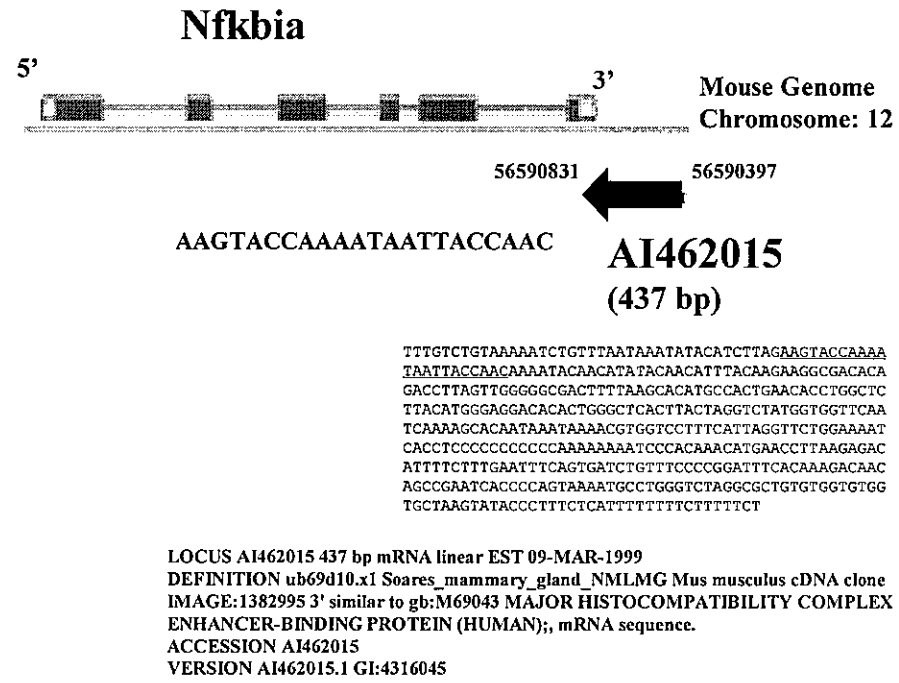
Figure 1



LOCUS AI462015 437 bp mRNA linear EST 09-MAR-1999
DEFINITION ub69d10.x1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone IMAGE:1382995 3' similar to gb:M69043 MAJOR HISTOCOMPATIBILITY COMPLEX ENHANCER-BINDING PROTEIN (HUMAN);, mRNA sequence.
ACCESSION AI462015
VERSION AI462015.1 GI:4316045

Figure 2

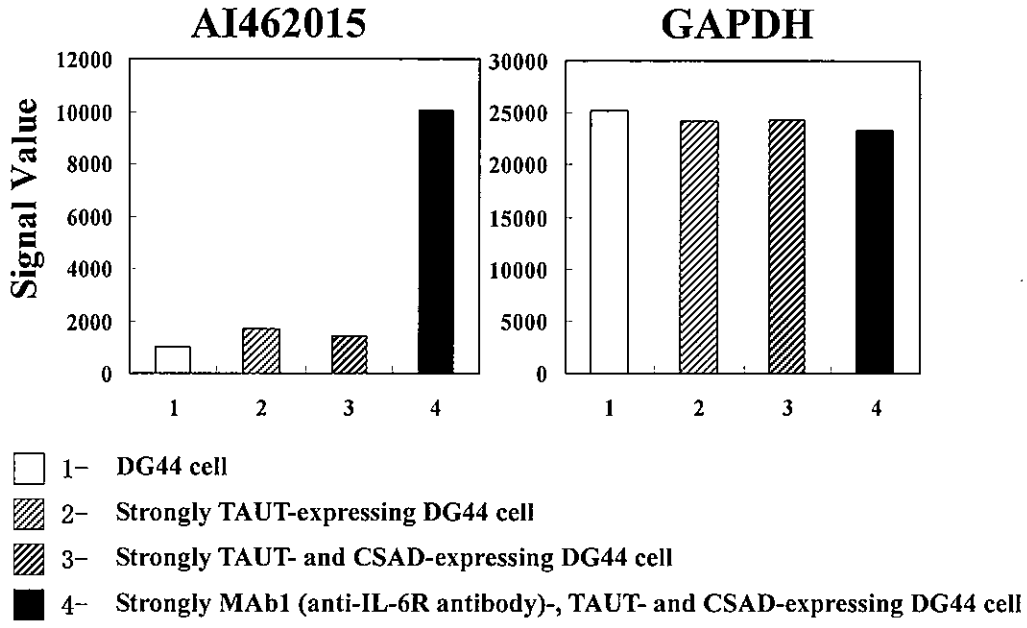


Figure 3

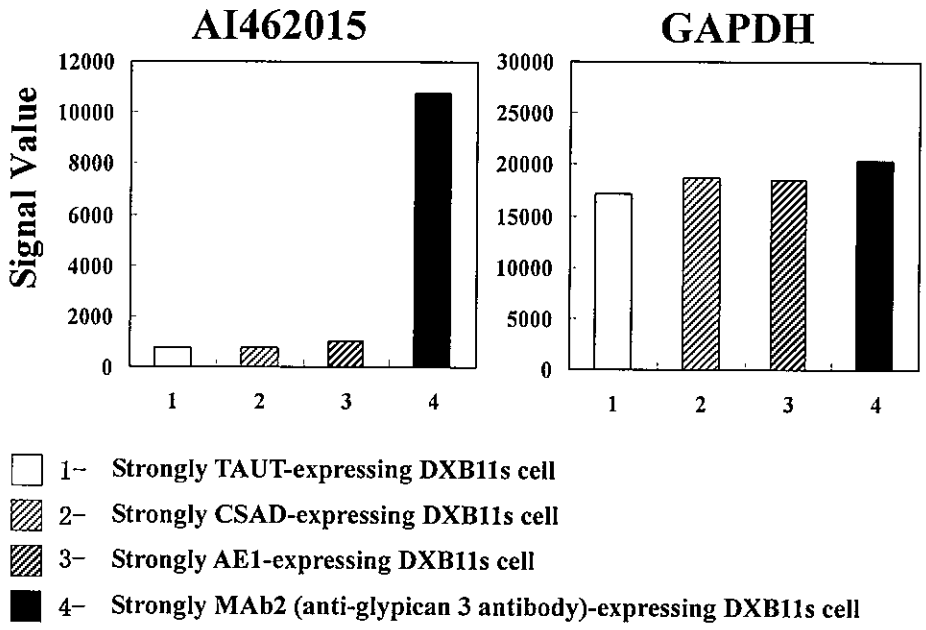


Figure 4

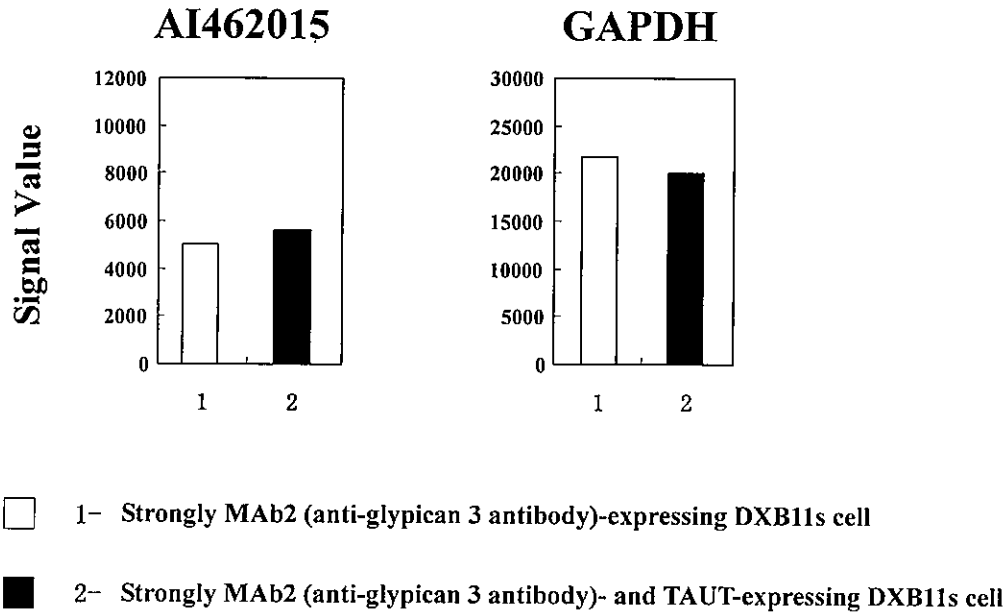
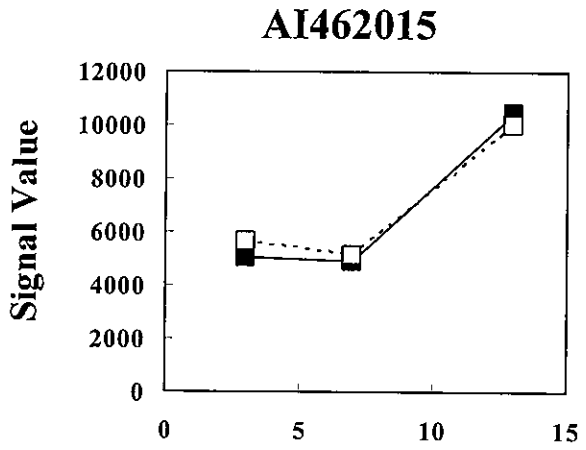


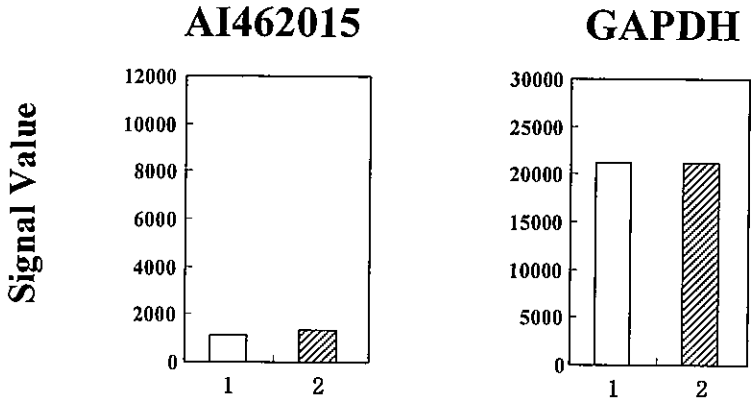
Figure 5



■ 1- Strongly MAb2 (anti-glypican 3 antibody)-expressing DXB11s cell

□ 2- Strongly MAb2 (anti-glypican 3 antibody)- and TAUT-expressing DXB11s cell

Figure 6



□ 1- Strongly MAb1 (anti-IL-6R antibody)-expressing DXB11s cell (Hy-Fish added)

▨ 2- Strongly MAb1 (anti-IL-6R antibody)-expressing DXB11s cell (Porcine Lysate added)

Figure 7

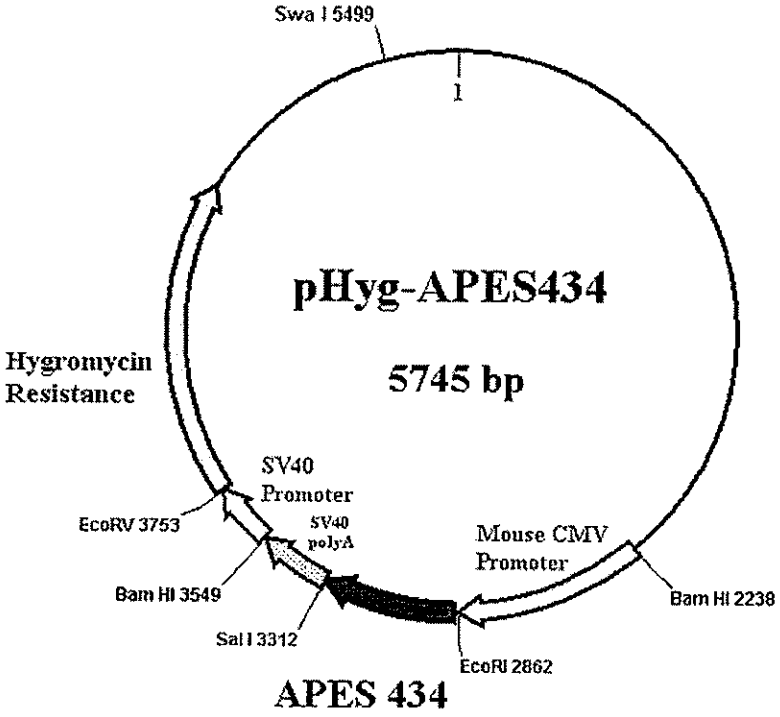


Figure 8

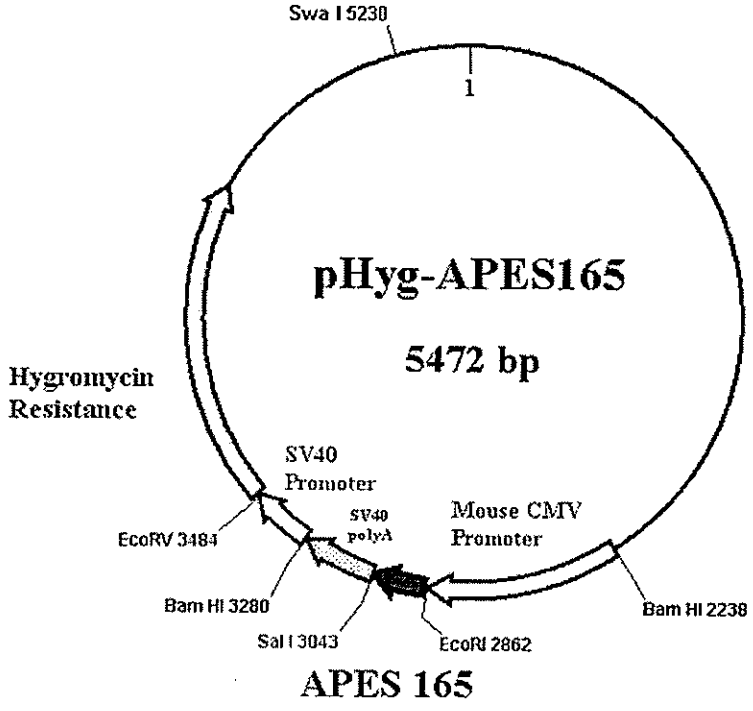


Figure 9

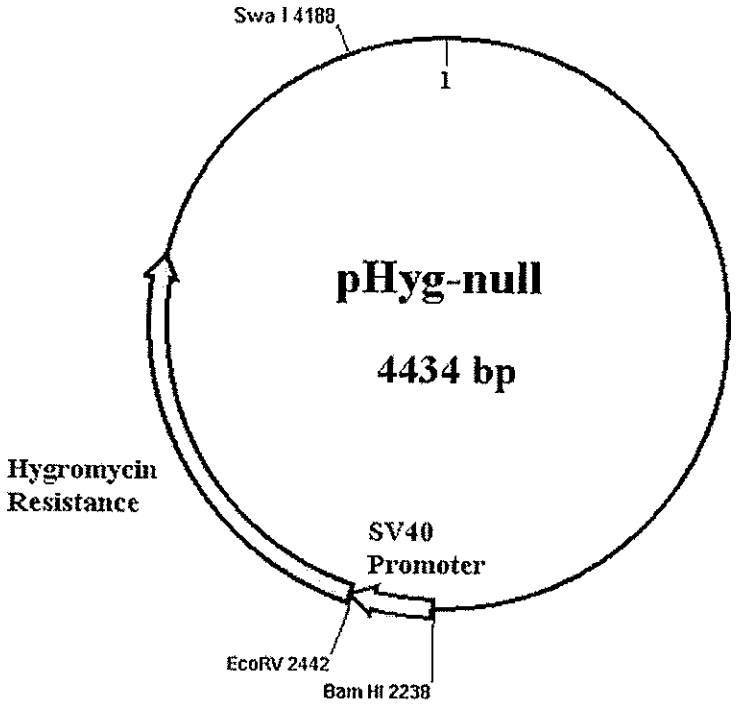


Figure 10

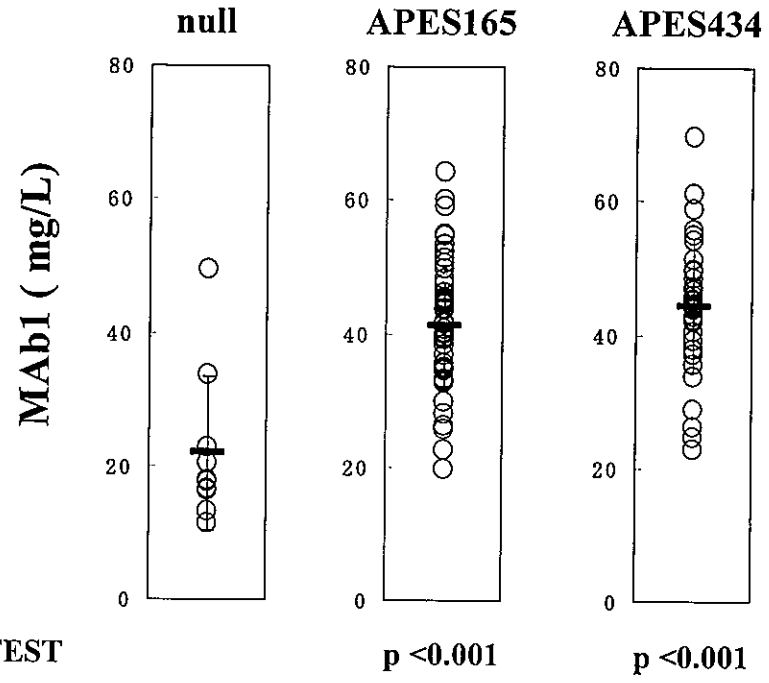
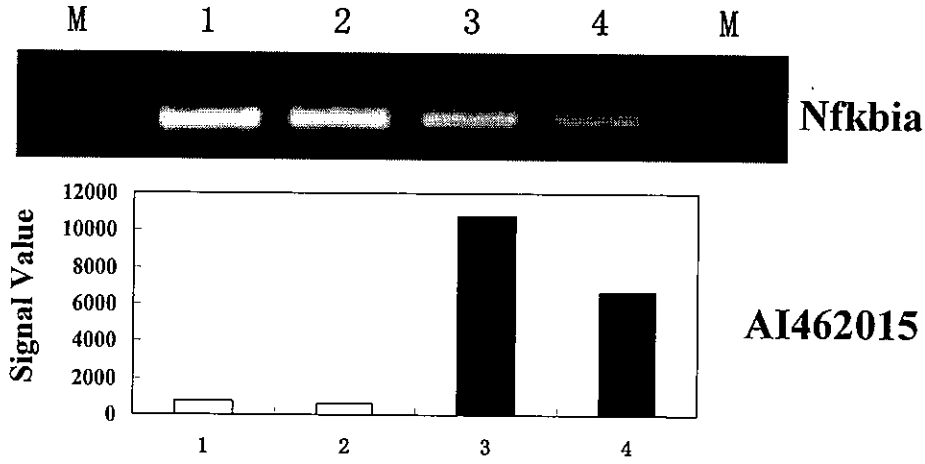


Figure 11



M- DNA MW marker (λ/HindIII + ϕX174/HaeIII)

1- Strongly TAUT-expressing DXB11s cell

2- Strongly CSAD-expressing DXB11s cell

3- Strongly MAb2 (anti-glypican 3 antibody)-expressing DXB11s cell

4- Strongly MAb2 (anti-glypican 3 antibody)- and TAUT-expressing DXB11s cell

Figure 12

A part of Hamster Nfkbia mRNA (134 bp)

```
          10         20         30         40         50
agtacccggatacagcagcagctgggccagctgacccgggaaaatcttca

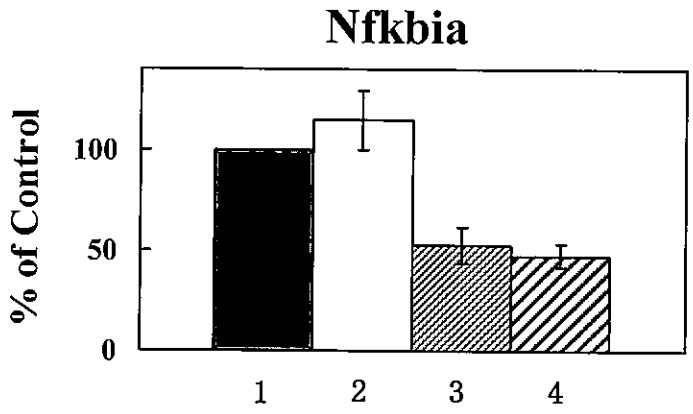
          60         70         80         90        100
gatgctgcccgagagtgaggatgaggagagctacgacacagagtcagaat

         110        120        130
tcacggaggatgagctgccctatgatgactgtgt
```

TaqMan Probe Set for Hamster Nfkbia mRNA

5′- cagctgacccgggaaaatc	Tm 59℃	19mer
5′- tgactctgtgtcgtagctctcctc	Tm 59℃	24mer
5′- FAM-tcagatgctgcccgagagtgagga-TAMRA	Tm 68℃	24mer

Figure 13



1- **Strongly TAUT-expressing DXB11s cell**

2- **Strongly CSAD-expressing DXB11s cell**

3- **Strongly MAb2 (anti-glypican 3 antibody)-expressing DXB11s cell**

4- **Strongly MAb2 (anti-glypican 3 antibody)- and TAUT-expressing DXB11s cell**

Figure 14

ctctgggctcgaatggcatgggggacagcttttatatggttaactccgcccgttttatgactagaaccaatagttttaatgccaaa
tgcactgaaatcccctaatttgcaaagccaaacgccccctatgtgagtaatacggggacttttacccaatttcccaagcggaaa
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gggtgagtcaacaggaaagttccattggagccaagtacattgagtcaatagggactttccaatgggttttgcccagtacataag
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Figure 15

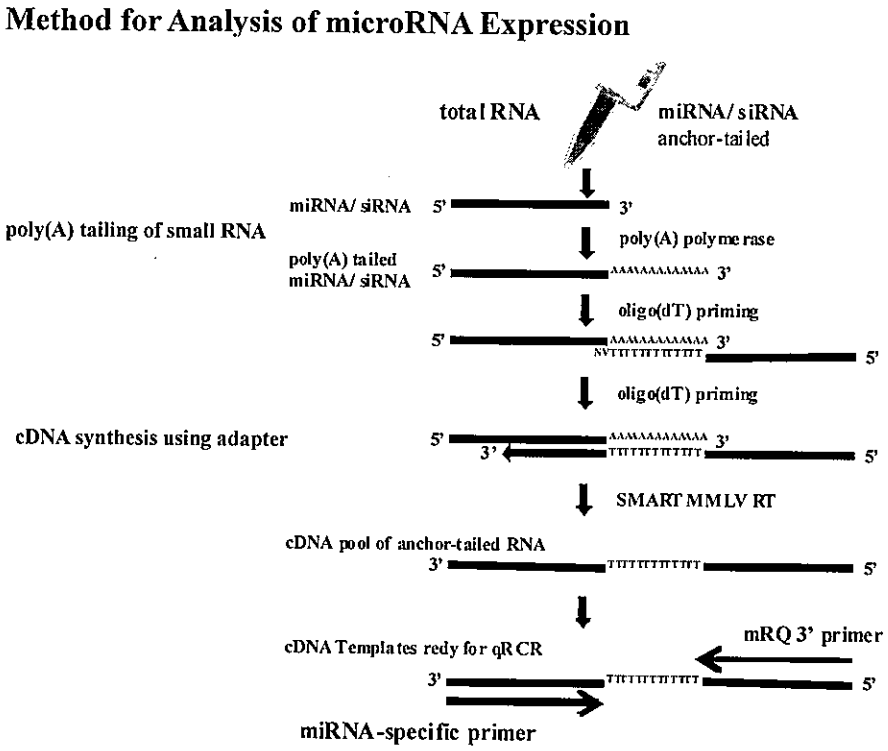
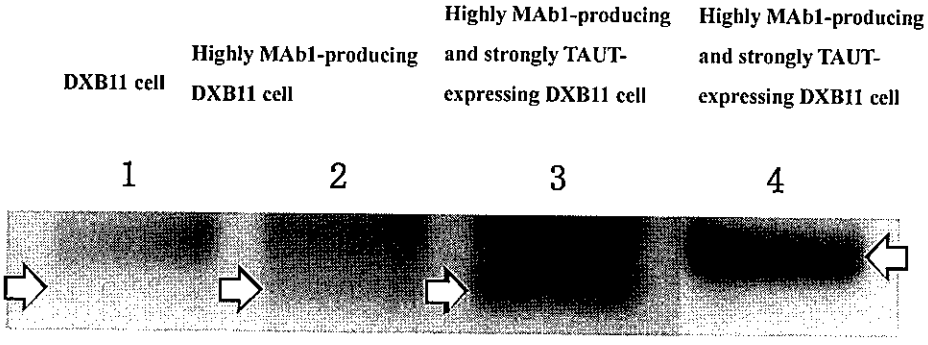


Figure 16



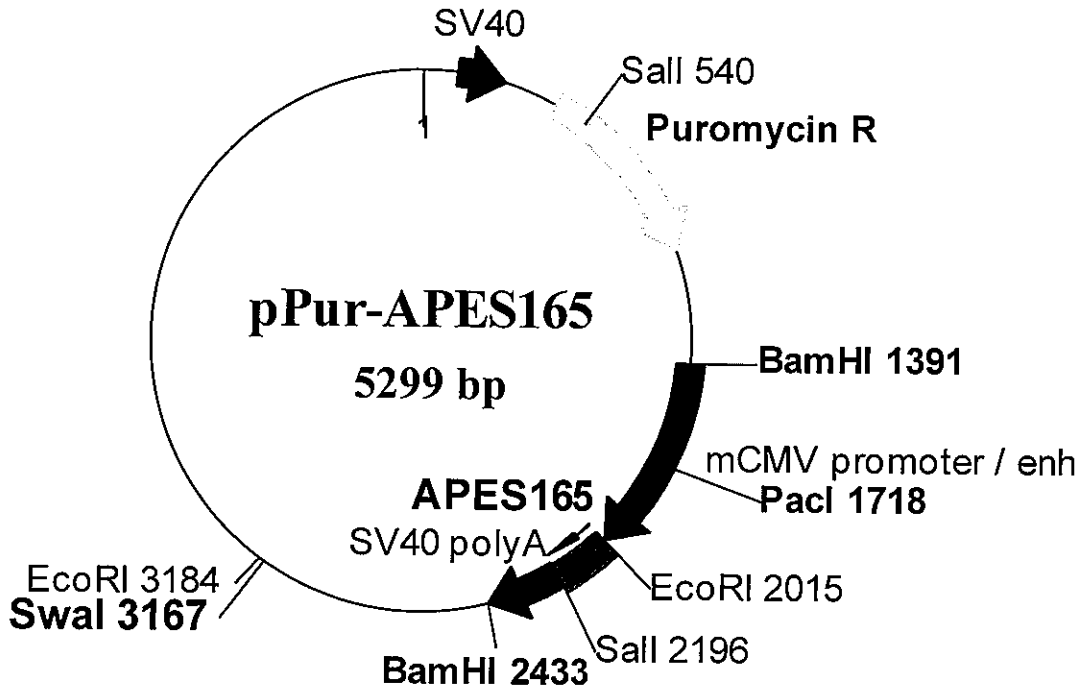
1, 2, 3 – APES 40-61 5' primer / mRQ 3' primer

4 – U6 snRNA 5' primer / mRQ 3' primer

⇨ – microRNA (APES 40-61)

⇦ – U6 snRNA

Figure 17


SV40
SalI 540
Puromycin R
pPur-APES165
5299 bp
BamHI 1391
mCMV promoter / enh
PacI 1718
APES165
SV40 polyA
EcoRI 2015
EcoRI 3184
SwaI 3167
SalI 2196
BamHI 2433

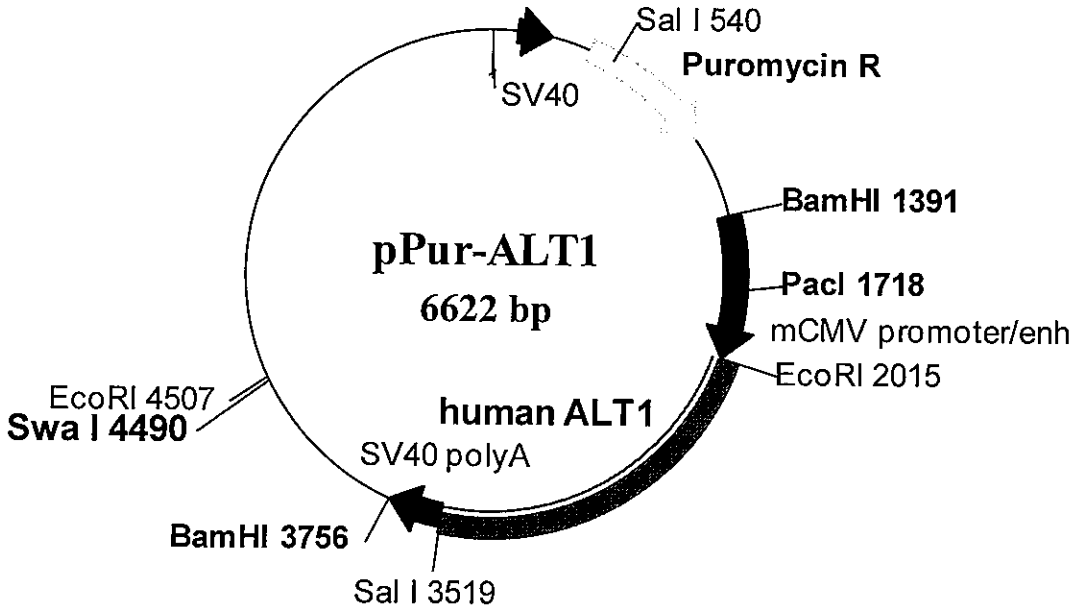

Sal I 540
Puromycin R
SV40
BamHI 1391
pPur-ALT1
6622 bp
PacI 1718
mCMV promoter/enh
EcoRI 2015
EcoRI 4507
Swa I 4490
human ALT1
SV40 polyA
BamHI 3756
Sal I 3519

Figure 18

MAb1-producing strain	Highest cell density (x10e6 cells/mL)	Amount of antibody production (g/L/14 days)
Strongly APES165-expressing strain	11.5 ±1.7	4.4±0.6
Strongly ALT1-expressing strain	8.9 ±1.8	4.0±0.6
Parent strain	4.1	3.4

Shaker fed-batch culture (n=3)

Figure 19

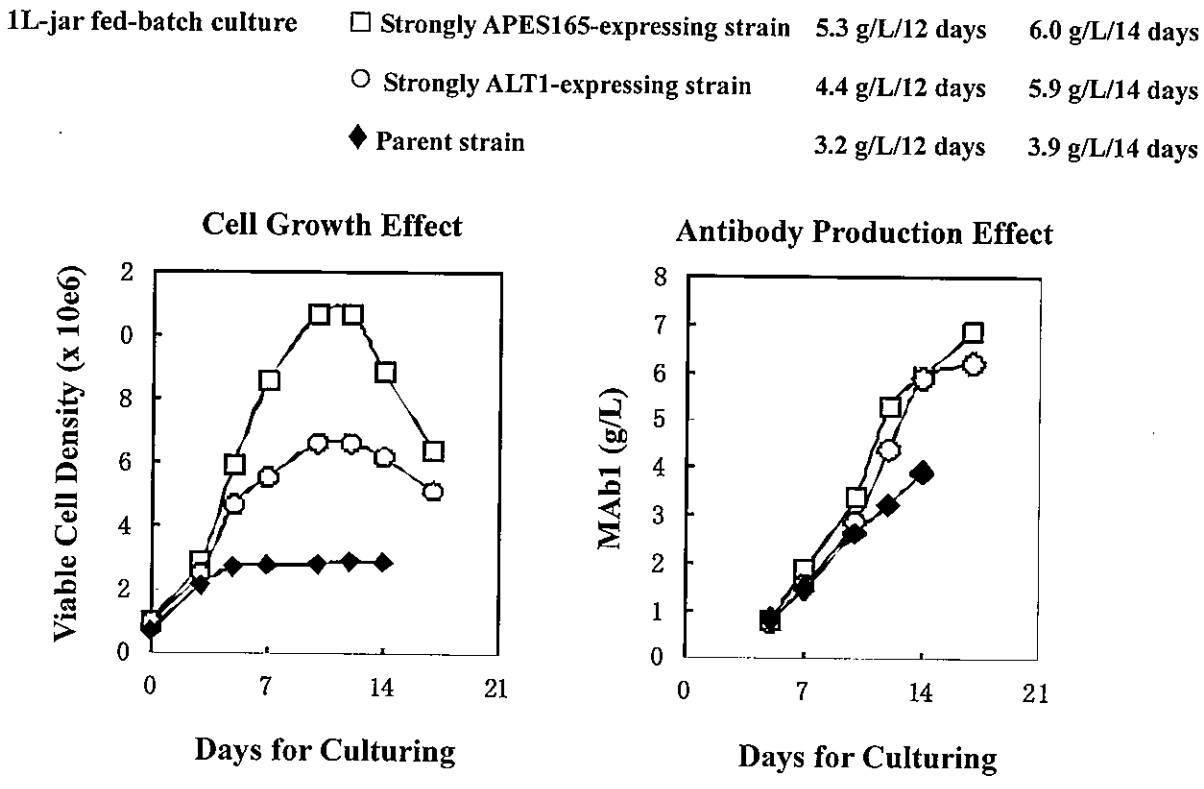


Figure 20

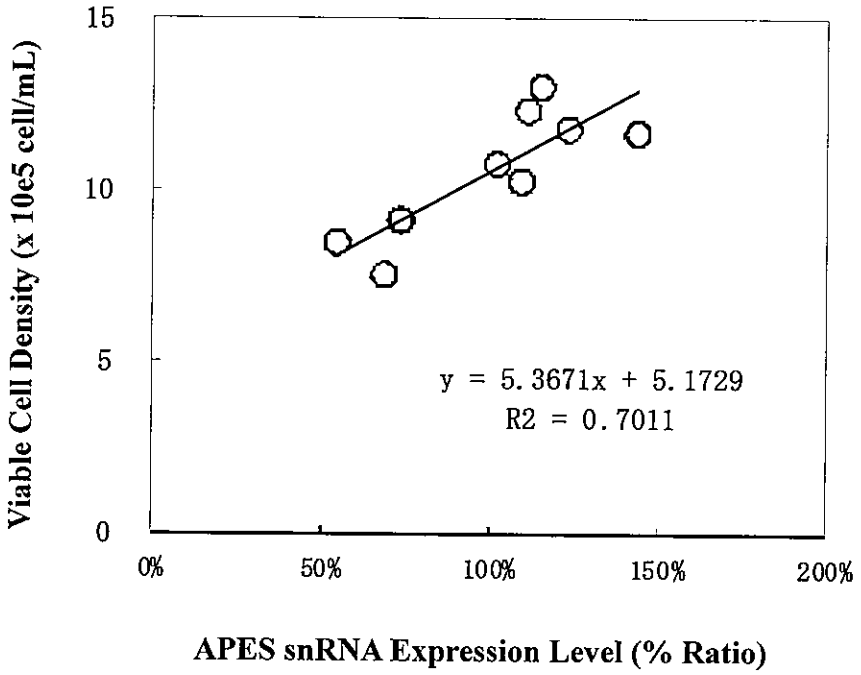


Figure 21

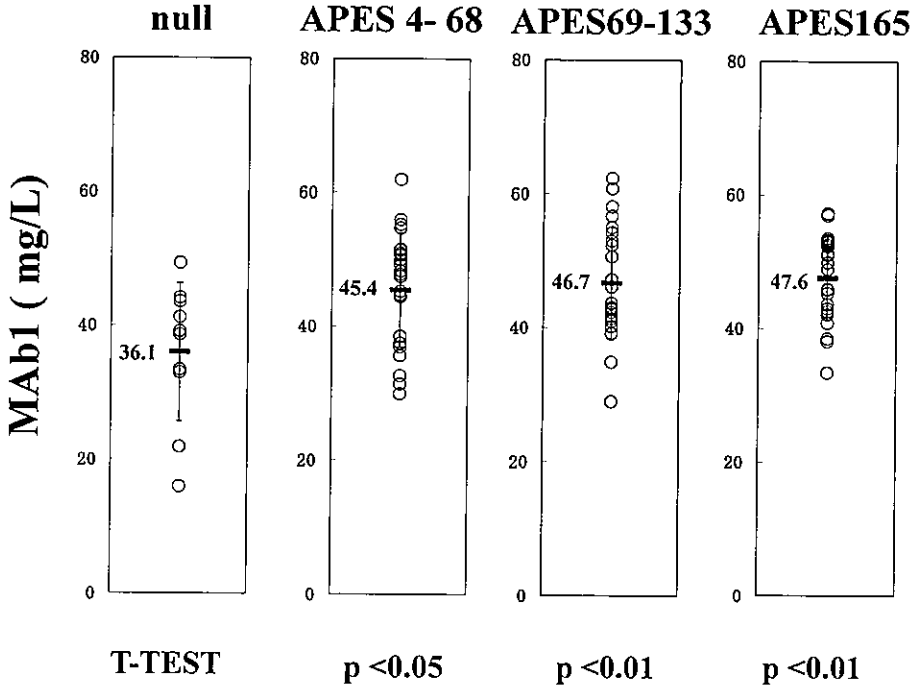


Figure 22

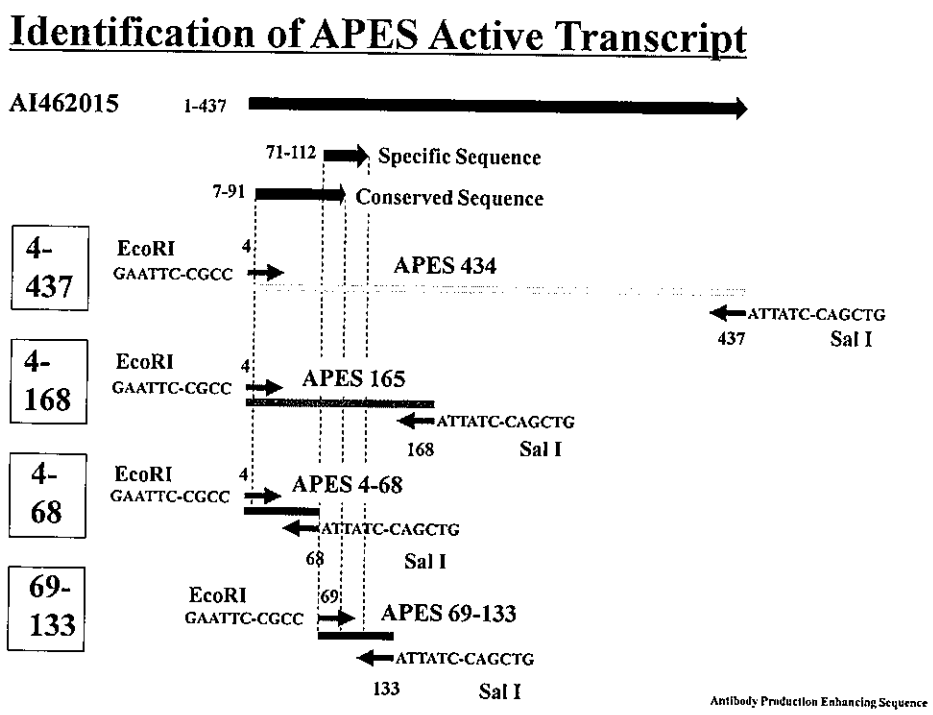


Figure 23

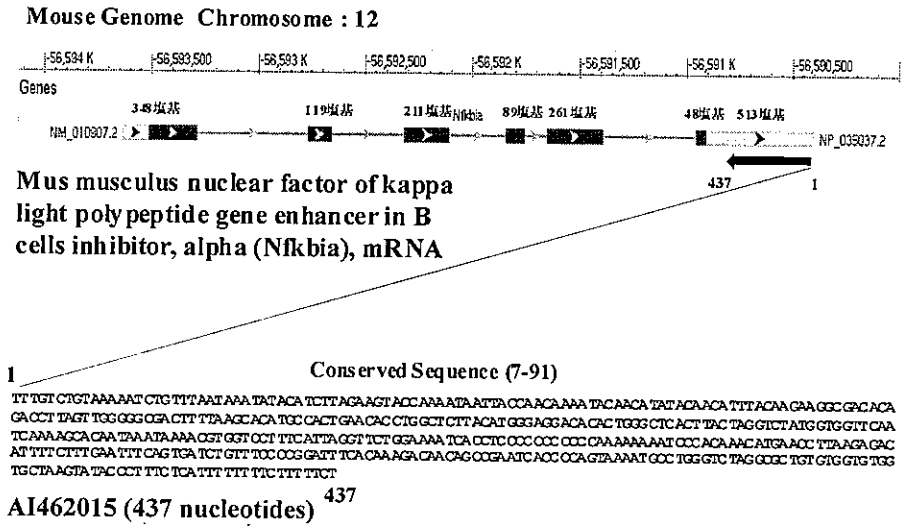


Figure 24

```
>gb|JH001217.1| Query1 on Cricetulus griseus cell line CHO-K1 unplaced genomic scaffold
scaffold4235, whole genome shotgun sequence Length=486540 Score = 378 bits (418), Expect = 3e-102
Identities = 352/440 (80%), Gaps = 33/440 (7%) Strand=Plus/Minus

Query 3      TGTCTGTAAAAATCTGTTTAATAAATATACATCTTAGAAGTACCAAAATAATTACCAACA 62      (AI462015)
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 385673 TGTCTGTAAAAATCTGTTTAATAAATATACATCTTAGAAGTACCAAAATAATTACCAACA 385614 (CHO-K1 genome)

Query 63     AAATACAACATATACAACATTTACAAGAAGGCGACACAGACCTTAGTTGGGGGCGACTTT 122     (AI462015)
             ||||||| |||||||||||||||||||| || ||| | |||| ||| ||| | ||||
Sbjct 385613 AAATACACCATATACAACATTTACAAGAGGGTAACAAAAACCTCAGTCGGGAGTGACT-- 385556 (CHO-K1 genome)

Query 123    TAAGCACATGCCACTGAACACCTGGCTCTTACATGGGAGGACACACTGGGCTCACTTACT 182     (AI462015)
             ||||||| ||||| |||||||||| || ||||| ||||||| || |||||| |||
Sbjct 385555 --AGCACATACCACTCAACACCTGGTTC-TACATGTGAGGACATACCAGGCTCAGCTACC 385499 (CHO-K1 genome)

Query 183    AGGTCTATGGTGGTTCAATCAAAAGCACAATAAATAAAACGTGGT-CCTTTCATTAGGTT 241     (AI462015)
             || |||| ||||| ||||||||||||||||| || ||||| |||||||| || |
Sbjct 385498 AGATCTA---CCGTTCAGTCAAAAGCACAATAAATAGAATGTGGTCCCTTTCATCAG--T 385444 (CHO-K1 genome)

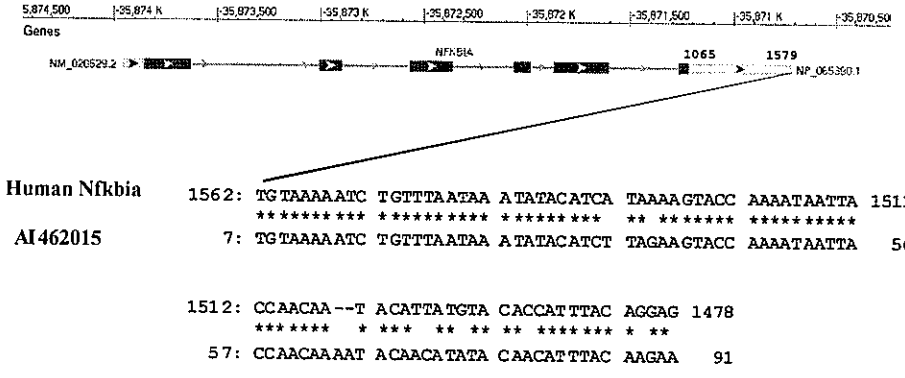
Query 242    CTGGAAAATCACCTccccccccccaaaaaaaTCCCACAAACATGAACCTTAAGAGACA 301     (AI462015)
             |||||||| |||||||| |||| | ||| || ||| | |||| |||||
Sbjct 385443 CTGGAAAACCACCTCCC----------AAAACCTCACGAATGTGAGCTTTAAAAGACA 385396 (CHO-K1 genome)

Query 302    TTTTCTTTGAATTTCAGTGATCTGTTTCCCCGGATTTCACAAAGACAACA----GCCGAA 357     (AI462015)
             |||||||||||||| || ||||||||||||||| |||||||||| | |||| ||| |
Sbjct 385395 TTTTCTTTGAATTCCAATGATCTGTTTCCCC--ATTTCACAAAAATAACAATCTGCC--A 385340 (CHO-K1 genome)

Query 358    TCACCCCAGTAAAATGCCTGGGTCTAGGCGCTGTGTGGTGTGGTGCTAAGTATA-CCCTT 416     (AI462015)
             ||||| ||||| |||| |||| |||| |||| |||||||| |||||||| |||||
Sbjct 385339 TCACCAGAGTAAGATGCTTGGGGGCAGGCTGTGTGCAGTGTGGTGGTAAGTATATCCCTT 385280 (CHO-K1 genome)

Query 417    TC-TCAttttttttctttttt 435
             || |  |||||||||||| ||
Sbjct 385279 TCTTTCTTTTTTTCTTCTT 385260
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Figure 25a

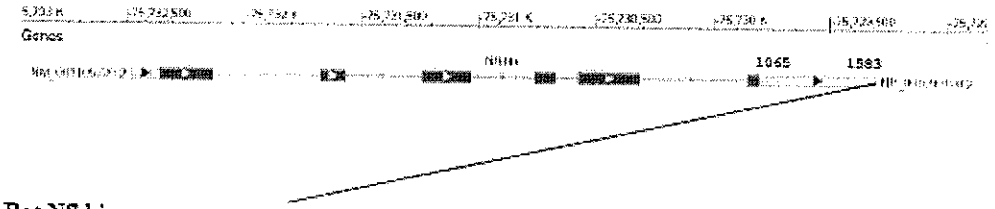



```
Human Nfkbia  1562: TGTAAAAATC TGTTTAATAA ATATACATCA TAAAAGTACC AAAATAATTA 1511
                    ********** ********** *********  ** ******* **********
AI462015         7: TGTAAAAATC TGTTTAATAA ATATACATCT TAGAAGTACC AAAATAATTA   56

              1512: CCAACAA--T ACATTATGTA CACCATTTAC AGGAG 1478
                    *******  * ***  ** ** ** ******* * **
                 57: CCAACAAAAT ACAACATATA CAACATTTAC AAGAA   91
```

Matching = 75/85 (88%)

Figure 25b

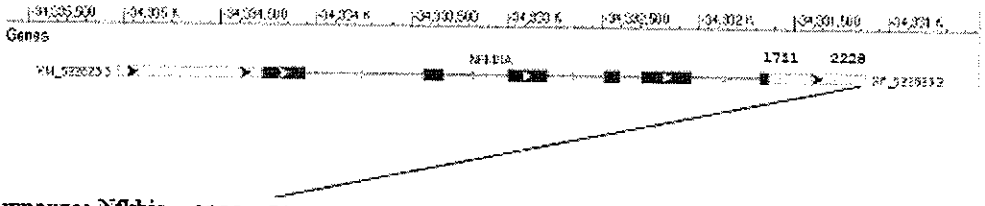



```
Rat Nfkbia      1562: TGTAAAAATC TGTTTAATAA ATATACATCT TAGAAGTACC AAAATAATTA 1511
                      ********** ********** ********** ********** **********
AI462015           7: TGTAAAAATC TGTTTAATAA ATATACATCT TAGAAGTACC AAAATAATTA   56

                1512: CCAACAAAAT ACACCATATA CAACATTTAC AAGAA 1478
                      ********** *** ****** ********** *****
                  57: CCAACAAAAT ACAACATATA CAACATTTAC AAGAA   91
```

Matching = 84/85 (99%)

Figure 25c

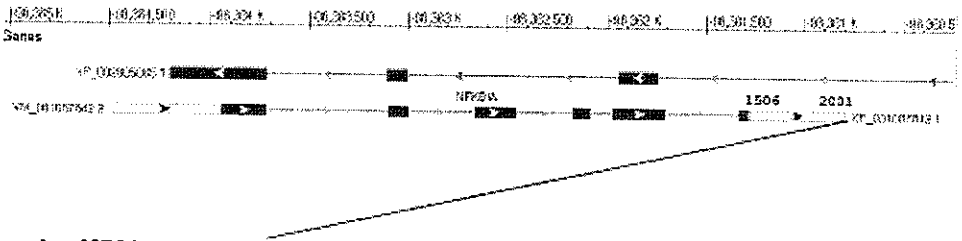



```
Chimpanzee Nfkbia 2209: TGTAAAAATC TGTTTAATAA ATATACATCA TAAAAGTACC AAAATAATTA 2158
                        ********** ********** *********  ** ******* **********
AI462015             7: TGTAAAAATC TGTTTAATAA ATATACATCT TAGAAGTACC AAAATAATTA   56

                  2159: CTAAC--AAT ACATTATGTA CATCATTTAC AGGAGGGTAA C 2121
                        * ***  *** ***  ** ** ** ******* *  **    *
                    57 : CCAACAAAAT ACAACATATA CAACATTTAC A--AG----A A   91
```

Matching = 75/85 (88%)

Figure 25d

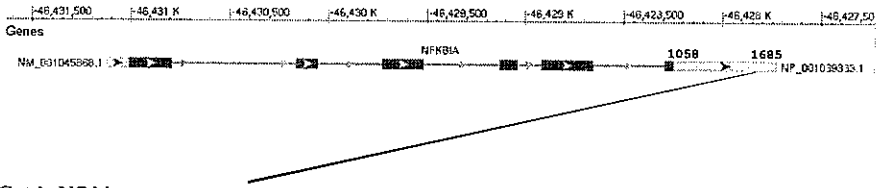



```
Rhesus monkey Nfkbia 1995: TGGAAAAATC TGTTTAATAA ATATACATAA TAAAAGTACC AAAATAATTA 1944
                     ** ******* ********** ********   ** ******* **********
AI462015          7: TGTAAAAATC TGTTTAATAA ATATACATCT TAGAAGTACC AAAATAATTA   56

                1945: CCAAC--AAT ACACTATGTA CACCATTTAC AGAAGGGTAA C 1907
                      *****  *** ***  ** ** ** *******   ***    *
                  57: CCAACAAAAT ACAACATATA CAACATTTAC --AAG----A A   91
```

Matching = 74/85 (87%)

Figure 25e




```
Cattle Nfkbia   1570: TGTAAAAATC TGTTTAATAA ATATACATCT TAAAAGTACC AAAATAATTA 1519
                      ********** ********** ********** ** ******* **********
AI462015           7: TGTAAAAATC TGTTTAATAA ATATACATCT TAGAAGTACC AAAATAATTA   56

                1520: CTGACAAAAT ACACTATGTA CACTATTTAC AGGAGGGGAA 1481
                      *  ******* ***  ** ** **  ****** *      ***
                  57: CCAACAAAAT ACAACATATA CAACATTTAC A-----AGAA   91
```

Matching = 76/85 (89%)