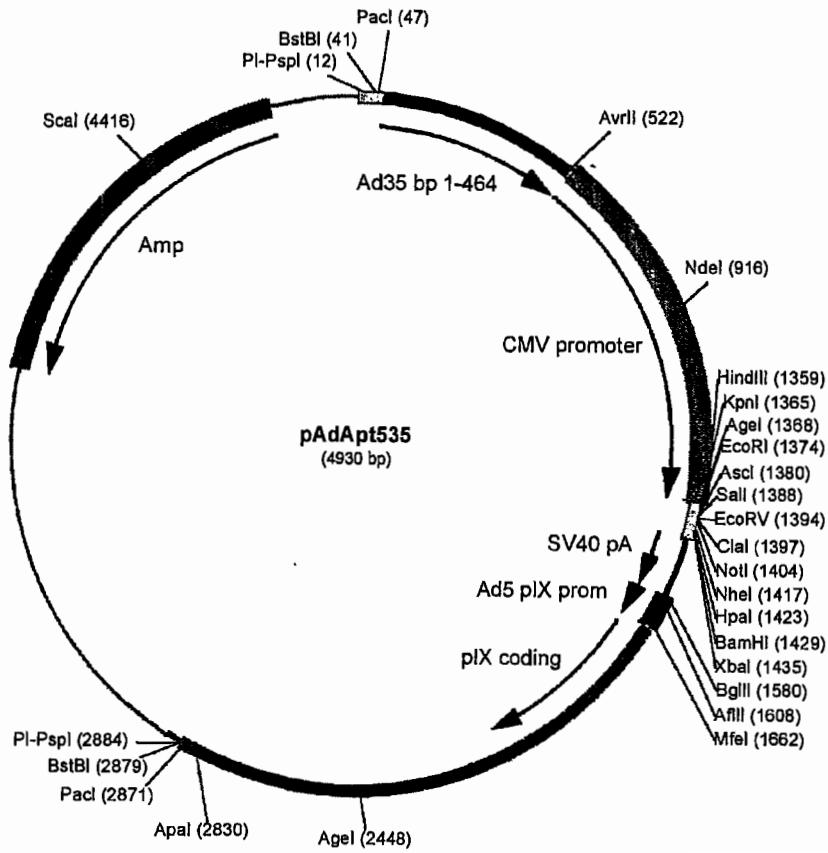

PacI (47)
BstBI (41)
PI-PspI (12)
ScaI (4416)
AvrII (522)
Ad35 bp 1-464
Amp
NdeI (916)
CMV promoter
HindIII (1359)
KpnI (1365)
AgeI (1368)
EcoRI (1374)
AscI (1380)
SalI (1388)
EcoRV (1394)
ClaI (1397)
NotI (1404)
NheI (1417)
HpaI (1423)
BamHI (1429)
XbaI (1435)
BglII (1580)
AflII (1608)
MfeI (1662)
pAdApt535
(4930 bp)
SV40 pA
Ad5 pIX prom
pIX coding
PI-PspI (2884)
BstBI (2879)
PacI (2871)
ApaI (2830)
AgeI (2448)

Fig. 6A

Transgene PCR on Ad35 E1deleted viruses

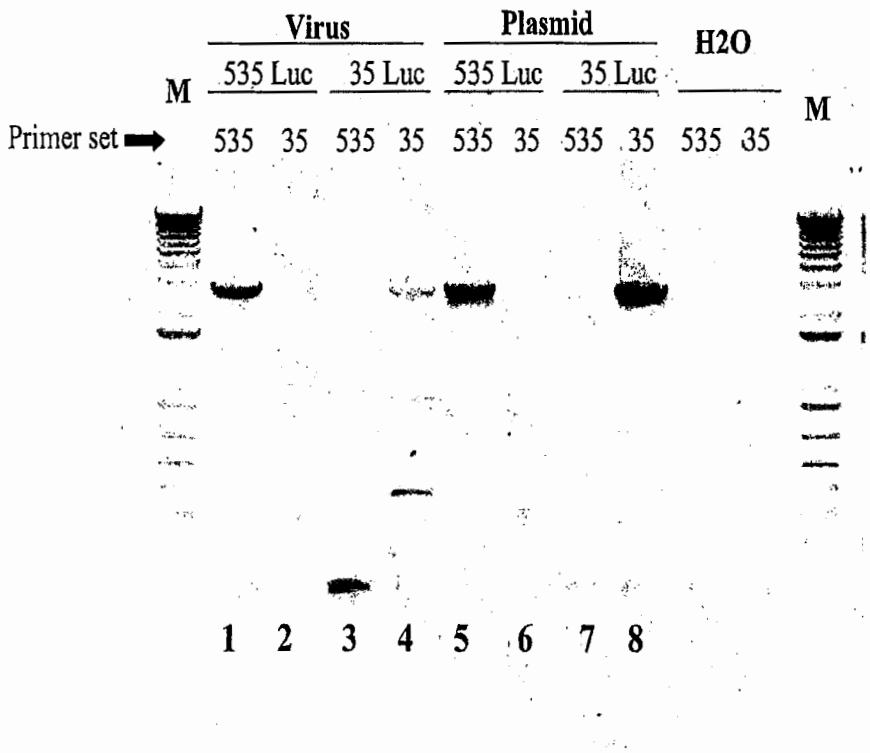


Fig. 6B

Transgene PCR on Ad35 E1/E3 deleted viruses

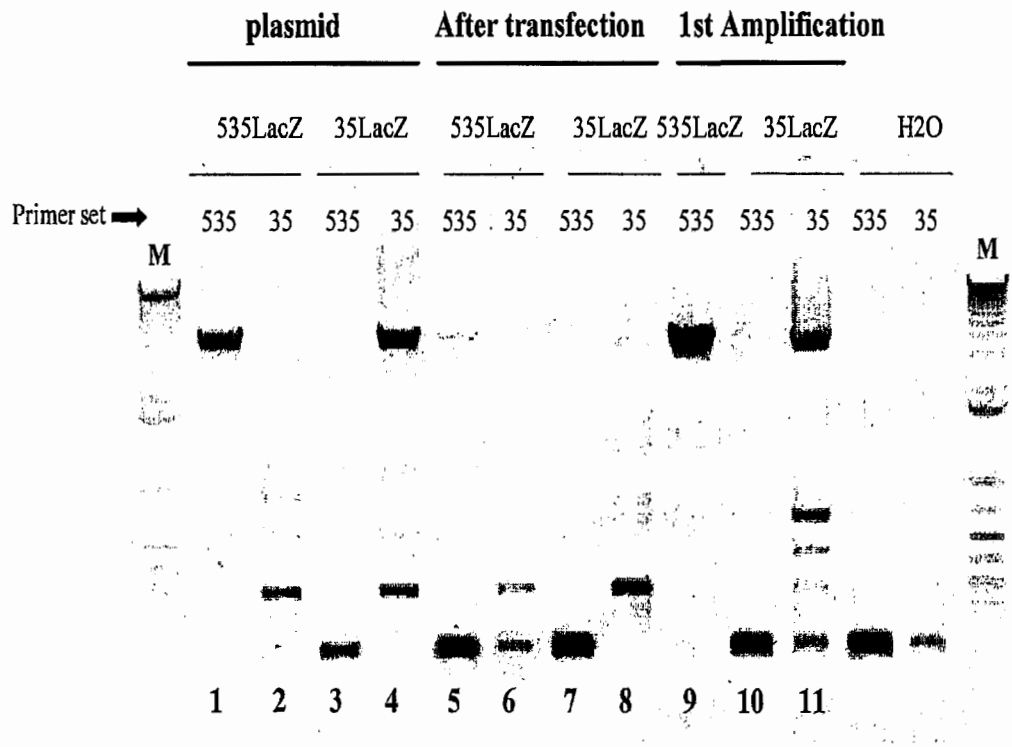


Fig. 7

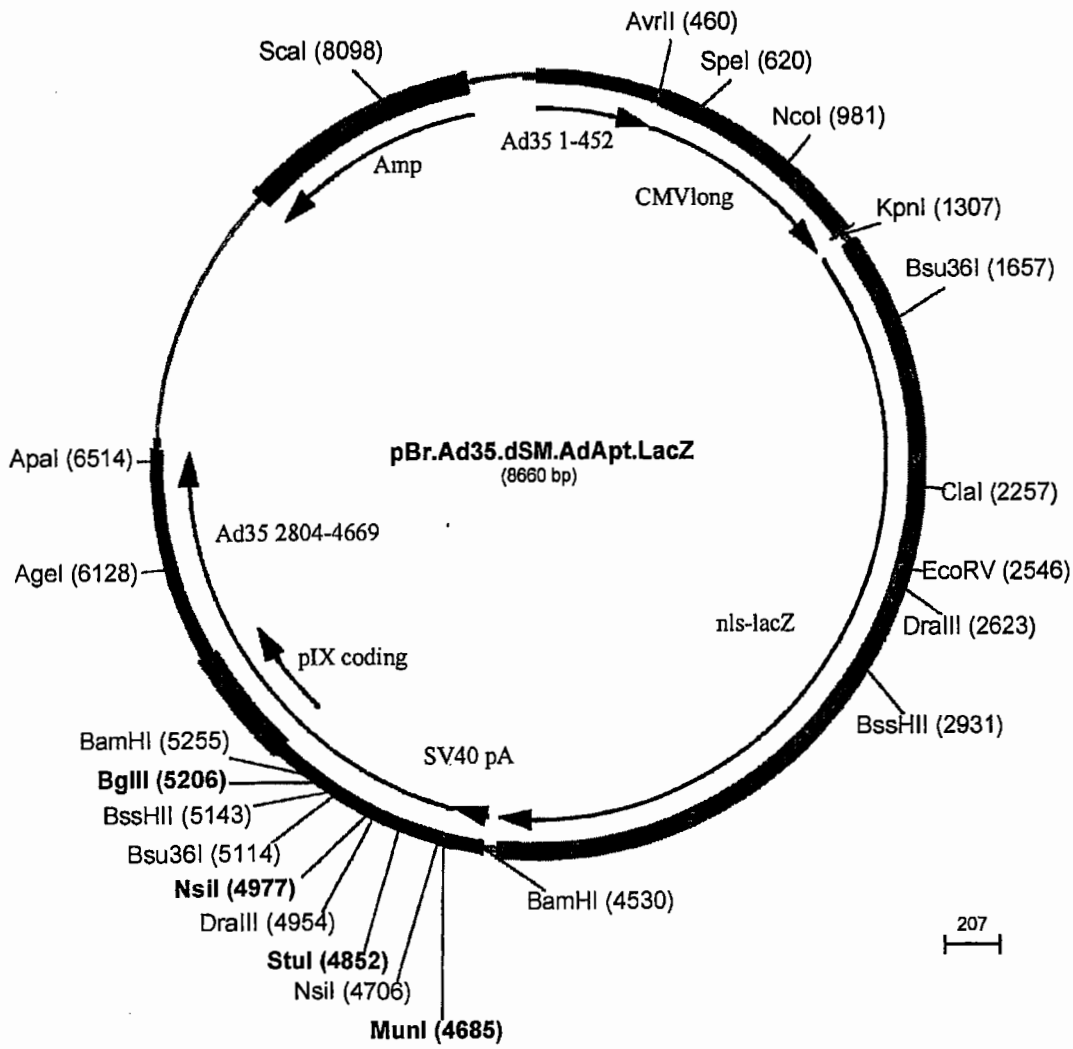

AvrII (460)
ScaI (8098)
SpeI (620)
NcoI (981)
Ad35 1-452
Amp
CMVlong
KpnI (1307)
Bsu36I (1657)
pBr.Ad35.dSM.AdApt.LacZ
(8660 bp)
ApaI (6514)
ClaI (2257)
Ad35 2804-4669
AgeI (6128)
EcoRV (2546)
nls-lacZ
DraIII (2623)
pIX coding
BssHII (2931)
BamHI (5255)
SV40 pA
BglII (5206)
BssHII (5143)
Bsu36I (5114)
NsiI (4977)
BamHI (4530)
DraIII (4954)
207
StuI (4852)
NsiI (4706)
MunI (4685)

Fig. 8

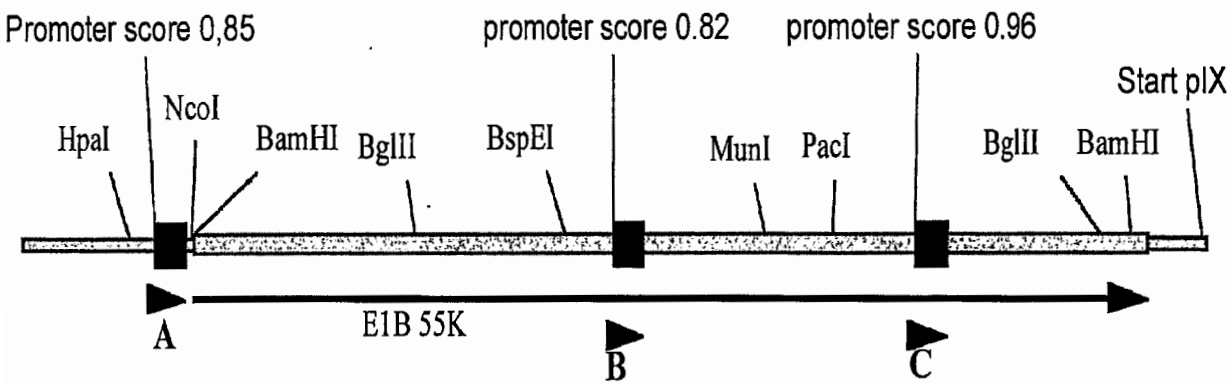

Promoter score 0,85
promoter score 0.82
promoter score 0.96
Start pIX
HpaI
NcoI
BamHI
BglII
BspEI
MunI
PacI
BglII
BamHI
E1B 55K
A
B
C

Fig. 9

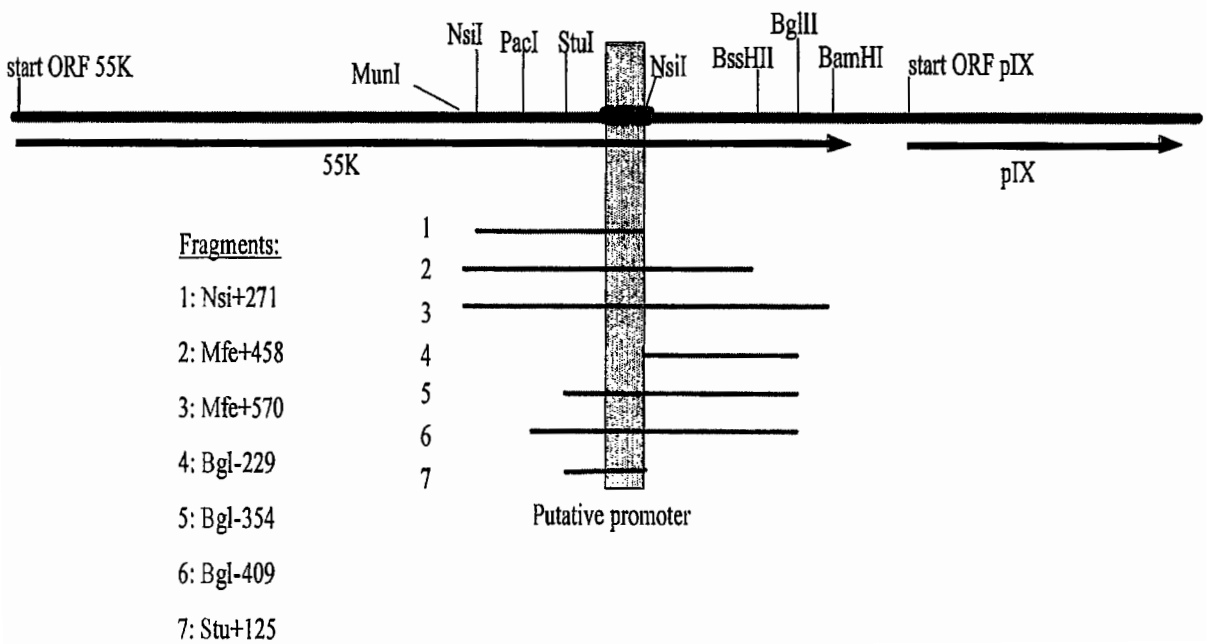

start ORF 55K
MunI
NsiI
PacI
StuI
NsiI
BssHII
BglII
BamHI
start ORF pIX
55K
pIX
Fragments:
1: Nsi+271
2: Mfe+458
3: Mfe+570
4: Bgl-229
5: Bgl-354
6: Bgl-409
7: Stu+125
1
2
3
4
5
6
7
Putative promoter

Fig. 10

Alignment Report of Align.E1B-pIX.35-11-7.MEG, using Clustal method with Weighted residue weight table.
Friday 4 October 2002 9:32

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1   AATAAAAATATGTTAACTGTTCACTGGTTTTTATTGCTTTTTGGGCGGGG Ad35.E1B-pIX.SEQ
1   AATAAAAATATGTTAACTGTTCACTGGTTTTTATTGCTTTTTGGGCGGGG Ad11.E1B-pIX.SEQ
1   AATAAAATTATGTCAGCTGCTGAGTG---TTTTATTACTTCTTGGGTGGGG Ad7.E1B-pIX.SEQ

51  ACTCAGGTATATAAGTAGAAGCAGACCTGTGTGGTTAGCTCATAGGAGCT Ad35.E1B-pIX.SEQ
51  ACTCAGGTATATAAGTAGAAGCAGACCTGTGTGGTTAGCTCATAGGAGCT Ad11.E1B-pIX.SEQ
49  TCTTGATATATAAGTAGGAGCAGATCTGTGTGGTTAGCTCACAGCAACT Ad7.E1B-pIX.SEQ

101 GGCTTTCATCCATGGAGGTTTGGGCCATTTTGGAAGACCTTAGGAAGACT Ad35.E1B-pIX.SEQ
101 GGCTTTCATCCATGGAGGTTTGGGCCATTTTGGAAGACCTTAGGAAGACT Ad11.E1B-pIX.SEQ
99  TGCTGCCATCCATGGAGGTTTGGGCTATCTTGGAAGACCTCAGACAGACT Ad7.E1B-pIX.SEQ

151 AGGCAACTGTTAGAGAGCGCTTCGGACGGAGTCTCCGGTTTTTGGAGATT Ad35.E1B-pIX.SEQ
151 AGGCAACTGTTAGAGAACGCTTCGGACGGAGTCTCCGGTTTTTGGAGATT Ad11.E1B-pIX.SEQ
149 AGGCTACTACTAGAAAACGCCTCGGACGGAGTCTCTGGCCTTTGGAGATT Ad7.E1B-pIX.SEQ

201 CTGGTTCGCTAGTGAATTAGCTAGGGTAGTTTTTAGGATAAAACAGGACT Ad35.E1B-pIX.SEQ
201 CTGGTTCGCTAGTGAATTAGCTAGGGTAGTTTTTAGGATAAAACAGGACT Ad11.E1B-pIX.SEQ
199 CTGGTTCGGTGGTGATCTAGCTAGGCTAGTGTTTAGGATAAAACAGGACT Ad7.E1B-pIX.SEQ

251 ATAAACAAGAATTTGAAAAGTTGTTGGTAGATTGCCCAGGACTTTTTGAA Ad35.E1B-pIX.SEQ
251 ATAAACAAGAATTTGAAAAGTTGTTGGTAGATTGCCCAGGACTTTTTGAA Ad11.E1B-pIX.SEQ
249 ACAGGGAAGAATTTGAAAAGTTATTGGACGACATTCCAGGACTTTTTGAA Ad7.E1B-pIX.SEQ

301 GCTCTTAATTTGGGCCATCAGGTTCACTTTAAAGAAAAAGTTTTATCAGT Ad35.E1B-pIX.SEQ
301 GCTCTTAATTTGGGCCATCAGGTTCACTTTAAAGAAAAAGTTTTATCAGT Ad11.E1B-pIX.SEQ
299 GCTCTTAACTTGGGCCATCAGGCTCATTTTAAGGAGAAGGTTTTATCAGT Ad7.E1B-pIX.SEQ

351 TTTAGACTTTTCAACCCCAGGTAGAACTGCTGCTGCTGTGGCTTTTCTTA Ad35.E1B-pIX.SEQ
351 TTTAGACTTTTCAACCCCAGGTAGAACTGCTGCTGCTGTGGCTTTTCTTA Ad11.E1B-pIX.SEQ
349 TTTAGATTTTTCTACTCCTGGTAGAACTGCTGCTGCTGTAGCTTTTCTTA Ad7.E1B-pIX.SEQ

401 CTTTTATATTAGATAAATGGATCCCGCAGACTCATTTCAGCAGGGGATAC Ad35.E1B-pIX.SEQ
401 CTTTTATATTAGATAAATGGATCCCGCAGACTCATTTCAGCAGGGGATAC Ad11.E1B-pIX.SEQ
399 CTTTTATATTGGATAAATGGATCCGCCAACTCACTTCAGCAAGGGATAC Ad7.E1B-pIX.SEQ

451 GTTTTGGATTTCATAGCCACAGCATTGTGGAGAACATGGAAGGTTCGCAA Ad35.E1B-pIX.SEQ
451 GTTTTGGATTTCATAGCCACAGCATTGTGGAGAACATGGAAGGTTCGCAA Ad11.E1B-pIX.SEQ
449 GTTTTGGATTTCATAGCAGCAGCTTTGTGGAGAACATGGAAGGCTCGCAG Ad7.E1B-pIX.SEQ

501 GATGAGGACAATCTTAGGTTACTGGCCAGTGCAGCCTTTGGGTGTAGCGG Ad35.E1B-pIX.SEQ
501 GATGAGGACAATCTTAGGTTACTGGCCAGTGCAGCCTTTGGGTGTAGCGG Ad11.E1B-pIX.SEQ
499 GATGAGGACAATCTTAGATTACTGGCCAGTGCAGCCTCTGGGAGTAGCAG Ad7.E1B-pIX.SEQ
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Fig. 10, Cont'd

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551  GAATCCTGAGGCATCCACCGGTCATGCCAGCGGTTCTGGAGGAGGAACAG Ad35.E1B-pIX.SEQ
551  GAATCCTGAGGCATCCACCGGTCATGCCAGCGGTTCTGGAGGAGGAACAG Ad11.E1B-pIX.SEQ
549  GGATACTGAGACACCCACCGACCATGCCAGCGGTTCTGCAGGAGGAGCAG Ad7.E1B-pIX.SEQ

601  CAAGAGGACAACCCGAGAGCCGGCCTGGACCCTCCAGTGGAGGAGGCGGA Ad35.E1B-pIX.SEQ
601  CAAGAGGACAACCCGAGAGCCGGCCTGGACCCTCCAGTGGAGGAGGCGGA Ad11.E1B-pIX.SEQ
599  CAGGAGGACAATCCGAGAGCCGGCCTGGACCCTCCGGTGGAGGAG----- Ad7.E1B-pIX.SEQ

651  GTAGCTGACTTGTCTCCTGAACTGCAACGGGTGCTTACTGGATCTACGTC Ad35.E1B-pIX.SEQ
651  GTAGCTGACTTGTCTCCTGAACTGCAACGGGTGCTTACTGGATCTACGTC Ad11.E1B-pIX.SEQ
644  -TAGCTGACCTGTTCCTGAACTGCGACGGGTGCTTACTAGGTCTACGAC Ad7.E1B-pIX.SEQ

701  CACTGGACGGGATAGGGGCGTTAAGAGGGAGAGGGCATCCAGTGGTACTG Ad35.E1B-pIX.SEQ
701  CACTGGACGGGATAGGGGCGTTAAGAGGGAGAGGGCATCTAGTGGTACTG Ad11.E1B-pIX.SEQ
693  CAGTGGACAGAACAGGGGAATTAAGAGGGAGAGGAATCCTAGTGGAATA Ad7.E1B-pIX.SEQ

751  ATGCTAGATCTGAGTTGGCTTTAAGTTTAATGAGTCGCAGACGTCCTGAA Ad35.E1B-pIX.SEQ
751  ATGCTAGATCTGAGTTGGCTTTAAGTTTAATGAGTCGCAGACGTCCTGAA Ad11.E1B-pIX.SEQ
743  ATTCAAGAACCGAGTTGGCTTTAAGTTTAATGAGCCGCAGGCGTCCTGAA Ad7.E1B-pIX.SEQ

801  ACCATTTGGTGGCATGAGGTTCAGAAAGAGGGAAGGGATGAAGTTTCTGT Ad35.E1B-pIX.SEQ
801  ACCATTTGGTGGCATGAGGTTCAGAAAGAGGGAAGGGATGAAGTTTCTGT Ad11.E1B-pIX.SEQ
793  ACTGTTTGGTGGCATGAGGTTCAGAGCGAAGGCAGGGATGAAGTTTCAAT Ad7.E1B-pIX.SEQ

851  ATTGCAGGAGAAATATTCACTGGAACAGGTGAAAACATGTTGGTTGGAGC Ad35.E1B-pIX.SEQ
851  ATTGCAGGAGAAATATTCACTGGAACAGGTGAAAACATGTTGGTTGGAGC Ad11.E1B-pIX.SEQ
843  ATTGCAGGAGAAATATTCACTAGAACAACTTAAGACCTGTTGGTTGGAAC Ad7.E1B-pIX.SEQ

901  CAGAGGATGATTGGGCGGTGGCCATTAAAAATTATGCCAAGATAGCTTTG Ad35.E1B-pIX.SEQ
901  CTGAGGATGATTGGGAGGTGGCCATTAAAAATTATGCCAAGATAGCTTTG Ad11.E1B-pIX.SEQ
893  CTGAGGATGATTGGGAGGTGGCCATTAGGAATTATGCTAAGATATCTCTG Ad7.E1B-pIX.SEQ

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951  AGGCCTGATAAACAGTATAAGATTACTAGACGGATTAATATCCGGAATGC Ad11.E1B-pIX.SEQ
943  AGGCCTGATAAACAATATAGAATTACTAAGAAGATTAATATTAGAAATGC Ad7.E1B-pIX.SEQ

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1001 TTGTTACATATCTGGAAATGGGGCTGAGGTGGTAATAGATACTCAAGACA Ad11.E1B-pIX.SEQ
993  ATGCTACATATCAGGGAATGGGGCAGAGGTTATAATAGATACACAAGATA Ad7.E1B-pIX.SEQ

1051 AGACAGTTATTAGATGCTGCATGATGGATATGTGGCCTGGAGTAGTCGGT Ad35.E1B-pIX.SEQ
1051 AGGCAGTTATTAGATGCTGCATGATGGATATGTGGCCTGGGGTAGTCGGT Ad11.E1B-pIX.SEQ
1043 AAGCAGCTTTAGATGTTGTATGATGGGTATGTGGCCAGGGGTTGTCGGC Ad7.E1B-pIX.SEQ
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Fig. 10, Cont'd

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1301 GAGTCAATTGTCTCTGAAGAAATGCATATTTCAAAGATGTAACCTGGGCA Ad11.E1B-pIX.SEQ
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1401 GGATGTTTTATTTTGATTAAGGGAAATGCCAGCGTAAAGCATAACATGAT Ad11.E1B-pIX.SEQ
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1443 CTGTGGACATTCGGATGAGAGGCCTTATCAGATGCTAACCTGCGCTGGTG Ad7.E1B-pIX.SEQ

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1501 GGCATTGTAATATGCTGGCTACTGTGCATATTGTTTCCCATCAACGCAAA Ad11.E1B-pIX.SEQ
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1551 AAATGGCCTGTTTTTGATCACAATGTGATGACGAAGTGTACCATGCATGC Ad11.E1B-pIX.SEQ
1543 AAATGGCCTGTATTTGAACATAATGTGATTACCAAGTGCACCATGCATAT Ad7.E1B-pIX.SEQ

1601 AGGTGGGCGTAGAGGAATGTTTATGCCTTACCAGTGTAACATGAATCATG Ad35.E1B-pIX.SEQ
1601 AGGTGGGCGTAGAGGAATGTTTATGCCTTACCAGTGTAACATGAATCATG Ad11.E1B-pIX.SEQ
1593 AGGTGGTCGCAGGGAATGTTTATGCCTTACCAGTGTAACATGAATCATG Ad7.E1B-pIX.SEQ
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Fig. 10, Cont'd

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1651 TGAAAGTGTTGTTGGAACCAGATGCCTTTTCCAGAATGAGCCTAACAGGA Ad11.E1B-pIX.SEQ
1643 TGAAGGTAATGTTGGAACCAGATGCCTTTTCCAGAGTGAGCGTAACAGGA Ad7.E1B-pIX.SEQ

1701 ATCTTTGACATGAACACGCAAATCTGGAAGATCCTGAGGTATGATGATAC Ad35.E1B-pIX.SEQ
1701 ATTTTTGACATGAACATGCAAATCTGGAAGATCCTGAGGTATGATGATAC Ad11.E1B-pIX.SEQ
1693 ATCTTTGATATGAATATTCAACTATGGAAGATCCTGAGATATGATGACAC Ad7.E1B-pIX.SEQ

1751 GAGATCGAGGGTGCGCGCATGCGAATGCGGAGGCAAGCATGCCAGGTTCC Ad35.E1B-pIX.SEQ
1751 GAGATCGAGGGTACGCGCATGCGAATGCGGAGGCAAGCATGCCAGGTTCC Ad11.E1B-pIX.SEQ
1743 TAAACCAAGGGTGCGCGCATGCGAATGCGGAGGCAAGCATGCTAGATTCC Ad7.E1B-pIX.SEQ

1801 AGCCGGTGTGTGTAGATGTGACCGAAGATCTCAGACCGGATCATTTGGTT Ad35.E1B-pIX.SEQ
1801 AGCCGGTGTGTGTAGATGTGACTGAAGATCTCAGACCGGATCATTTGGTT Ad11.E1B-pIX.SEQ
1793 AGCCGGTGTGCGTGGATGTGACTGAAGACCTGAGGCCCGATCATTTGGTG Ad7.E1B-pIX.SEQ

1851 ATTGCCCGCACTGGAGCAGAGTTCGGATCCAGTGGAGAAGAAACTGACTA Ad35.E1B-pIX.SEQ
1851 ATTGCCCGCACTGGAGCAGAGTTCGGATCCAGTGGAGAAGAAACTGACTA Ad11.E1B-pIX.SEQ
1843 CTTGCCTGCACTGGAGCGGAGTTCGGTTCTAGTGGTGAAGAAACTGACTA Ad7.E1B-pIX.SEQ

1901 AGGTGAGTATTGGGA--AAACTTTGGGGTGGGATTTTCAG---------A Ad35.E1B-pIX.SEQ
1901 AGGTGAGTATTGGGA--AAACTTTGGGGTGGGATTTTCAG---------A Ad11.E1B-pIX.SEQ
1893 AAGTAAGTAGTGGGGGCAAAAATGTGGATGGGGACTTTCAGGTTGGTAAGG Ad7.E1B-pIX.SEQ

1940 TGGACAGATTGAGTAAAAATTTGTTTTTTCTGTCTTGCAGCTGACATGAG Ad35.E1B-pIX.SEQ
1940 TGGACAGATTGAGTAAAAATTTGTTTTTTCTGTCTTGCAGCTGTCATGAG Ad11.E1B-pIX.SEQ
1943 TGGACAAATTGGGTAAATTTTGTTAATTTCTGTCTTGCAGCTGCCATGAG Ad7.E1B-pIX.SEQ

1990 TGGAAATGCTTCTTTTTAAGGGGGGAGTCTTCAGCCCTTATCTGACAGGGC Ad35.E1B-pIX.SEQ
1990 TGGAAACGCTTCTTTTTAAGGGGGGAGTCTTCAGCCCTTATCTGACAGGGC Ad11.E1B-pIX.SEQ
1993 TGGAAGCGCTTCTTTTTGAGGGGGGAGTATTTAGCCCTTATCTGACGGCA Ad7.E1B-pIX.SEQ

2040 GTCTCCCATCCTGGGCAGGAGTTCGTCAGAATGTTATGGGATCTACTGTG Ad35.E1B-pIX.SEQ
2040 GTCTCCCATCCTGGGCAGGAGTTCGTCAGAATGTTATGGGATCTACTGTG Ad11.E1B-pIX.SEQ
2043 GGCTCCCACCCATGGGCAGGAGTTCGTCAGAATGTCATGGGATCCCACTGTG Ad7.E1B-pIX.SEQ

2090 GATGGAAGACCCGTTCAACCCGCCAATTCTTCAACGCTGACCTATGCTAC Ad35.E1B-pIX.SEQ
2090 GATGGAAGACCCGTCCAACCCGCCAATTCTTCAACGCTGACCTATGCTAC Ad11.E1B-pIX.SEQ
2093 GATGGGAGACCCGTCCAGCCCGCCAATTCCTCAACGCTGACCTATGCCAC Ad7.E1B-pIX.SEQ

2140 TTTAAGTTCTTCACCTTTGGACGCAGCTGCAGCCGCTGCCGCCGCCTCTG Ad35.E1B-pIX.SEQ
2140 TTTAAGTTCTTCACCTTTGGACGCAGCTGCAGCTGCCGCCGCCTTCTG Ad11.E1B-pIX.SEQ
2143 TTTGAGTTCGTCACCATTGGATGCAGCTGCAGCCGCCGCCGCTAC---TG Ad7.E1B-pIX.SEQ
```

Fig. 10, Cont'd

```
2190 TCGCCGCTAACACTGTGCTTGGAATGGGTTACTATGGAAGCATCGTGGCT Ad35.E1B-pIX.SEQ
2190 TTGCCGCTAACACTGTGCTTGGAATGGGTTACTATGGAAGCATCATGGCT Ad11.E1B-pIX.SEQ
2190 CTGCCGCCAACACCATCCTTGGAATGGGCTATTACGGAAGCATTGTTGCC Ad7.E1B-pIX.SEQ

2240 AATTCCACTTCCTCTAATAACCCTTCTACACTGACTCAGGACAAGTTACT Ad35.E1B-pIX.SEQ
2240 AATTCCACTTCCTCTAATAACCCTTCTACCCTGACTCAGGACAAGTTACT Ad11.E1B-pIX.SEQ
2240 AATTCCAGTTCCTCTAATAATCCTTCAACCCTGGCTGAGGACAAGCTACT Ad7.E1B-pIX.SEQ

2290 TGTCCTTTTGGCCCAGCTGGAGGCTTTGACCCAACGTCTGGGTGAACTTT Ad35.E1B-pIX.SEQ
2290 TGTCCTTTTGGCCCAGCTGGAGGCTTTGACCCAACGTCTGGGTGAACTTT Ad11.E1B-pIX.SEQ
2290 TGTTCTCTTGGCTCAGCTCGAGGCCTTAACCCAACGCTTAGGCGAACTGT Ad7.E1B-pIX.SEQ

2340 CTCAGCAGGTGGCCGAGTTGCGAGTACAAACTGAGTCTGCTGTCGGCACG Ad35.E1B-pIX.SEQ
2340 CTCAGCAGGTGGTCGAGTTGCGAGTACAAACTGAGTCTGCTGTCGGCACG Ad11.E1B-pIX.SEQ
2340 CTAAGCAGGTGGCCCAGTTGCGTGAGCAAACTGAGTCTGCTGTTGCCACA Ad7.E1B-pIX.SEQ

2390 GCAAAGTCTAAATAAAAAAAAATTCCAGAATCAATGAATAAA Ad35.E1B-pIX.SEQ
2390 GCAAAGTCTAAATAAAAAAAA-TCCCAGAATCAATGAATAAA Ad11.E1B-pIX.SEQ
2390 GCAAAGTCTAAATAAAGA---TCTCA-AATCAATAAATAAA Ad7.E1B-pIX.SEQ

Decoration 'Decoration #1': Box residues that differ from Ad35.E1B-pIX.SEQ.
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Fig. 11

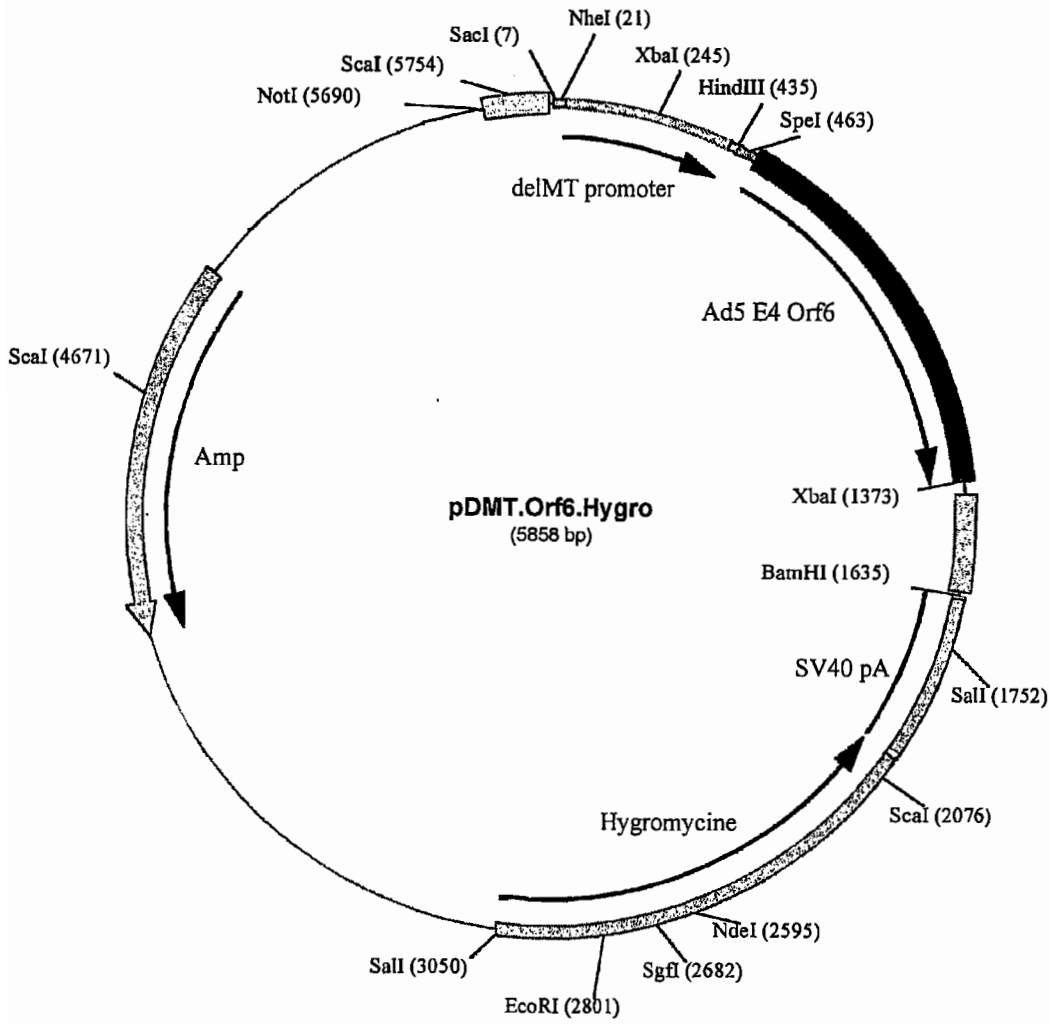

NheI (21)
SacI (7)
XbaI (245)
ScaI (5754)
HindIII (435)
NotI (5690)
SpeI (463)
delMT promoter
Ad5 E4 Orf6
ScaI (4671)
Amp
pDMT.Orf6.Hygro
(5858 bp)
XbaI (1373)
BamHI (1635)
SV40 pA
SalI (1752)
ScaI (2076)
Hygromycine
NdeI (2595)
SalI (3050)
SgfI (2682)
EcoRI (2801)

Fig. 12

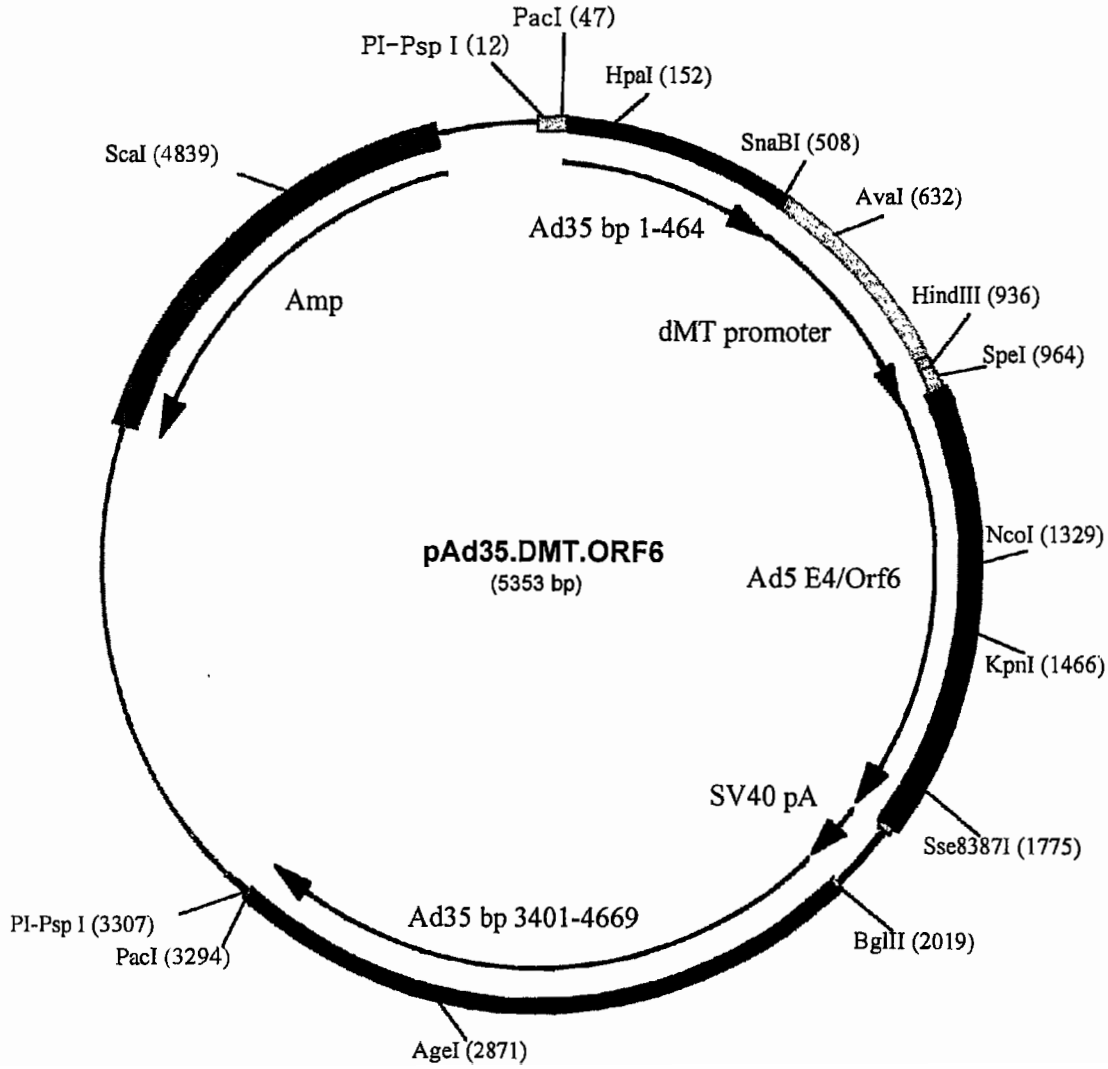

PacI (47)
PI-Psp I (12)
HpaI (152)
SnaBI (508)
ScaI (4839)
AvaI (632)
Ad35 bp 1-464
Amp
HindIII (936)
dMT promoter
SpeI (964)
pAd35.DMT.ORF6
(5353 bp)
Ad5 E4/Orf6
NcoI (1329)
KpnI (1466)
SV40 pA
Sse8387I (1775)
PI-Psp I (3307)
Ad35 bp 3401-4669
BglII (2019)
PacI (3294)
AgeI (2871)

Fig. 13

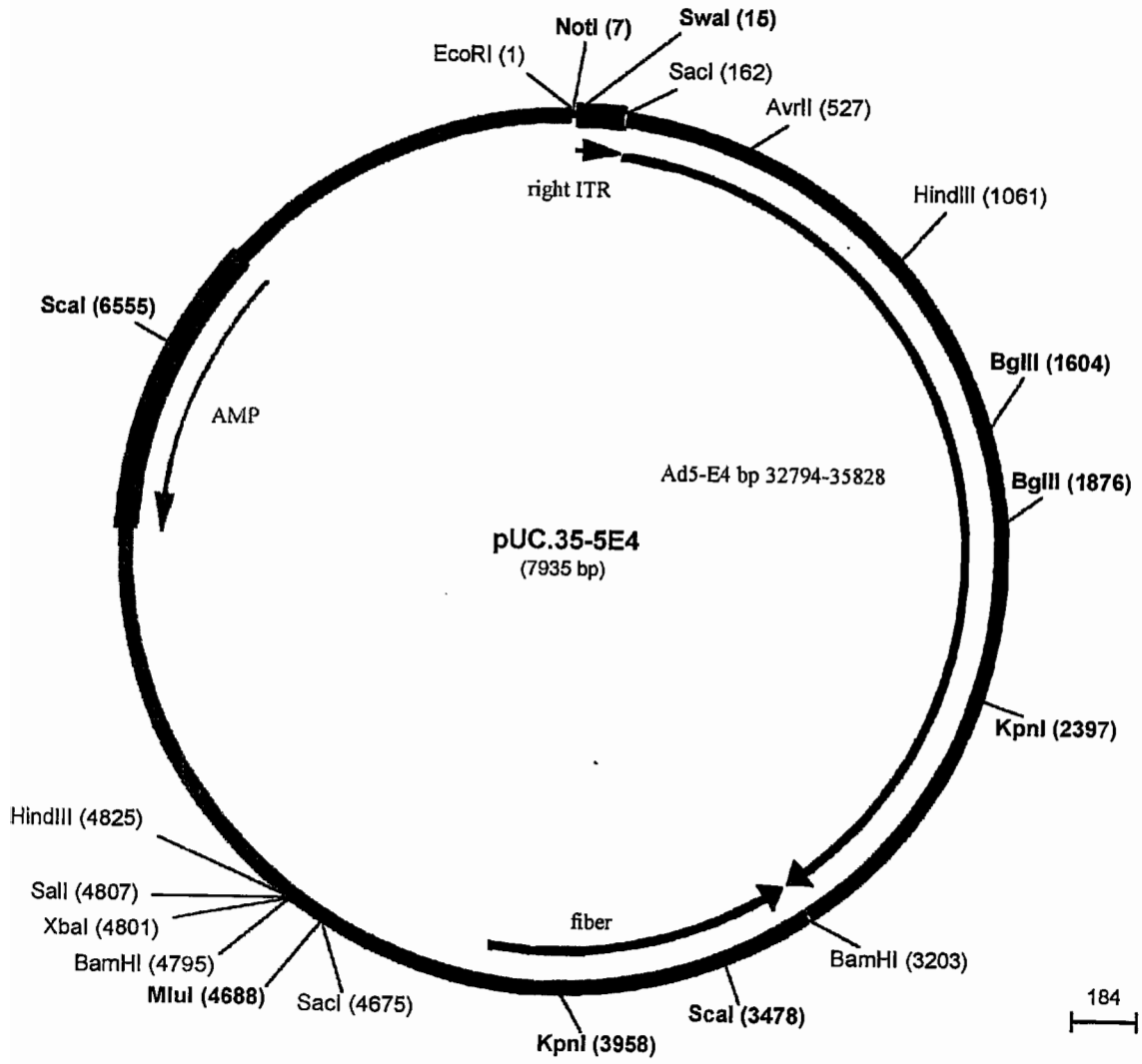

NotI (7)
SwaI (15)
EcoRI (1)
SacI (162)
AvrII (527)
right ITR
HindIII (1061)
ScaI (6555)
BglII (1604)
AMP
Ad5-E4 bp 32794-35828
BglII (1876)
pUC.35-5E4
(7935 bp)
KpnI (2397)
HindIII (4825)
SalI (4807)
XbaI (4801)
fiber
BamHI (4795)
BamHI (3203)
MluI (4688)
SacI (4675)
ScaI (3478)
184
KpnI (3958)

Fig. 14: Cloning steps for pUC.35-5E4

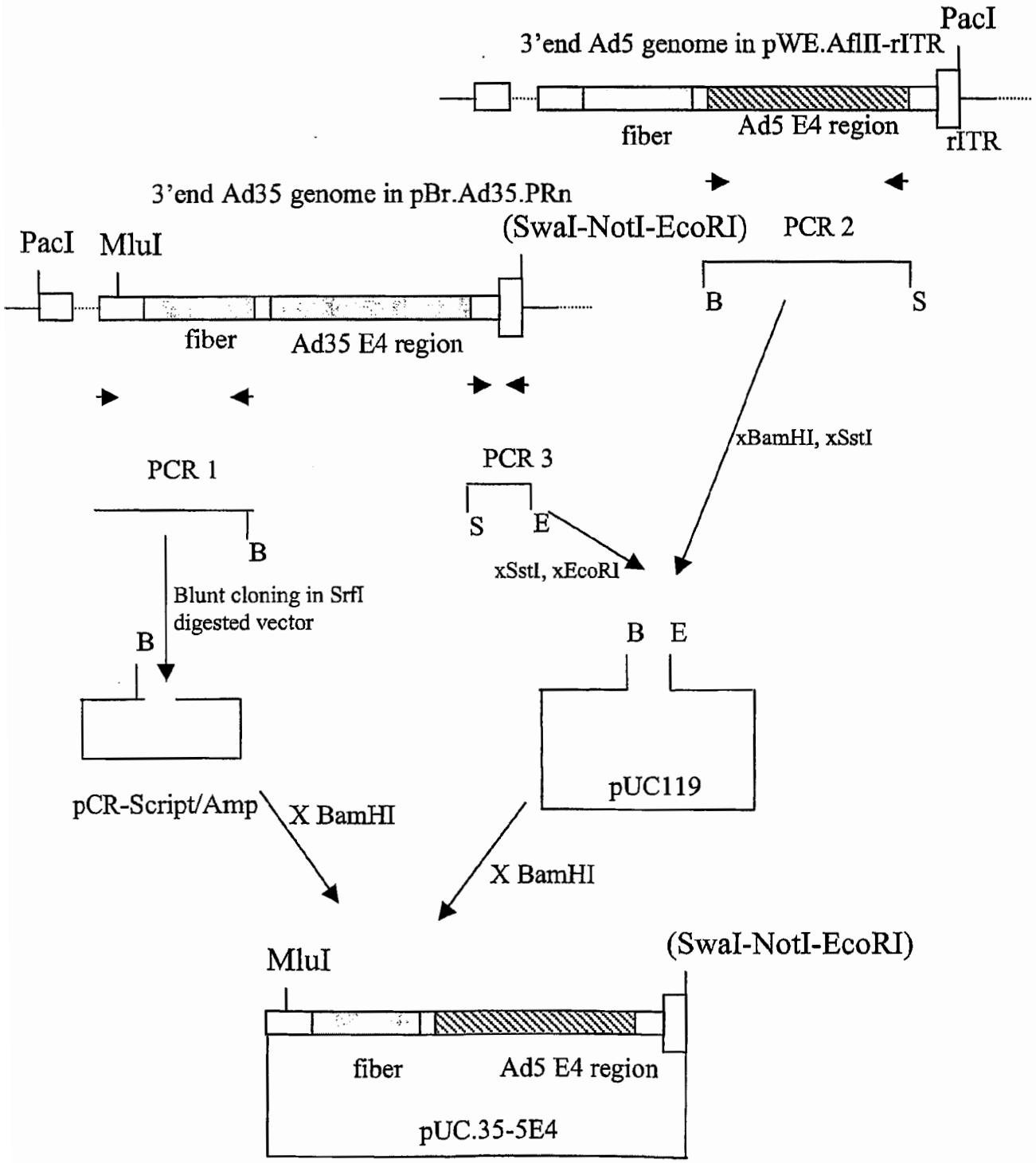


Fig. 15

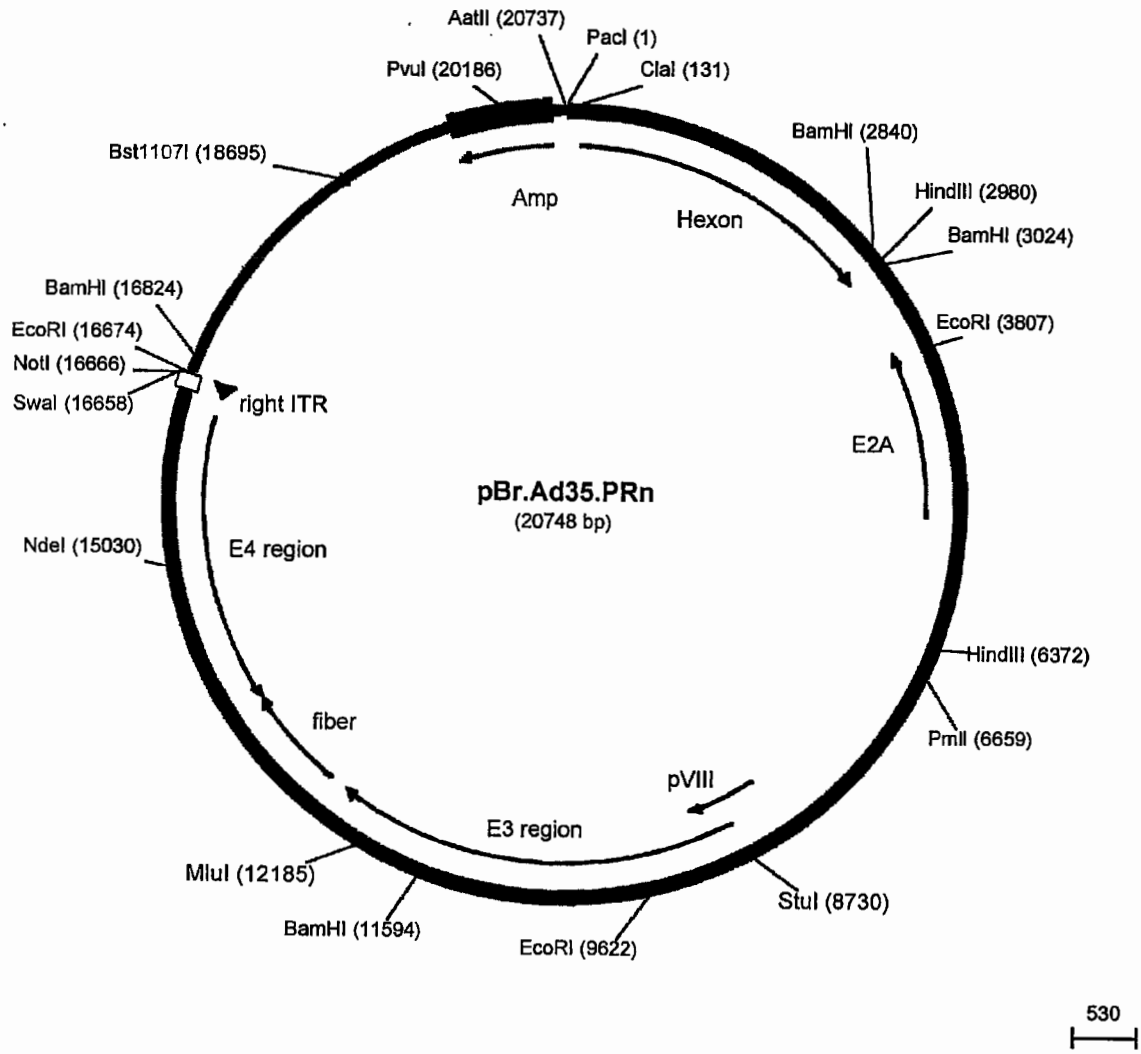

AatII (20737)
PacI (1)
PvuI (20186)
ClaI (131)
BamHI (2840)
Bst1107I (18695)
HindIII (2980)
Amp
Hexon
BamHI (3024)
BamHI (16824)
EcoRI (16674)
NotI (16666)
SwaI (16658)
right ITR
EcoRI (3807)
E2A
pBr.Ad35.PRn
(20748 bp)
NdeI (15030)
E4 region
HindIII (6372)
PmlI (6659)
fiber
pVIII
E3 region
MluI (12185)
StuI (8730)
BamHI (11594)
EcoRI (9622)
530

Fig. 16

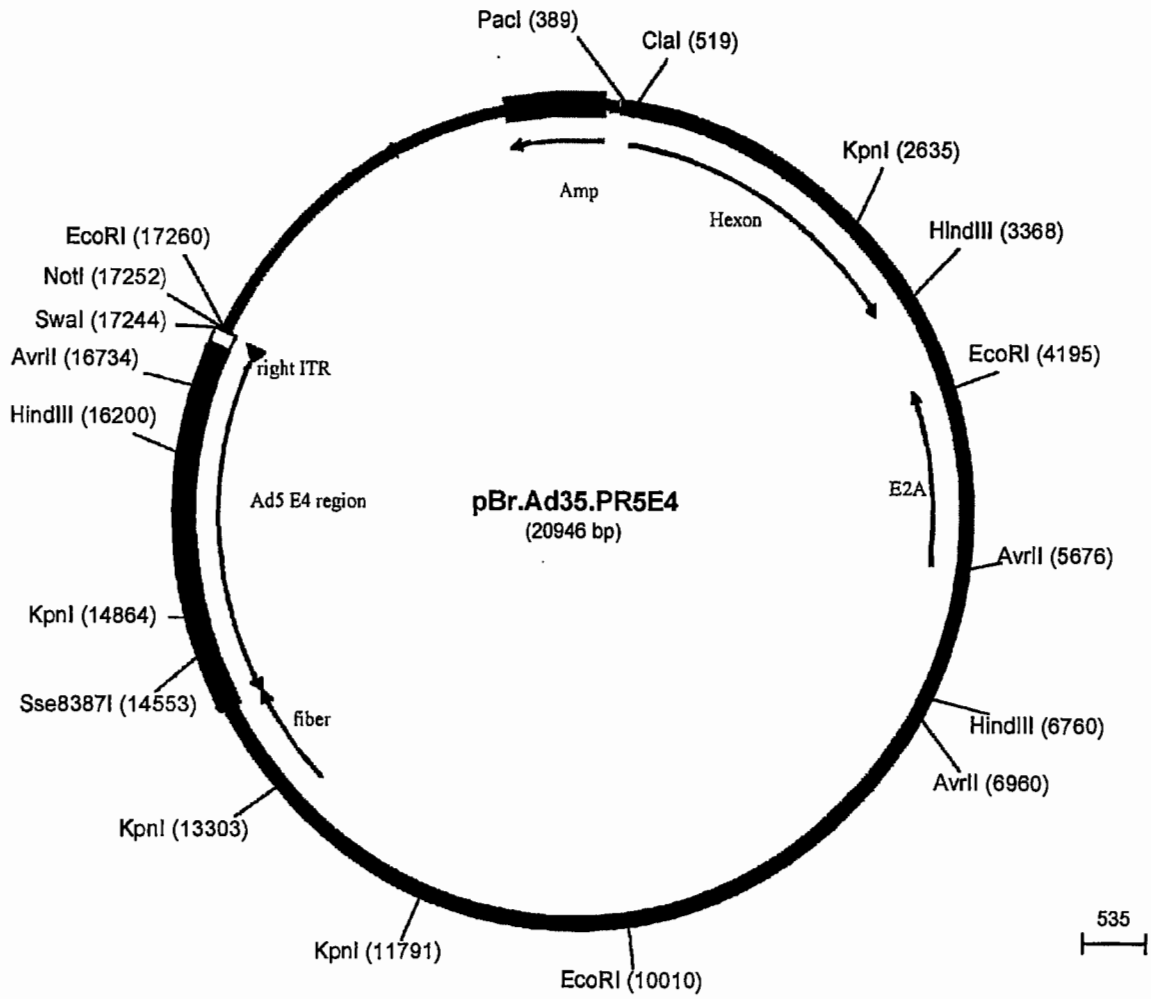

PacI (389)
ClaI (519)
KpnI (2635)
HindIII (3368)
EcoRI (4195)
AvrII (5676)
HindIII (6760)
AvrII (6960)
EcoRI (10010)
KpnI (11791)
KpnI (13303)
Sse8387I (14553)
KpnI (14864)
HindIII (16200)
AvrII (16734)
SwaI (17244)
NotI (17252)
EcoRI (17260)
Amp
Hexon
E2A
right ITR
fiber
Ad5 E4 region
pBr.Ad35.PR5E4
(20946 bp)
535

Fig. 17

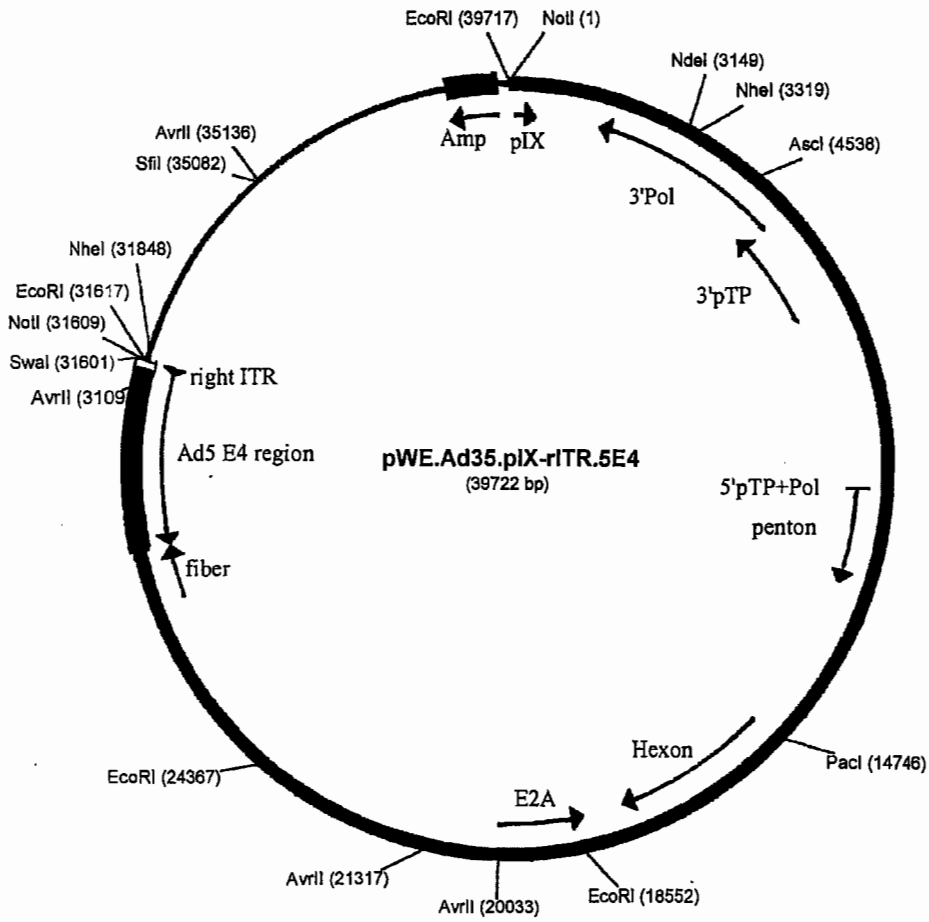

EcoRI (39717)
NotI (1)
NdeI (3149)
NheI (3319)
AscI (4538)
3'Pol
3'pTP
5'pTP+Pol
penton
PacI (14746)
Hexon
E2A
EcoRI (18552)
AvrII (20033)
AvrII (21317)
EcoRI (24367)
fiber
Ad5 E4 region
right ITR
SwaI (31601)
NotI (31609)
EcoRI (31617)
NheI (31848)
SfiI (35082)
AvrII (35136)
Amp
pIX
pWE.Ad35.pIX-rITR.5E4
(39722 bp)

Fig. 18

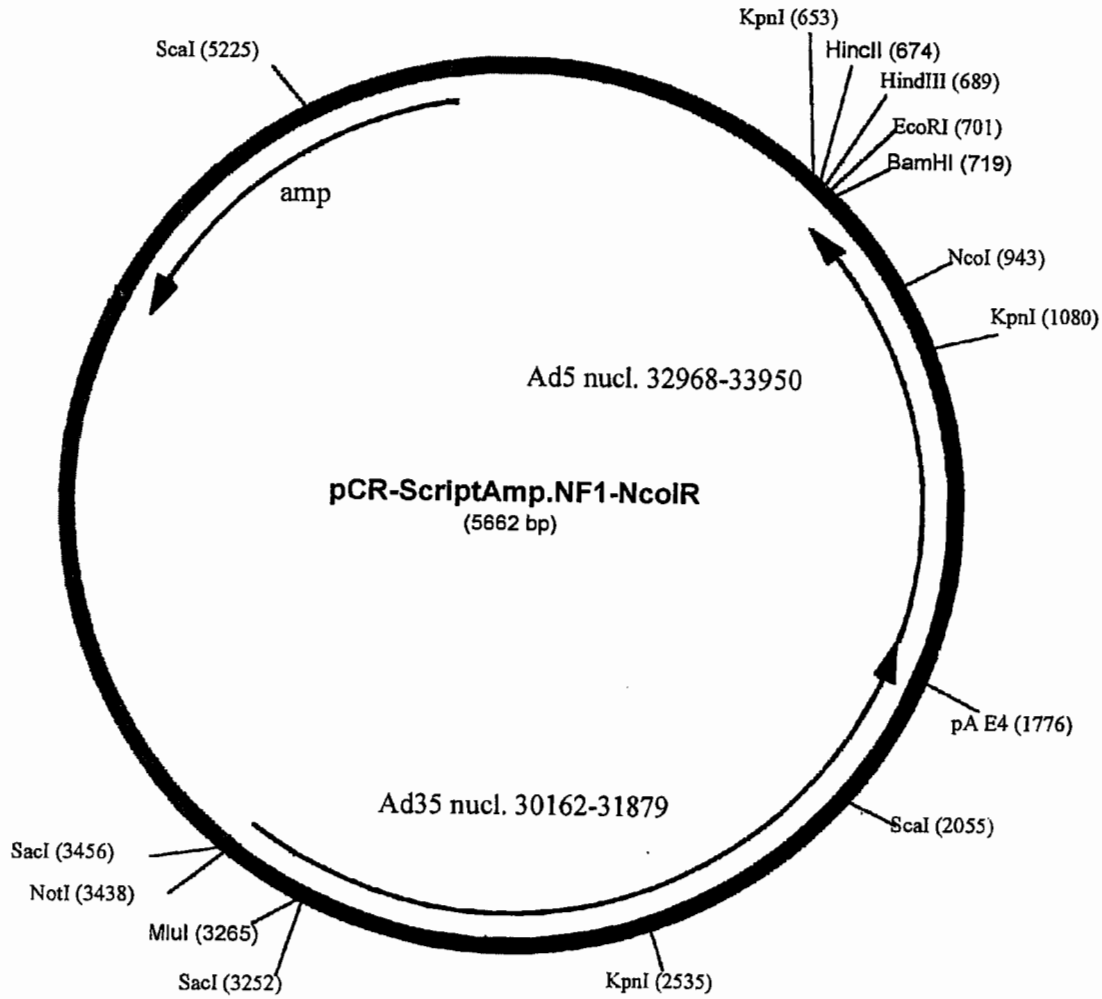

KpnI (653)
HincII (674)
HindIII (689)
EcoRI (701)
BamHI (719)
ScaI (5225)
amp
NcoI (943)
KpnI (1080)
Ad5 nucl. 32968-33950
pCR-ScriptAmp.NF1-NcoIR
(5662 bp)
pA E4 (1776)
Ad35 nucl. 30162-31879
ScaI (2055)
SacI (3456)
NotI (3438)
MluI (3265)
SacI (3252)
KpnI (2535)

Fig. 19

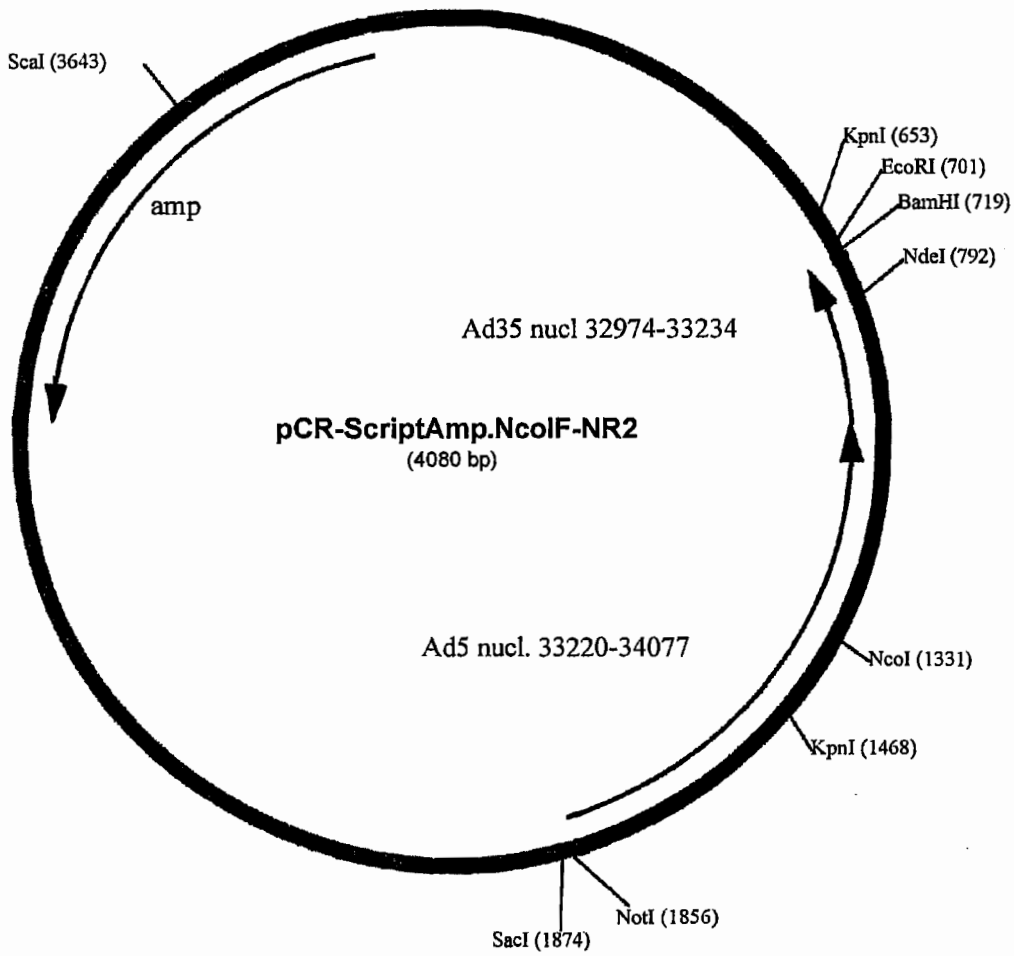

ScaI (3643)
amp
KpnI (653)
EcoRI (701)
BamHI (719)
NdeI (792)
Ad35 nucl 32974-33234
pCR-ScriptAmp.NcoIF-NR2
(4080 bp)
Ad5 nucl. 33220-34077
NcoI (1331)
KpnI (1468)
NotI (1856)
SacI (1874)

Fig. 20

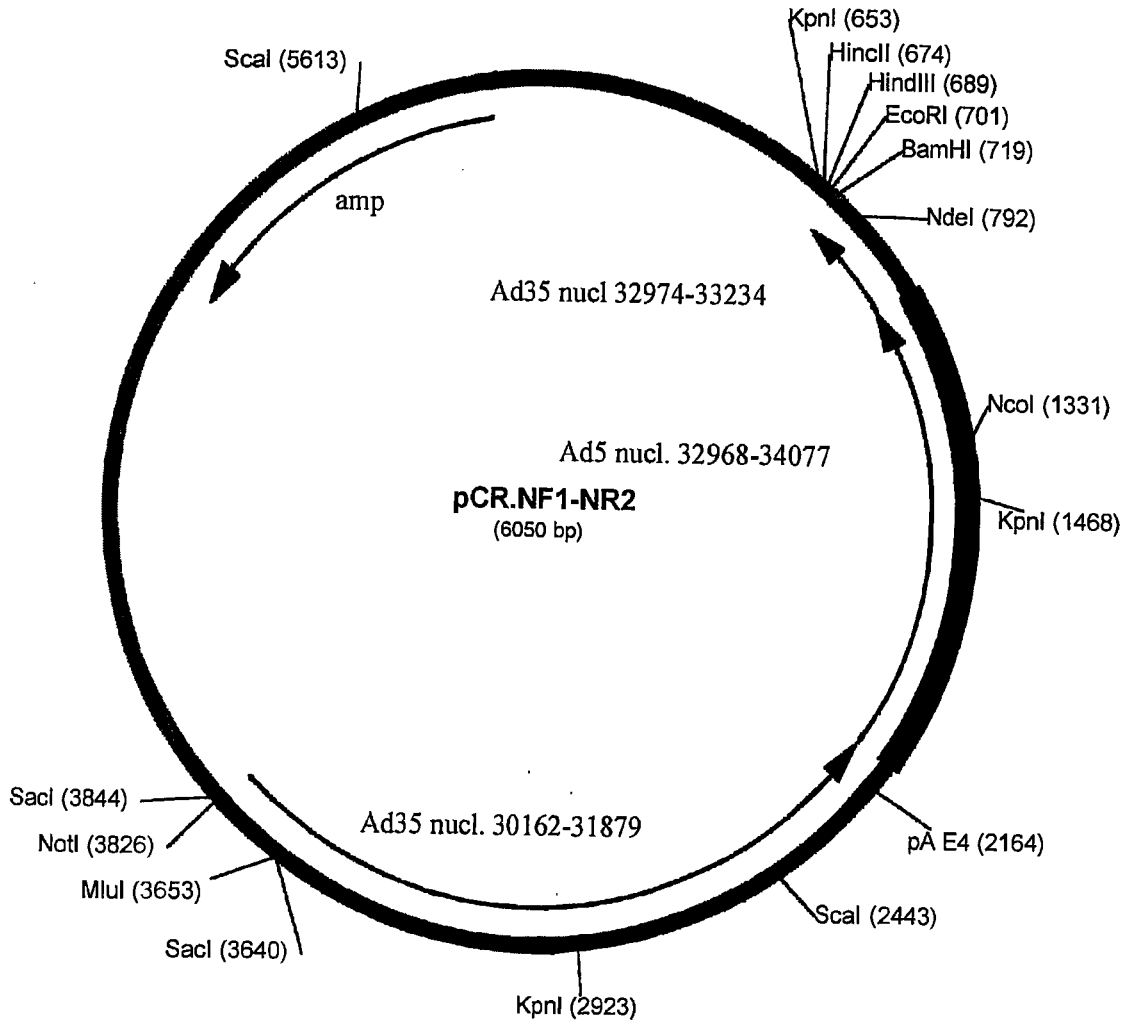
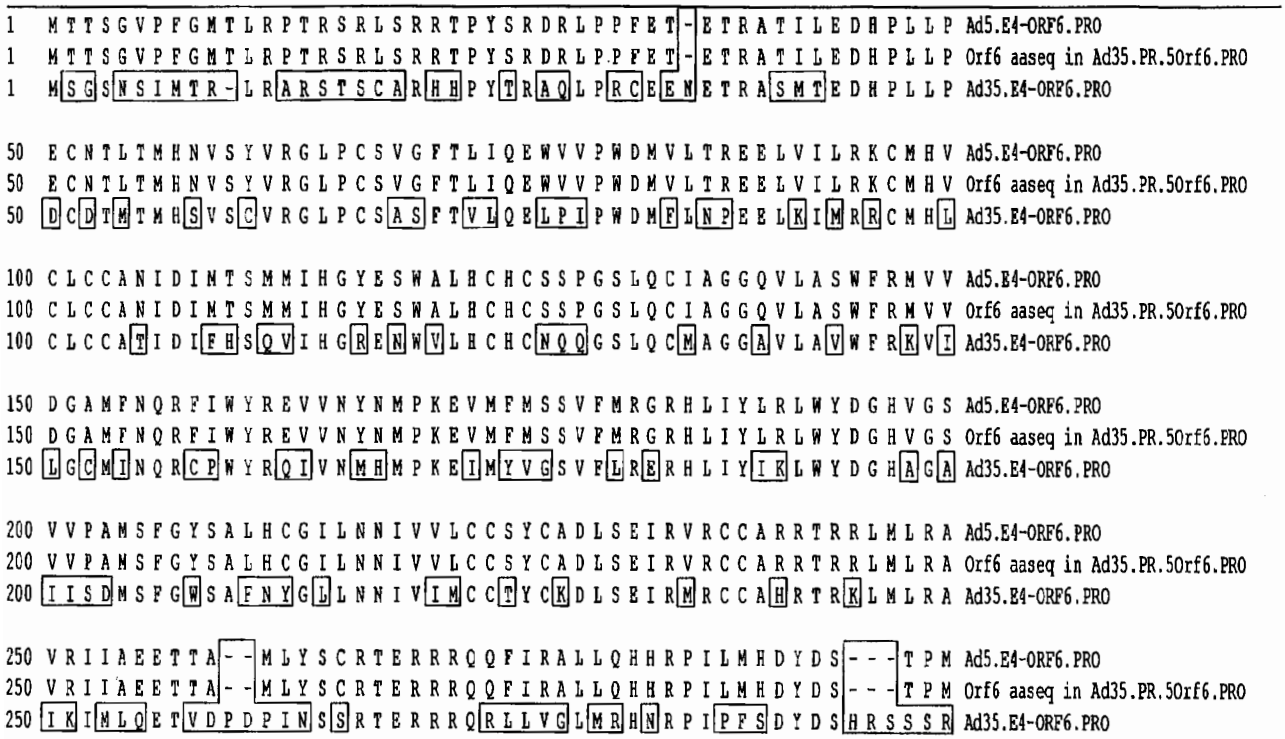

KpnI (653)
HincII (674)
HindIII (689)
EcoRI (701)
BamHI (719)
NdeI (792)
ScaI (5613)
amp
Ad35 nucl 32974-33234
NcoI (1331)
Ad5 nucl. 32968-34077
pCR.NF1-NR2
(6050 bp)
KpnI (1468)
SacI (3844)
NotI (3826)
MluI (3653)
SacI (3640)
Ad35 nucl. 30162-31879
pA E4 (2164)
ScaI (2443)
KpnI (2923)

Fig. 21



Decoration 'Decoration #1': Box residues that differ from Ad5.E4-ORF6.PRO.

Fig. 22

```
1   M T T S G V P F G M T L R P T R S R L S R R T P Y S R D R L P P F E T - E T R A Ad5.E4-ORF6+7.PRO
1   M T T S G V P F G M T L R P T R S R L S R R T P Y S R D R L P P F E T - E T R A Orf6+7 aaseq in Ad35.PR5Orf6.PRO
1   M S G S N - S I M T R L R A R S T S C A R H H P Y T R A Q L P R C E E N E T R A Ad35.E4-ORF6+7.pro

40  T I L E D H P L L P E C N T L T M H N A W T S P S P P V K Q P Q V G Q Q P V A Q Ad5.E4-ORF6+7.PRO
40  T I L E D H P L L P E C N T L T M H N A W T S P S P P V K Q P Q V G Q Q P V A Q Orf6+7 aaseq in Ad35.PR5Orf6.PRO
40  S M T E D H P L L P D C D T M T M H S M T V I Q T P - - - - - - - - - E S H P Q Ad35.E4-ORF6+7.pro

80  Q L D S D M N L S E L P G E F I N I T D E R L A R Q E T V W N I T P K N M S V T Ad5.E4-ORF6+7.PRO
80  Q L D S D M N L S E L P G E F I N I T D E R L A R Q E T V W N I T P K N M S V T Orf6+7 aaseq in Ad35.PR5Orf6.PRO
71  Q L D C E S A L K D Y R D G F L S I T D P R L A R S E T V W N V E S K T M S I S Ad35.E4-ORF6+7.pro

120 H D M M L F K A S R G E R T V Y S V C W E G G G R L N T R V L                   Ad5.E4-ORF6+7.PRO
120 H D M M L F K A S R G E R T V Y S V K W E G G G K I T T R I L                   Orf6+7 aaseq in Ad35.PR5Orf6.PRO
111 N G I Q M F K A V R G E R L V Y S V K W E G G G K I T T R I L                   Ad35.E4-ORF6+7.pro

Decoration 'Decoration #1': Box residues that differ from Ad5.E4-ORF6+7.PRO.
```

Fig. 23

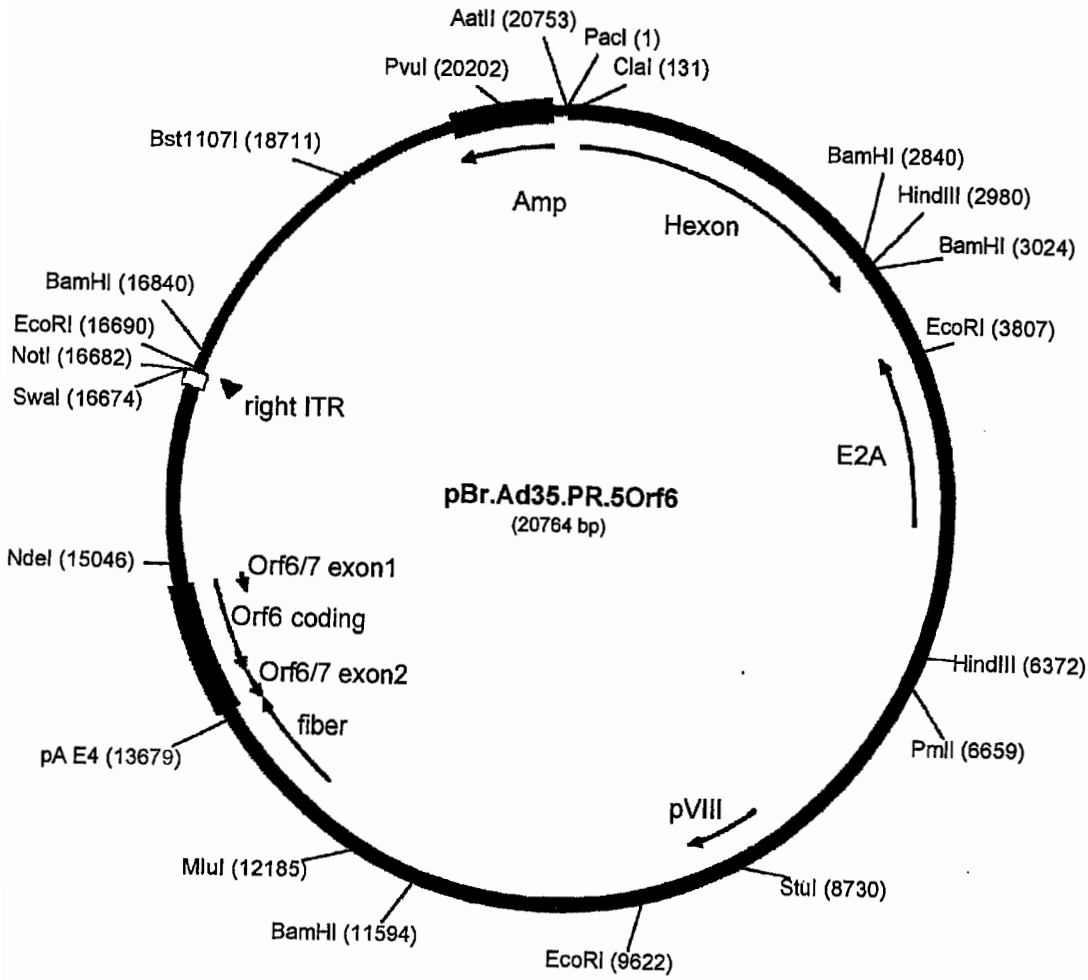

AatII (20753)
PacI (1)
PvuI (20202)
ClaI (131)
Bst1107I (18711)
BamHI (2840)
HindIII (2980)
BamHI (3024)
Amp
Hexon
BamHI (16840)
EcoRI (16690)
NotI (16682)
SwaI (16674)
right ITR
EcoRI (3807)
E2A
pBr.Ad35.PR.5Orf6
(20764 bp)
NdeI (15046)
Orf6/7 exon1
Orf6 coding
Orf6/7 exon2
fiber
HindIII (6372)
PmlI (6659)
pA E4 (13679)
pVIII
MluI (12185)
StuI (8730)
BamHI (11594)
EcoRI (9622)

Fig. 24

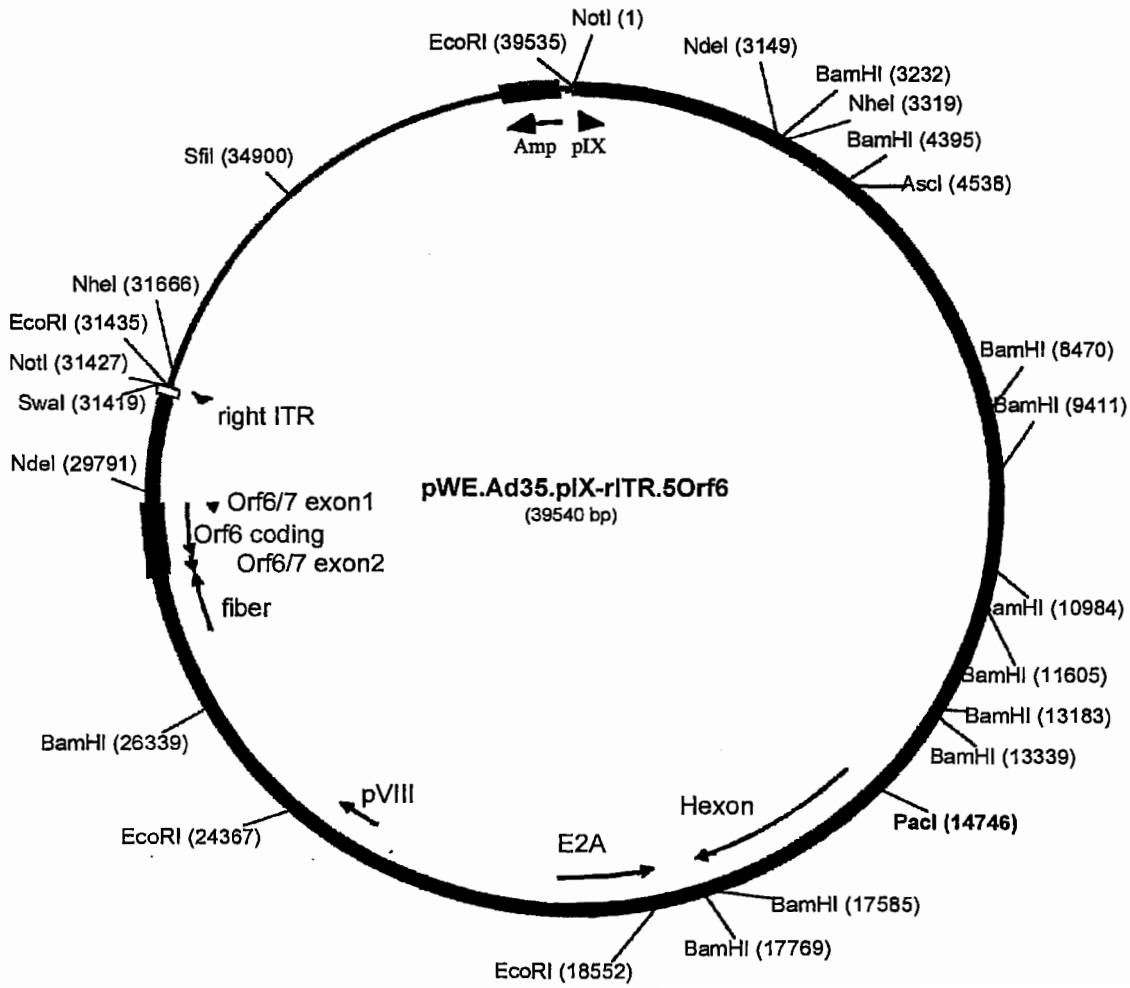

NotI (1)
EcoRI (39535)
NdeI (3149)
BamHI (3232)
NheI (3319)
BamHI (4395)
AscI (4538)
Amp
pIX
SfiI (34900)
NheI (31666)
EcoRI (31435)
NotI (31427)
SwaI (31419)
right ITR
NdeI (29791)
pWE.Ad35.pIX-rITR.5Orf6
(39540 bp)
Orf6/7 exon1
Orf6 coding
Orf6/7 exon2
fiber
BamHI (8470)
BamHI (9411)
amHI (10984)
BamHI (11605)
BamHI (13183)
BamHI (13339)
PacI (14746)
BamHI (26339)
pVIII
EcoRI (24367)
Hexon
E2A
BamHI (17585)
BamHI (17769)
EcoRI (18552)

Fig. 25

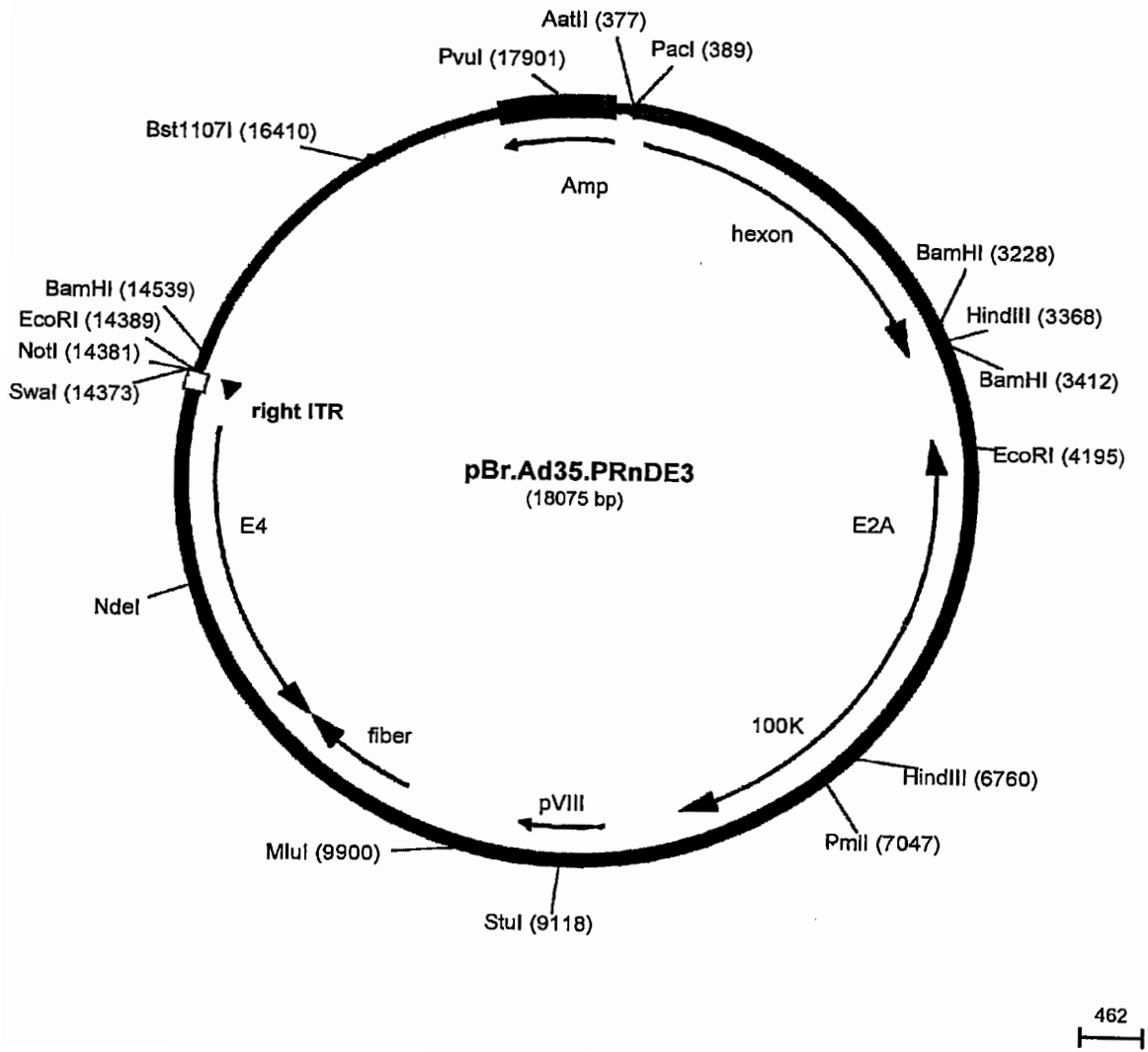

AatII (377)
PacI (389)
PvuI (17901)
Bst1107I (16410)
Amp
hexon
BamHI (3228)
HindIII (3368)
BamHI (3412)
EcoRI (4195)
BamHI (14539)
EcoRI (14389)
NotI (14381)
SwaI (14373)
right ITR
pBr.Ad35.PRnDE3
(18075 bp)
E4
E2A
NdeI
fiber
100K
HindIII (6760)
pVIII
PmlI (7047)
MluI (9900)
StuI (9118)
462

Fig. 26

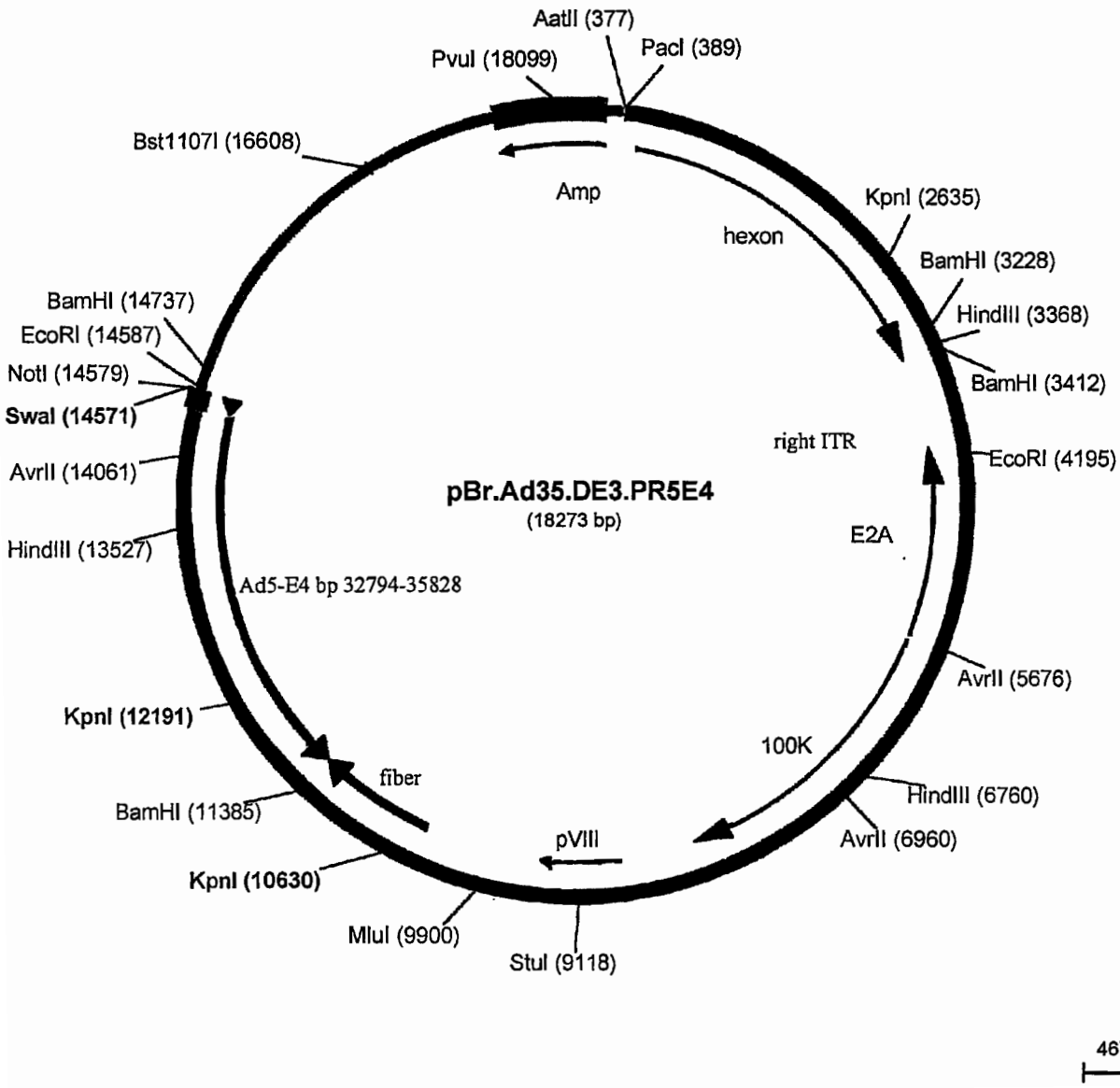

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PacI (389)
PvuI (18099)
Bst1107I (16608)
Amp
KpnI (2635)
hexon
BamHI (3228)
HindIII (3368)
BamHI (3412)
BamHI (14737)
EcoRI (14587)
NotI (14579)
SwaI (14571)
right ITR
EcoRI (4195)
AvrII (14061)
pBr.Ad35.DE3.PR5E4
(18273 bp)
E2A
HindIII (13527)
Ad5-E4 bp 32794-35828
AvrII (5676)
KpnI (12191)
100K
fiber
HindIII (6760)
BamHI (11385)
AvrII (6960)
pVIII
KpnI (10630)
MluI (9900)
StuI (9118)
467

Fig. 27

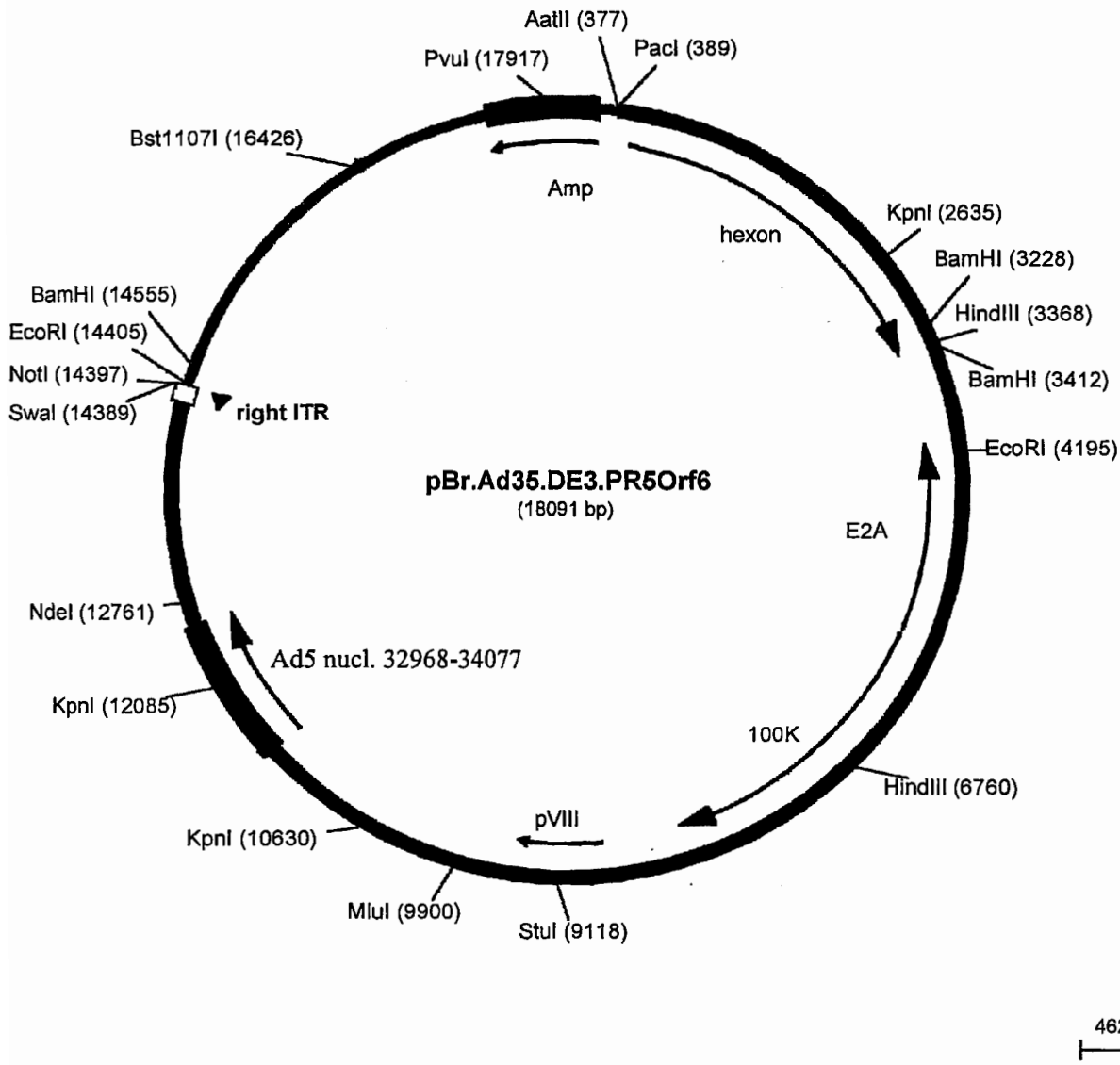
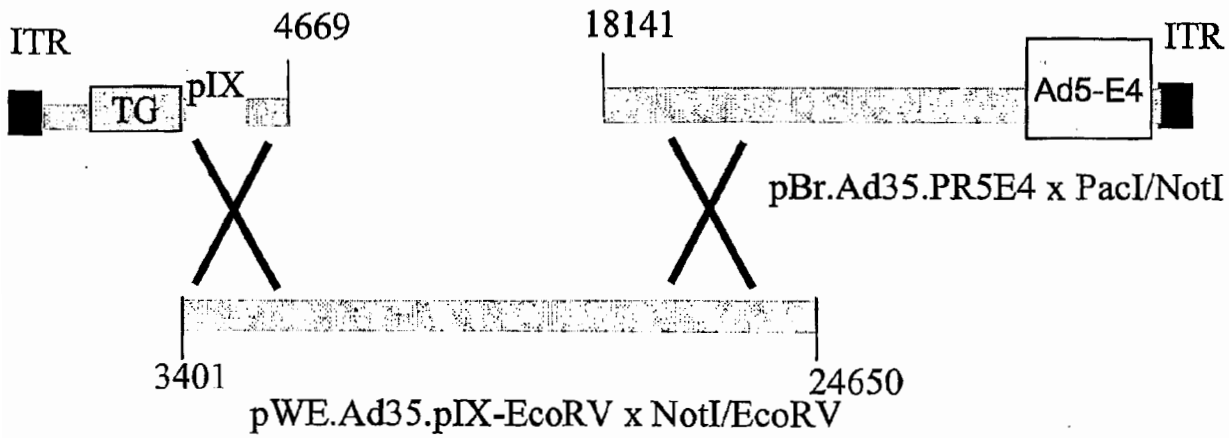

AatII (377)
PacI (389)
PvuI (17917)
Bst1107I (16426)
Amp
hexon
KpnI (2635)
BamHI (3228)
HindIII (3368)
BamHI (3412)
EcoRI (4195)
BamHI (14555)
EcoRI (14405)
NotI (14397)
SwaI (14389)
right ITR
pBr.Ad35.DE3.PR5Orf6
(18091 bp)
E2A
NdeI (12761)
Ad5 nucl. 32968-34077
KpnI (12085)
100K
HindIII (6760)
pVIII
KpnI (10630)
MluI (9900)
StuI (9118)
462

FIG. 28: Generation of E1-deleted Ad35 vectors via double homologous recombination in PER.C6 cells



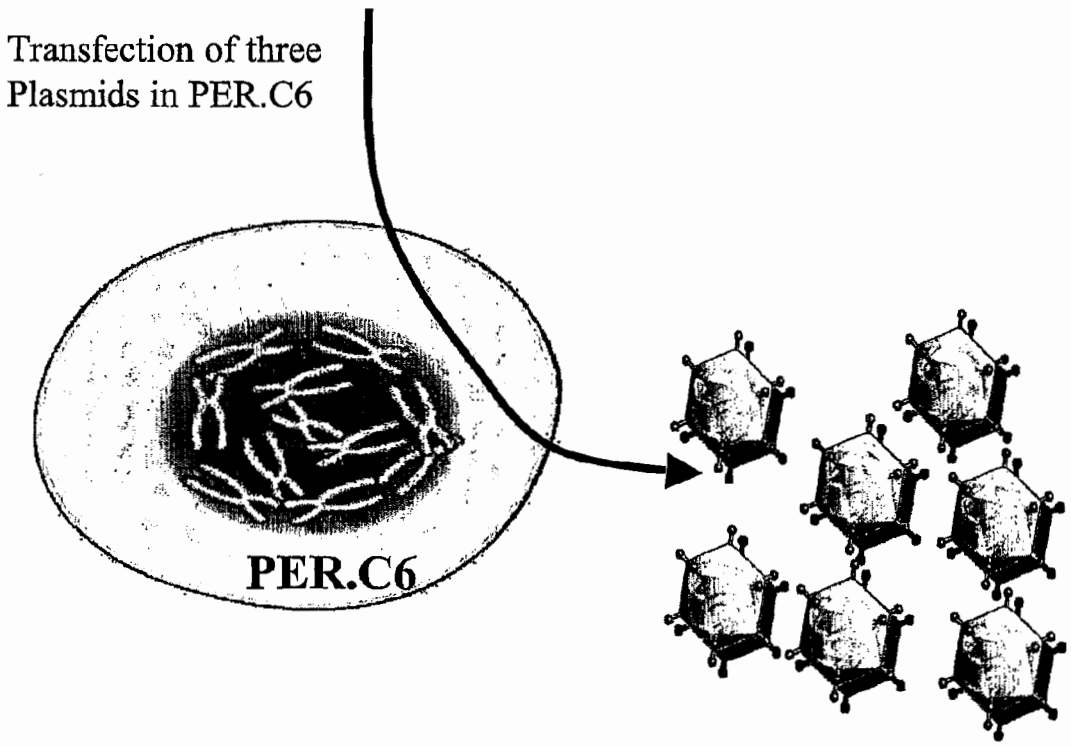


Fig. 29

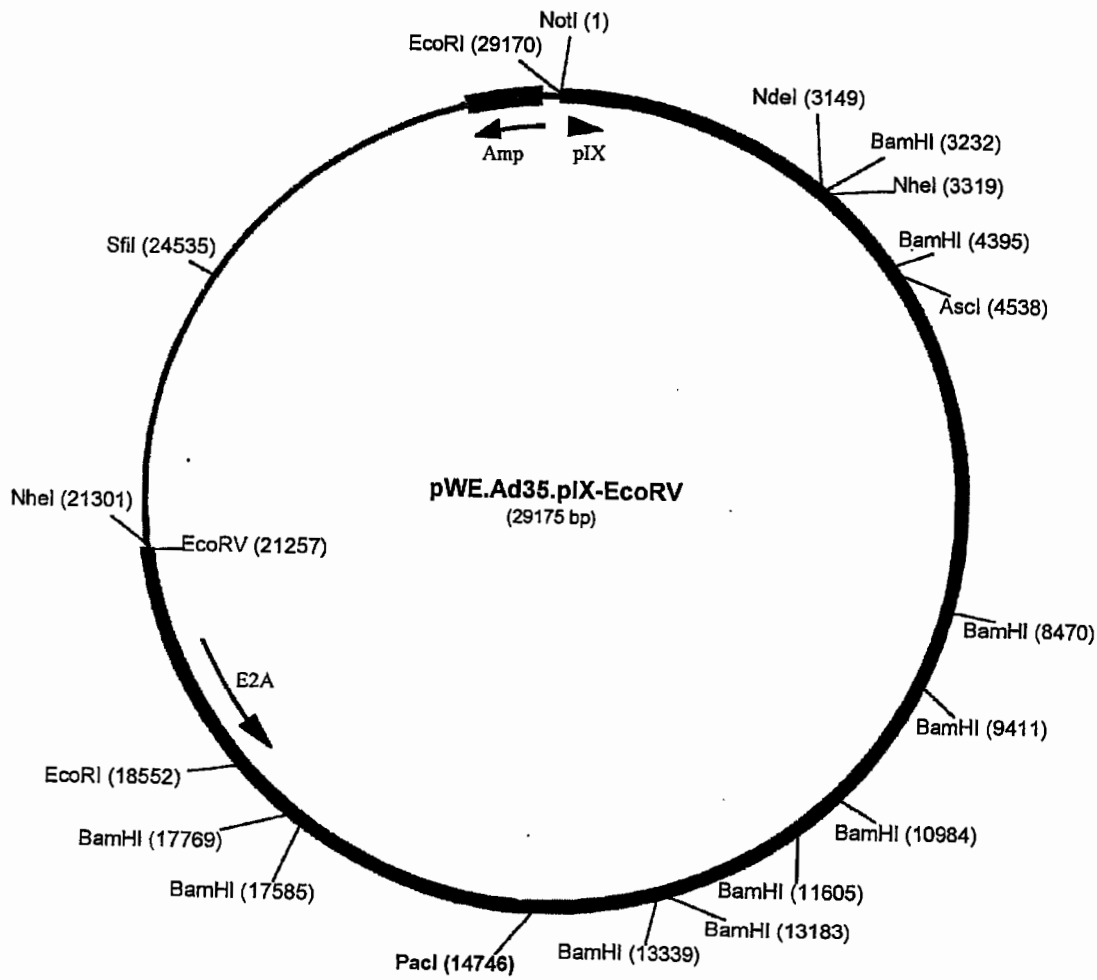

NotI (1)
EcoRI (29170)
NdeI (3149)
BamHI (3232)
NheI (3319)
BamHI (4395)
AscI (4538)
SfiI (24535)
Amp
pIX
pWE.Ad35.pIX-EcoRV
(29175 bp)
NheI (21301)
EcoRV (21257)
BamHI (8470)
E2A
BamHI (9411)
EcoRI (18552)
BamHI (10984)
BamHI (17769)
BamHI (17585)
BamHI (11605)
BamHI (13183)
PacI (14746)
BamHI (13339)

Fig. 30

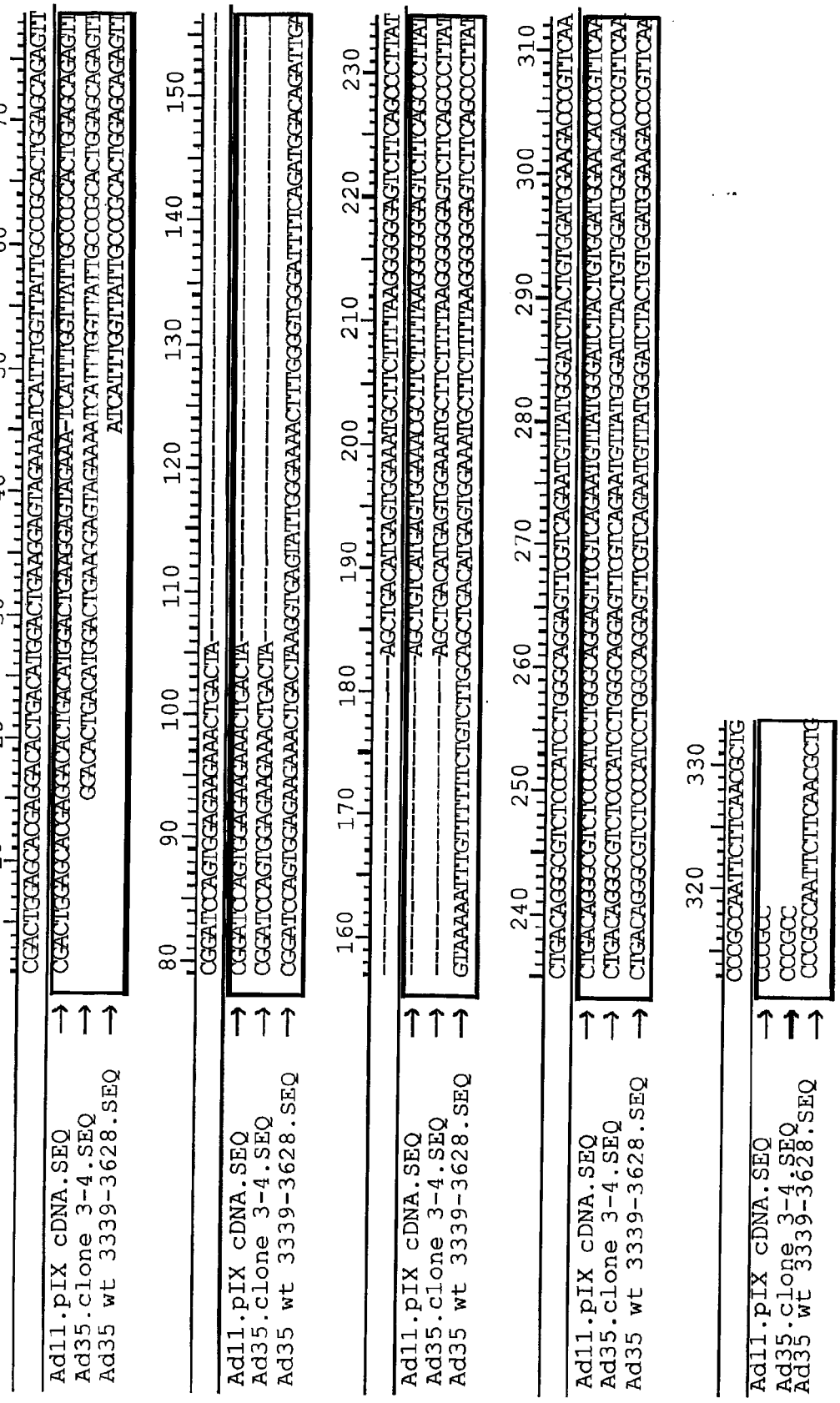


Fig. 31.

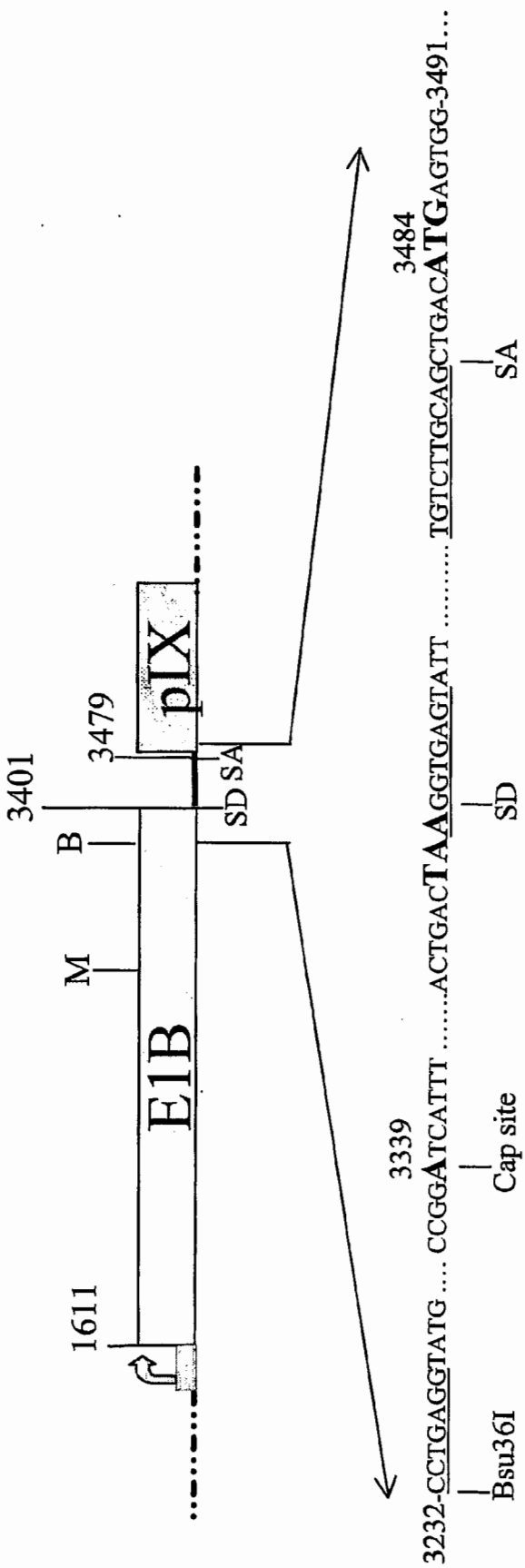
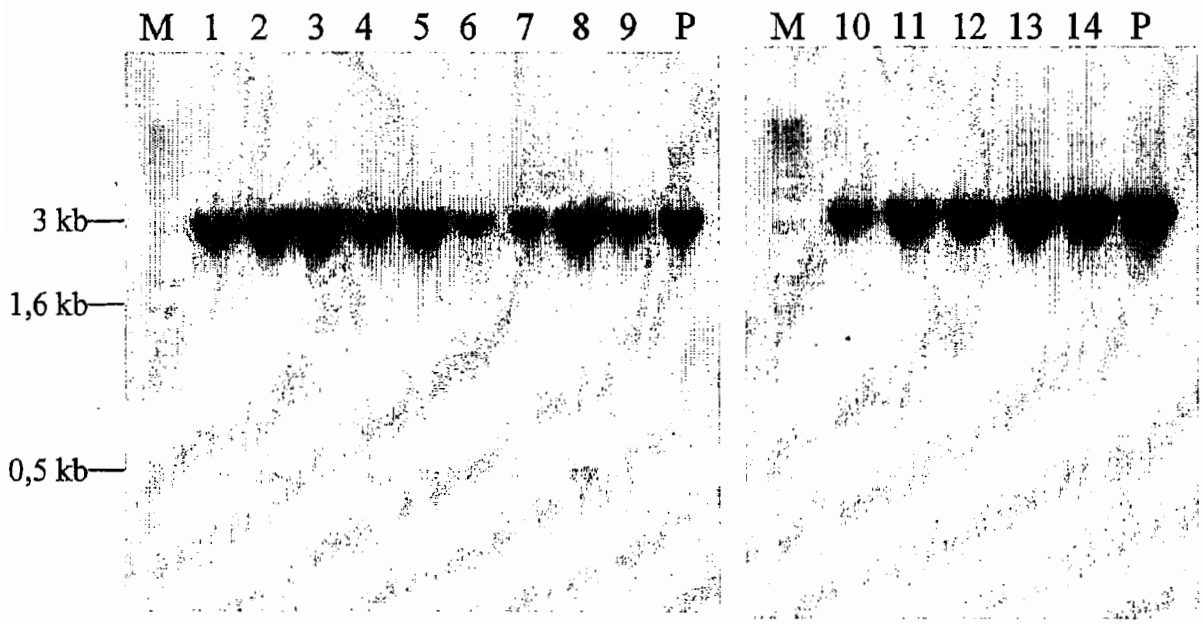

1611
M
B
3401
3479
SD SA
pIX
E1B
3484
3339
3232-CCTGAGGTATG .... CCGGATCATTT .....ACTGACTAAGGTGAGTATT ..... TGTCTTGCAGCTGACATGAGTGG-3491...
Bsu36I
Cap site
SD
SA

Fig. 32.


M 1 2 3 4 5 6 7 8 9 P
M 10 11 12 13 14 P
3 kb
1,6 kb
0,5 kb
Ad35.AdAptBsuLuc5Orf6
Ad35.AdAptBsuLuc