FIG. 1a

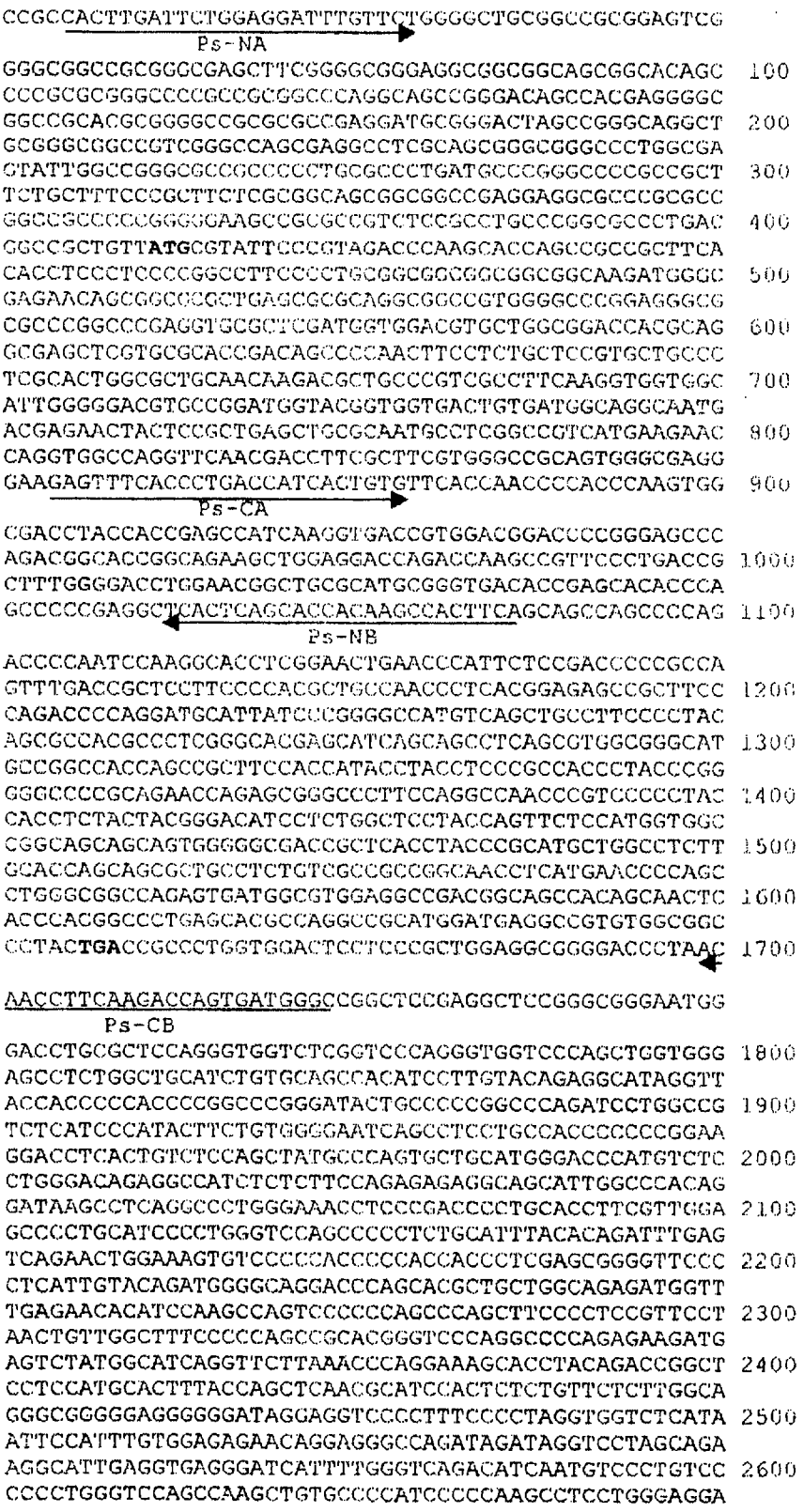


FIG. 1b

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TAATCTAACGTTTTCAAACACAAGGTCTCTTACAGGTATAGTTCCGTGAT
TATGATAGCTCTGTGATTATAAGCAACATCCCCGCCCCCTCTCCCCCCCG 2900
CGGACCCCCAGCTGCCTCCTGAGGGTGTGGGGTTATTAGGGTCTCAATAC
TTTCTCAAGGGGCTACACTCCCCATCAGGCAGCATCCCACCAGCCTGCAC 3000
CACAGGCTCCCCTGGGAGGACGAGGGAAACGCTGATGAGACGCTGGGCAT
CTCTCCTCTGTGGCTCTAGGACATCTGTCCAGGAGGCTGGGCGGAGGTGG 3100
GCAGGATGTGAGAGGTGGGGAGTACTGGCTGTGCGTGGCAGGACAGAAGC
ACTGTAAAGGGCTCTCCAGCCGCAGCTCAGCTGCACTGCGTTCCGAGGTG 3200
AAGTCTTGCCCCTGAATTTTGCAAAATGGGAAAGTGGGCGCTTGCCCAAG
GGCCAGGCTGCATGGATTCTCACATCAGAGTTCTCTGGCCCTAGAAAGGC 3300
TTAGAAAAGGCGTAAGGGAACTCATAAAGGCTAGCAGCATGCGGTATTTT
AACTTTCTGCCTCGGCCTCTGTGGATGCAGAAATCTGCCCTACAAAATGC 3400
TCTTCATTGGTTGTCTCTGTGAGAGCACTGTCCCCACCCAACCTGTCACA
ACGGCCAGAACCATACACCAGAGACACACTGGCAGGTTAGGCAGTCCTTC 3500
TGGTGATCCTATTCCATTCCCTCCTGCTGCGGTTTCTCTTGGCCTGTCCT
CACTGGAAAAACAGTCTCCATCTCCTCAAAATAGTTGCTGACTCCCTGCA 3600
CCCAAGGGGCCTCTCCATGCCTTCTTAGGAAGCAGCTATGAATCCATTGT
CCTTGTAGTTTCTTCCCTCCTGTTCTCTGGTTATAGCTGGTCCCAGGTCA 3700
GCGTGGGAGGCACCTTTGGGTTCCCAGTGCCCAGCACTTTGTAGTCTCAT
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ATTGCTCTTCCTACCCCATCCCCCATCCCCTGACAAAAAGTGACGGCAGC
CGTACTGAGTCTGTAAGGCCCAAAGTGGGTACAGACAGCCTGGGCTGGTA 3900
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CACTGATGTAGGAAGCACGAGGAAAGGAAGACGTTTTGATATAGTGTTAC 4000
TGTGAGCCTGTCAGTAGTGGGTACCAATCTTTTGTGACATATTGTCATGC
TGAGGTGTGACACCTGCTGCACTCATCTGATGTAAAACCATCCCAGAGCT 4100
GGCGAGAGGATGGAGCTGGGTGGAAACTGCTTTGCACTATCGTTTGCTTG
GTGTTTGTTTTTAACGCACAACTTGCTTGTACAGTAAACTGTCTTCTGTA 4200
CTATTTAACTGTA 3'
```

FIG. 1c

MRIPVDPSTSRRFTPPSPAFPCGGGGGKMGENSGALSAQAAVGPGGRARP
EVRSMVDVLADHAGELVRTDSPNFLCSVLPSHWRCNKTLPVAFKVVALGD
VPDGTVVTVMAGNDENYSAELRNASAVMKNQVARFNDLRFVGRSGRGKSF
TLTITVFTNPTQVATYHRAIKVTVDGPREPRRHRQKLEDQTKPFPDRFGD
LERLRMRVTPSTPSPRGSLSTTSHFSSQPQTPIQGTSELNPFSDPRQFDR
SFPTLPTLTESRFPDPRMHYPGAMSAAFPYSATPSGTSISSLSVAGMPAT
SRFHHTYLPPPYPGAPQNQSGPFQANPSPYHLYYGTSSGSYQFSMVAGSS
SGGDRSPTRMLASCTSSAASVAAGNLMNPSLGGQSDGVEADGSHSNSPTA
LSTPGRMDEAVWRPY

FIG. 2a

CCTTCTGCTTCCTAGCCCTGCTGTGGACAACTTAGGGTGCTCTTAGGTGG
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GGAGAAAAGACGACGGTCCATGCCAACTGGGGAAGGGCGAGGGTGTCTGC
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CAGGCAGTGCCTTGGCGAAGCTGTCCGCGGTCCCTGCGGCGCAGCCGGAG
CGCACGGGCCCAAGAAGAAGTGGGGTTGGACCCGCAGAGGCCACTTTCCA
CCCGCATGGAGAAAGAAAATTCTCTCCTCTGAAAGCGAGGGCCCTTAGCT
TTGCAGCCACTGCTGTTTTTCTTTTGCCACCGACGCGCGTACCGTTTCAC
GATGCAGGACCGTGGTTACATGCGTAAAGGAAAAAAAGAAAAACGCATTT
TGCAGGCCTCGTCGTGTTTTTCAAAGAGCCACAGGCCGCCACAACGAAGA

FIG. 2b

ACGACGCCGCGAGGCCTGCAAGATCCTGAAACTTGTTTTGAGGGGAGAGC
AGAGAGGAAAGGGGTTGTTGGCCCCAGGCTACTTAGGGTCCCTAGGAGAC
TCCCTTCCGCCTGTCCCCGGTTTGGCACAGGGGCCACCGAGGCTGGGACC
AAAGCCGCGCAGGGCTGGGAGCAGCAAAGGCCGCCGGCCGGGCGTGGACG
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CCGCTTCTCGCGGCAGCGGCGGCCGAGGAGGCGCCCGCGCCGGCCGCCCC
CGGGGGAAGCCGCGCCGTCTCCGCCTGCCCGGCGCCCTGACGGCCGCTGT
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CCCCGGCCTTCCCCTGCGGCGGCGGCGGCGGCAAGATGGGCGAGAACAGC
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FIG. 3

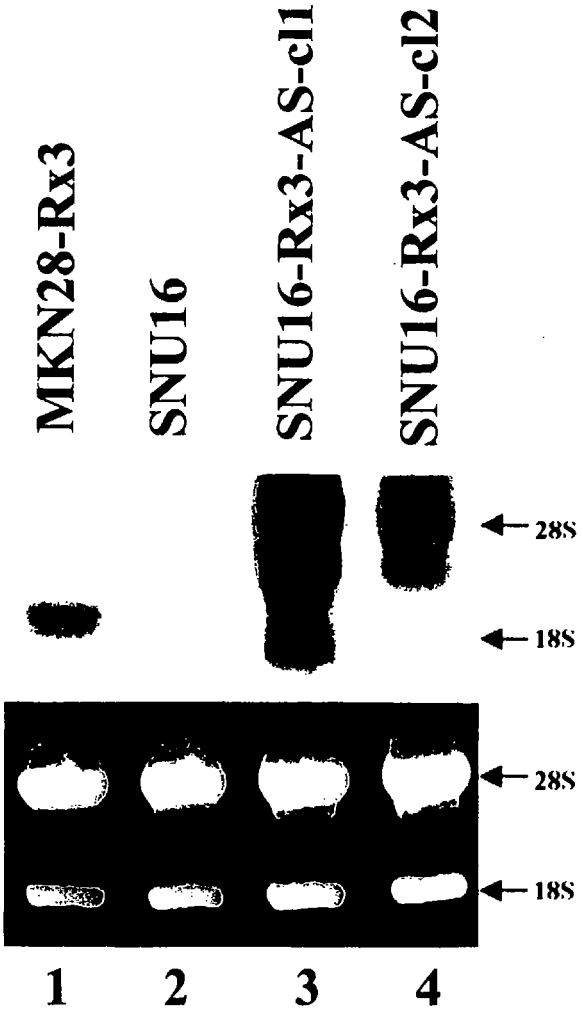

MKN28-Rx3
SNU16
SNU16-Rx3-AS-cl1
SNU16-Rx3-AS-cl2
28S
18S
28S
18S
1
2
3
4

FIG. 4a

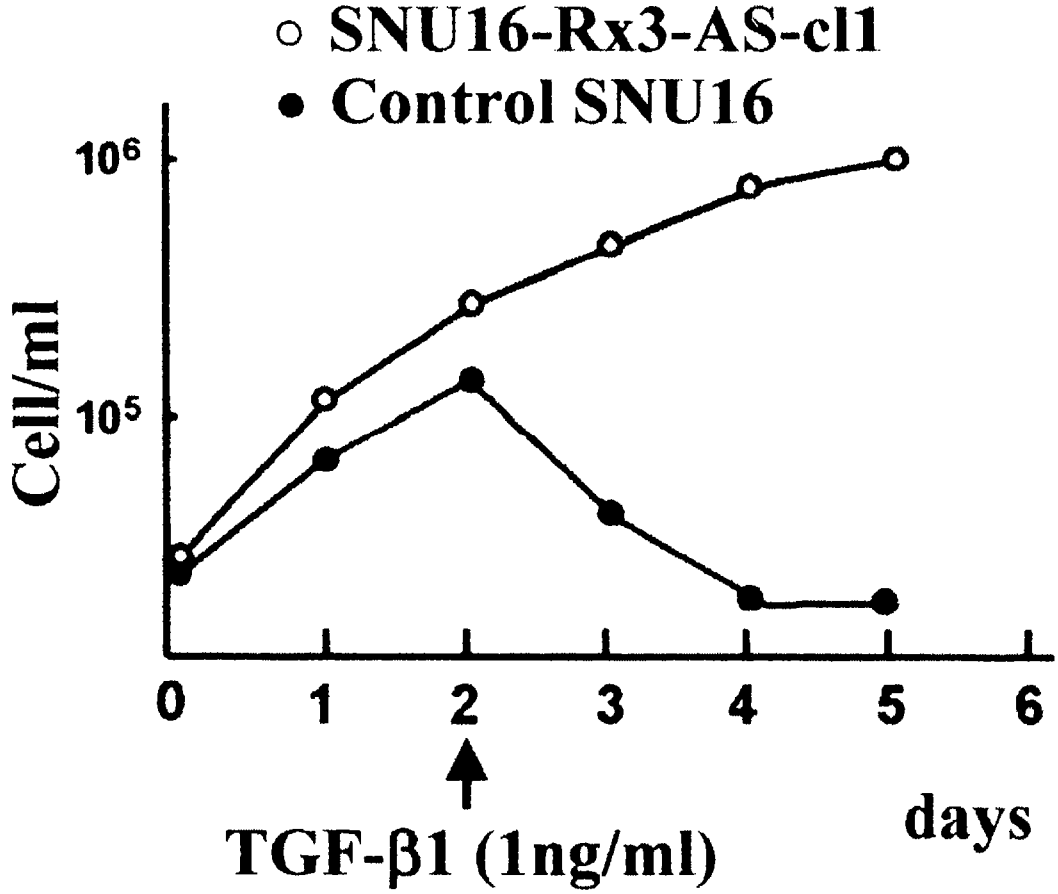

○ SNU16-Rx3-AS-cl1
● Control SNU16
Cell/ml
10^6
10^5
0
1
2
3
4
5
6
days
TGF-β1 (1ng/ml)

FIG. 4b

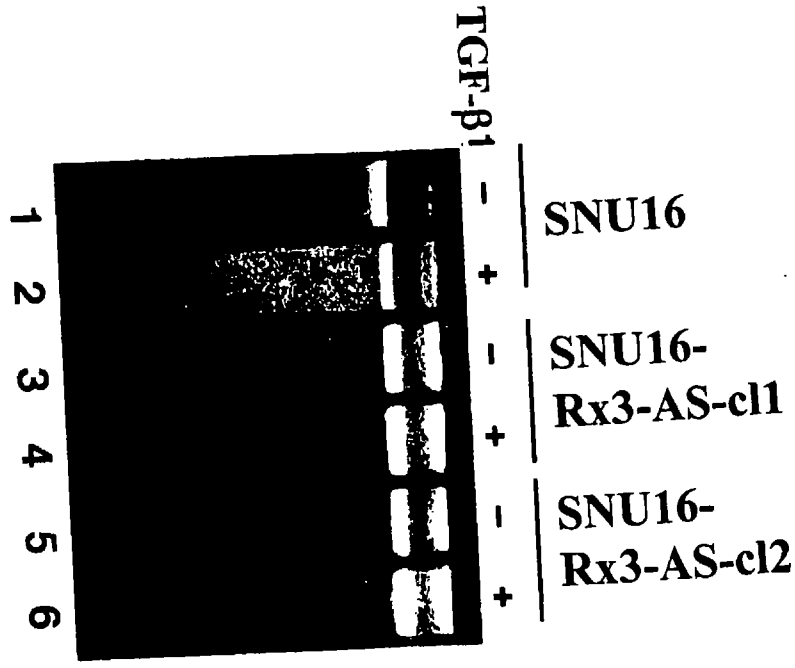


FIG. 5a

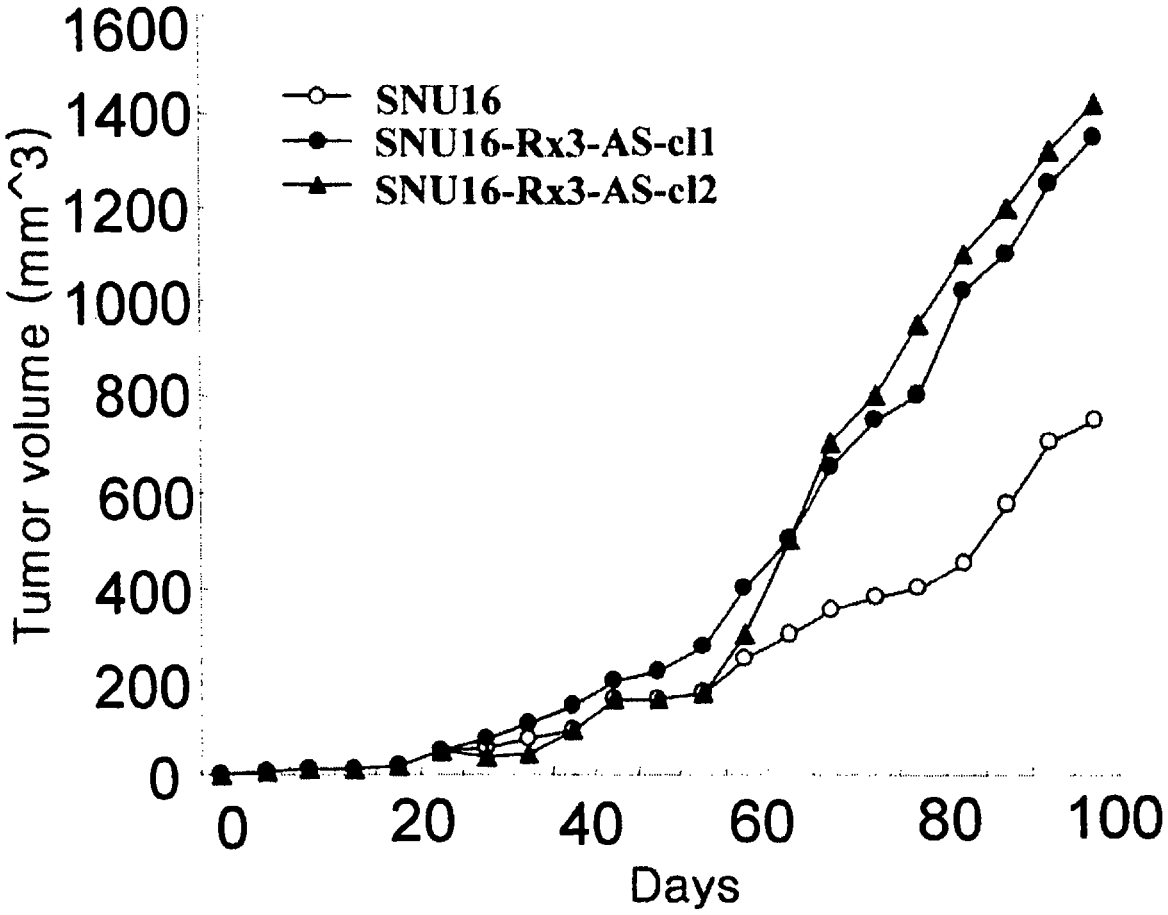

1600
1400
1200
1000
800
600
400
200
0
Tumor volume (mm^3)
SNU16
SNU16-Rx3-AS-cl1
SNU16-Rx3-AS-cl2
0
20
40
60
80
100
Days

FIG. 5b

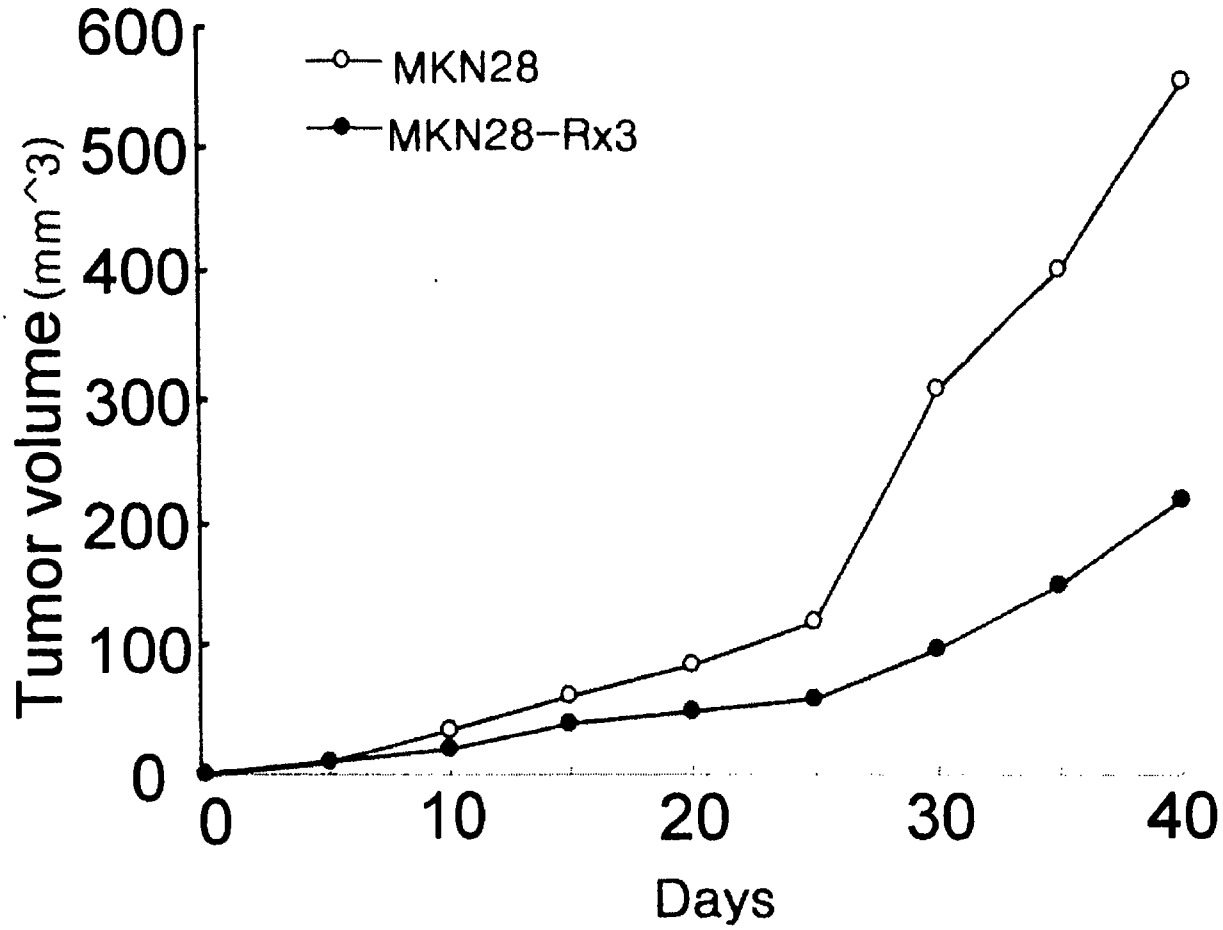

600
500
400
300
200
100
0
Tumor volume (mm^3)
MKN28
MKN28-Rx3
0
10
20
30
40
Days

FIG. 5c

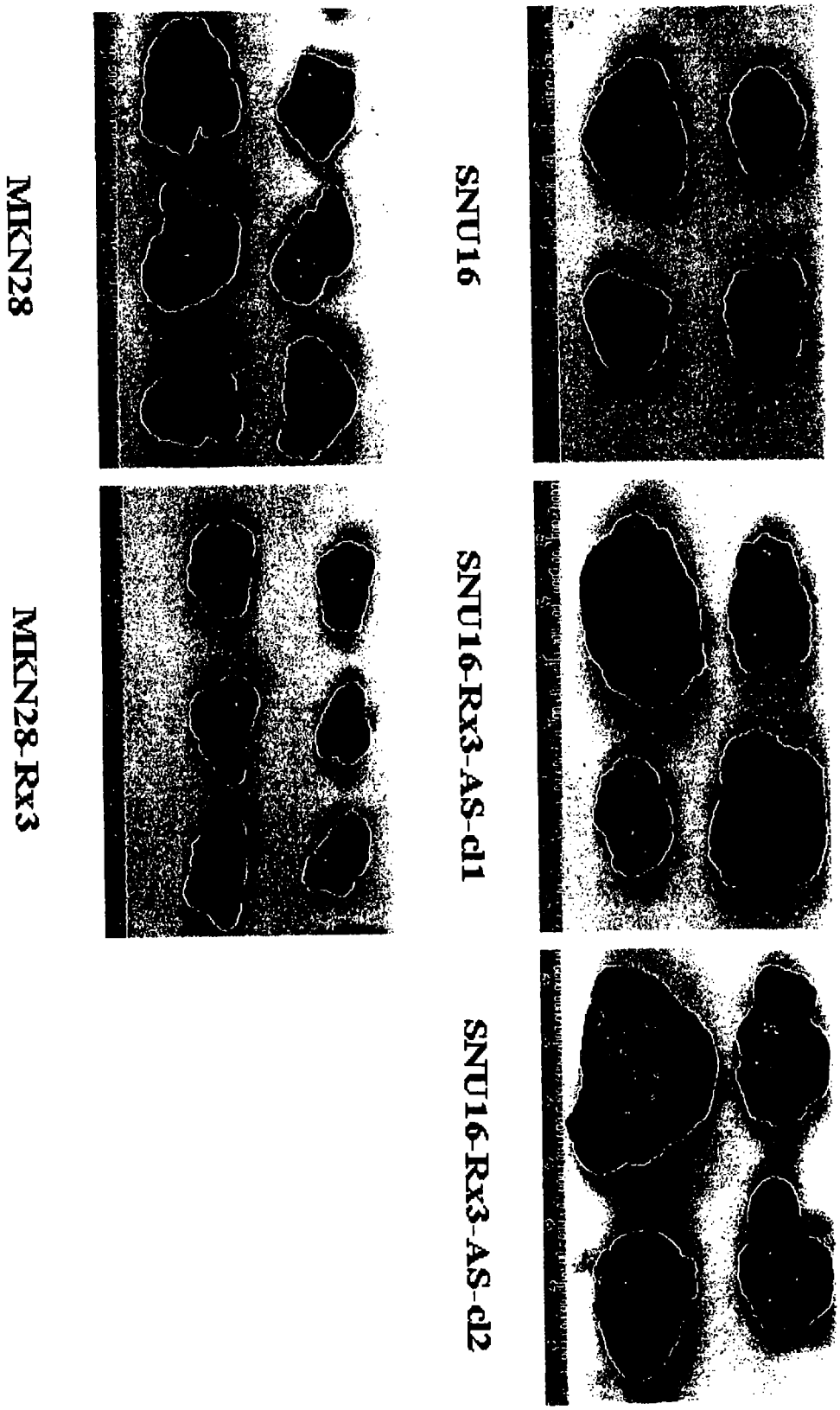


FIG. 6a

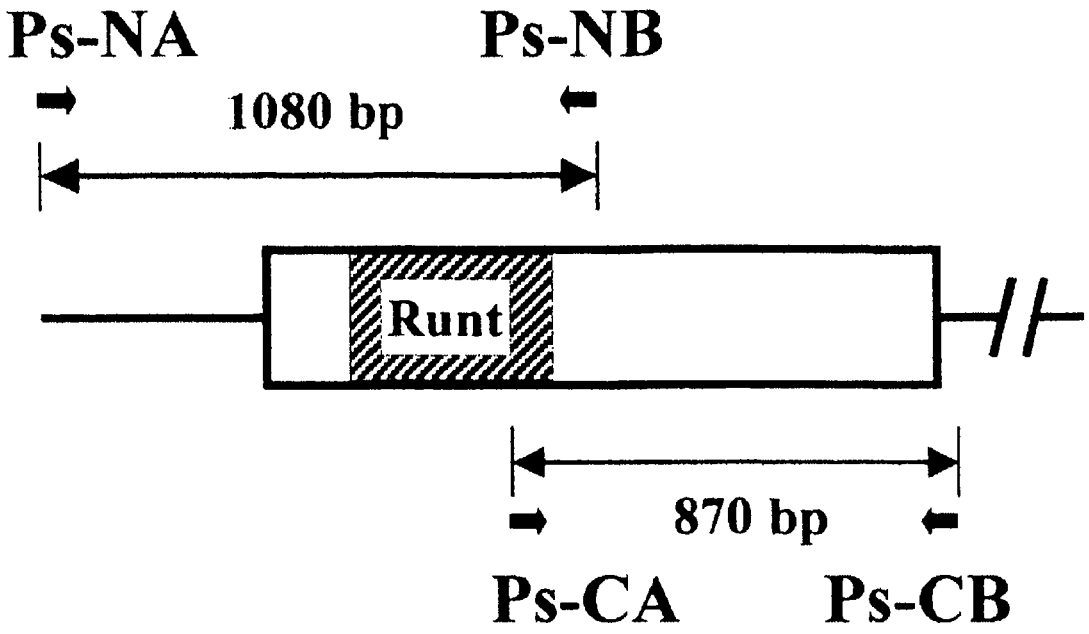


FIG. 6b

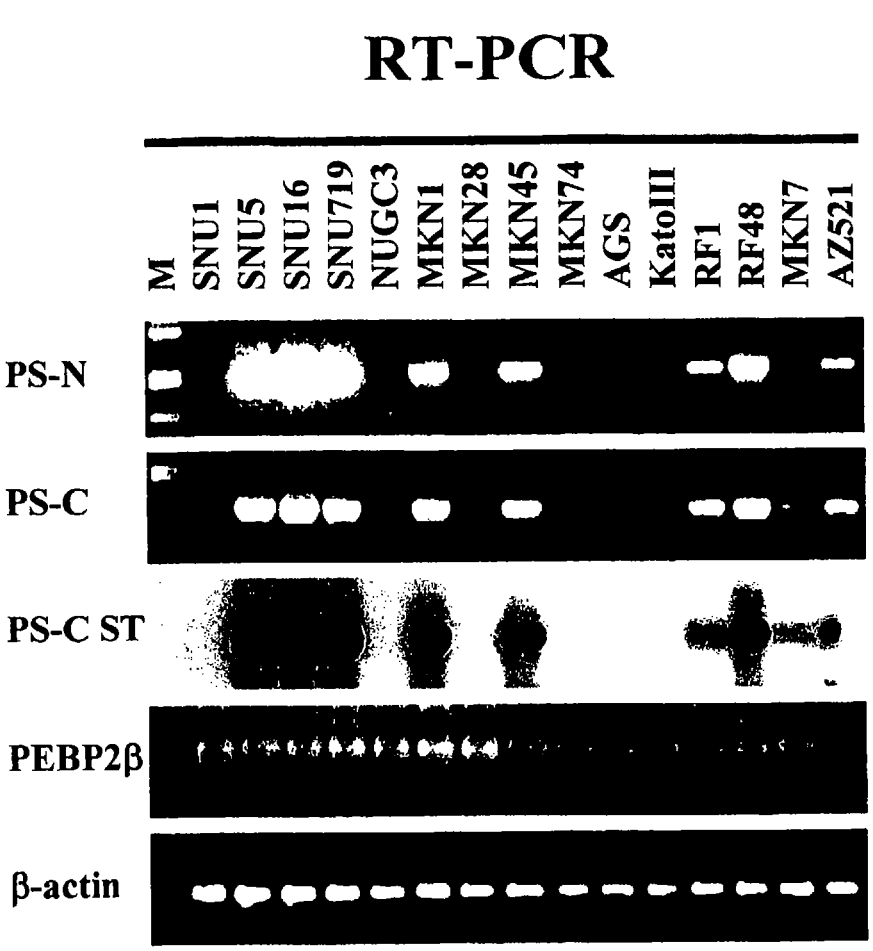

RT-PCR
M
SNU1
SNU5
SNU16
SNU719
NUGC3
MKN1
MKN28
MKN45
MKN74
AGS
KatoIII
RF1
RF48
MKN7
AZ521
PS-N
PS-C
PS-C ST
PEBP2β
β-actin

FIG. 6c

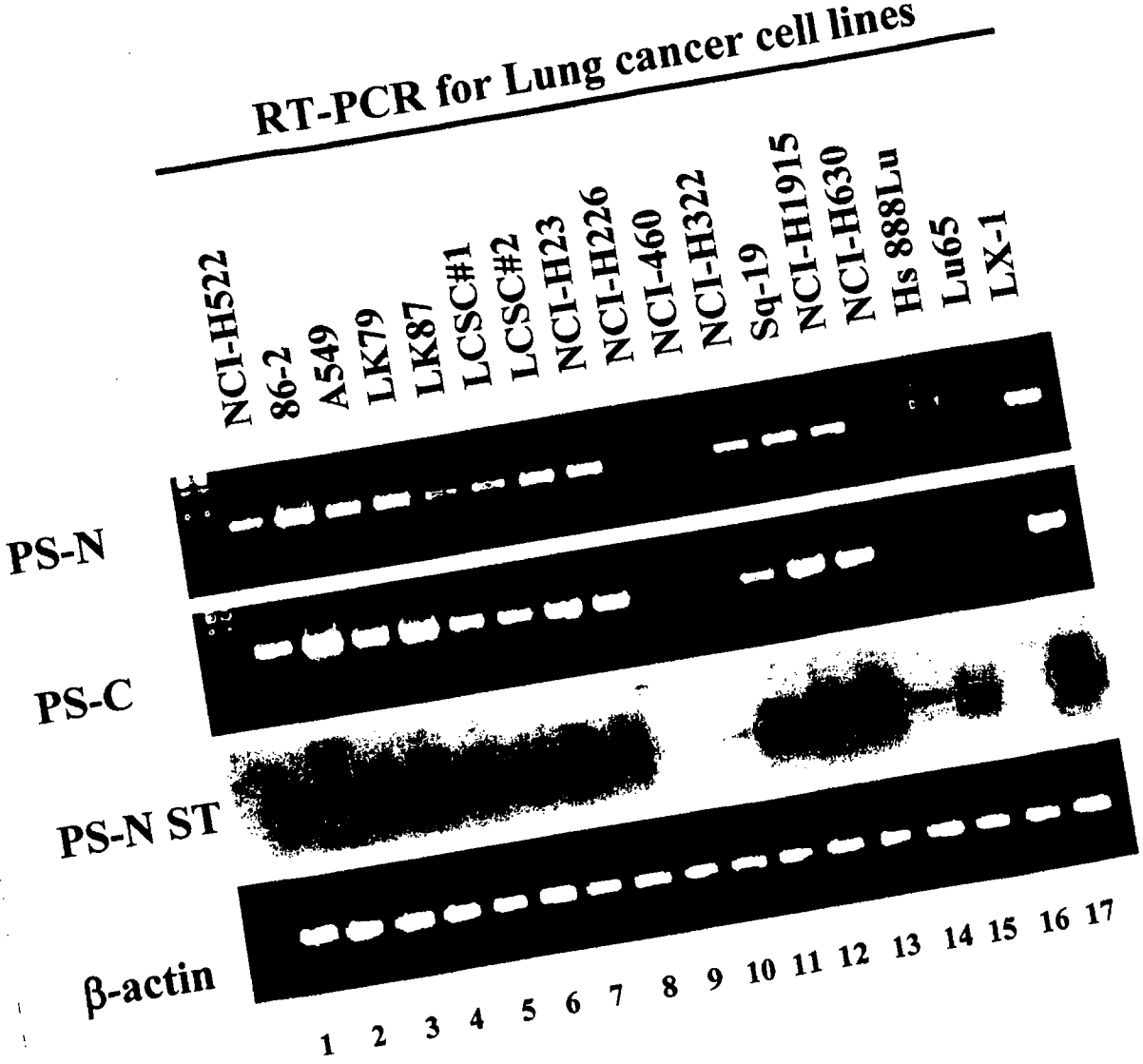

RT-PCR for Lung cancer cell lines
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86-2
A549
LK79
LK87
LCSC#1
LCSC#2
NCI-H23
NCI-H226
NCI-460
NCI-H322
Sq-19
NCI-H1915
NCI-H630
Hs 888Lu
Lu65
LX-1
PS-N
PS-C
PS-N ST
β-actin
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17

FIG. 7a

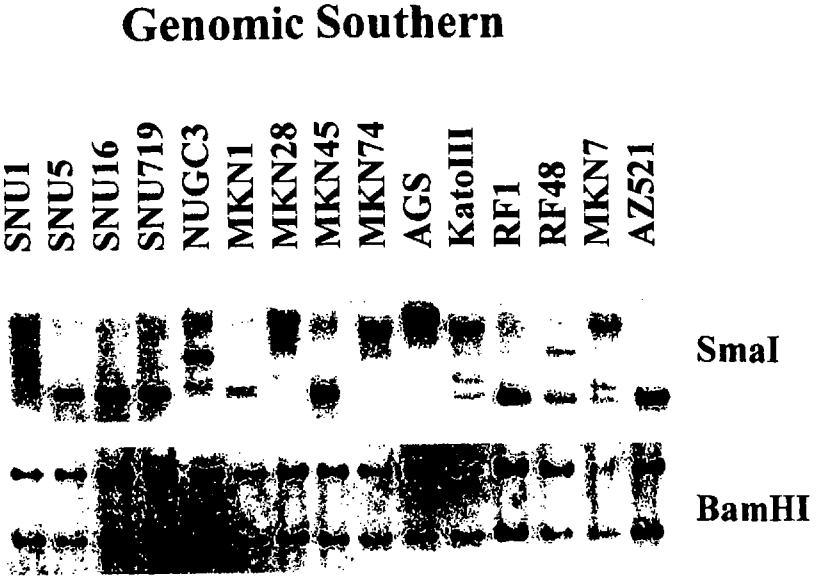

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SNU5
SNU16
SNU719
NUGC3
MKN1
MKN28
MKN45
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AGS
KatoIII
RF1
RF48
MKN7
AZ521
SmaI
BamHI

FIG. 7b

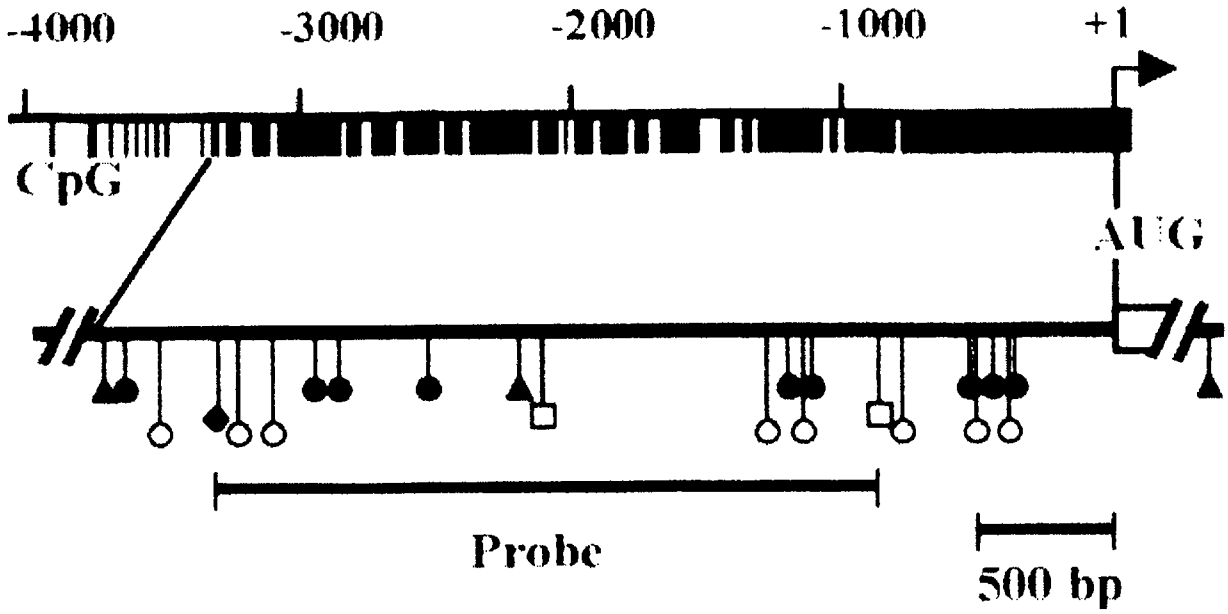
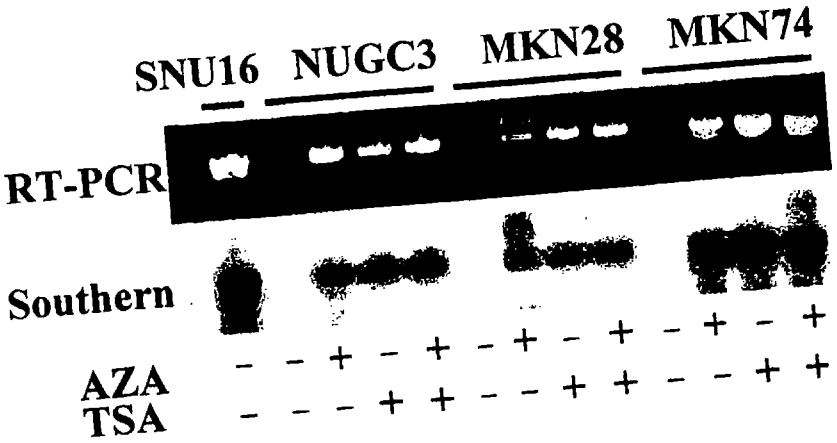

-4000
-3000
-2000
-1000
+1
CpG
ATG
Probe
500 bp
○: SmaI ●: HaeII ▲: BamHI □: MluI ◆: NheI

FIG. 8



SEQUENCE LISTINGS

<110> BAE, Seok-Cheol

<120> RUNX3 gene showing anti-tumor activity and use thereof

<130> Ofpo-12-21

<160> 11

<170> KopatentIn 1.55

<210> 1
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<400> 1

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gcccaggcag ccgggacagc cacgaggggc ggccgcacgc ggggccgcgc gccgaggatg 180

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gtaccaatct tttgtgacat attgtcatgc tgaggtgtga cacctgctgc actcatctga 4080

tgtaaaacca tcccagagct ggcgagagga tggagctggg tggaaactgc tttgcactat 4140

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ctatttaact gta 4213

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<213> human SNUX3 protein

<400> 2

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1 5 10 15

Ser Pro Ala Phe Pro Cys Gly Gly Gly Gly Gly Lys Met Gly Glu Asn
20 25 30

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        35                  40                  45

Arg Pro Glu Val Arg Ser Met Val Asp Val Leu Ala Asp His Ala Gly
    50                  55                  60

Glu Leu Val Arg Thr Asp Ser Pro Asn Phe Leu Cys Ser Val Leu Pro
65                  70                  75                  80

Ser His Trp Arg Cys Asn Lys Thr Leu Pro Val Ala Phe Lys Val Val
                85                  90                  95

Ala Leu Gly Asp Val Pro Asp Gly Thr Val Val Thr Val Met Ala Gly
            100                 105                 110

Asn Asp Glu Asn Tyr Ser Ala Glu Leu Arg Asn Ala Ser Ala Val Met
        115                 120                 125

Lys Asn Gln Val Ala Arg Phe Asn Asp Leu Arg Phe Val Gly Arg Ser
    130                 135                 140

Gly Arg Gly Lys Ser Phe Thr Leu Thr Ile Thr Val Phe Thr Asn Pro
145                 150                 155                 160

Thr Gln Val Ala Thr Tyr His Arg Ala Ile Lys Val Thr Val Asp Gly
                165                 170                 175

Pro Arg Glu Pro Arg Arg His Arg Gln Lys Leu Glu Asp Gln Thr Lys
            180                 185                 190

Pro Phe Pro Asp Arg Phe Gly Asp Leu Glu Arg Leu Arg Met Arg Val
        195                 200                 205

Thr Pro Ser Thr Pro Ser Pro Arg Gly Ser Leu Ser Thr Thr Ser His
    210                 215                 220

Phe Ser Ser Gln Pro Gln Thr Pro Ile Gln Gly Thr Ser Glu Leu Asn
225                 230                 235                 240

Pro Phe Ser Asp Pro Arg Gln Phe Asp Arg Ser Phe Pro Thr Leu Pro
                245                 250                 255
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Thr Leu Thr Glu Ser Arg Phe Pro Asp Pro Arg Met His Tyr Pro Gly
260 265 270

Ala Met Ser Ala Ala Phe Pro Tyr Ser Ala Thr Pro Ser Gly Thr Ser
275 280 285

Ile Ser Ser Leu Ser Val Ala Gly Met Pro Ala Thr Ser Arg Phe His
290 295 300

His Thr Tyr Leu Pro Pro Pro Tyr Pro Gly Ala Pro Gln Asn Gln Ser
305 310 315 320

Gly Pro Phe Gln Ala Asn Pro Ser Pro Tyr His Leu Tyr Tyr Gly Thr
325 330 335

Ser Ser Gly Ser Tyr Gln Phe Ser Met Val Ala Gly Ser Ser Ser Gly
340 345 350

Gly Asp Arg Ser Pro Thr Arg Met Leu Ala Ser Cys Thr Ser Ser Ala
355 360 365

Ala Ser Val Ala Ala Gly Asn Leu Met Asn Pro Ser Leu Gly Gly Gln
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Ser Asp Gly Val Glu Ala Asp Gly Ser His Ser Asn Ser Pro Thr Ala
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Leu Ser Thr Pro Gly Arg Met Asp Glu Ala Val Trp Arg Pro Tyr
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