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(12) **Reissued Patent**
Thompson

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- (54) **METHOD FOR IDENTIFYING METASTATIC SEQUENCES**
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- (73) Assignee: **Baylor College of Medicine**, Houston, TX (US)
- (21) Appl. No.: **09/985,799**
- (22) Filed: **Nov. 6, 2001**

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- (63) Continuation of application No. 09/977,371, filed on Oct. 16, 2001, which is a continuation of application No. 09/469,316, filed on Dec. 22, 1999, now abandoned.
- (51) **Int. Cl.⁷** **C12N 5/00**; C12N 15/63;
C12N 15/70; A61K 48/00
- (52) **U.S. Cl.** **424/93.21**; 424/9.2; 435/6;
435/69.1; 435/375; 435/455; 800/10
- (58) **Field of Search** 424/9.2, 93.21;
435/6, 69.1, 375, 455; 800/10

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(57) **ABSTRACT**

The invention relates to methods for the identification of metastatic sequences. Cells from a cell line or an animal tissue are treated to form a cell line predisposed to metastasis. Treated cells are implanted in an animal [of] at a primary site and incubated for a period of time sufficient for the cells to proliferate and develop metastases at secondary sites. Expressed sequences from cells at the primary and secondary sites are amplified by differential display polymerase chain reaction and compared. Differentially expressed sequences are [identical] identified and can be cloned and sequenced. These sequences can be used as probes in the diagnosis of metastatic disorders, as probes to isolate metastatic sequences and as a therapeutic agent.

43 Claims, 63 Drawing Sheets

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INCREMENTAL MULTISTEP MODEL

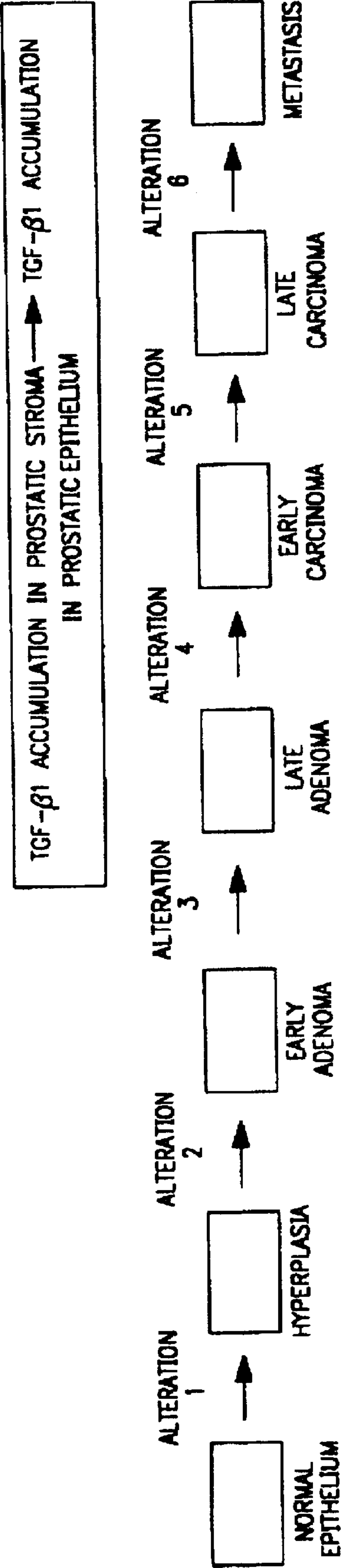


FIG. 1A

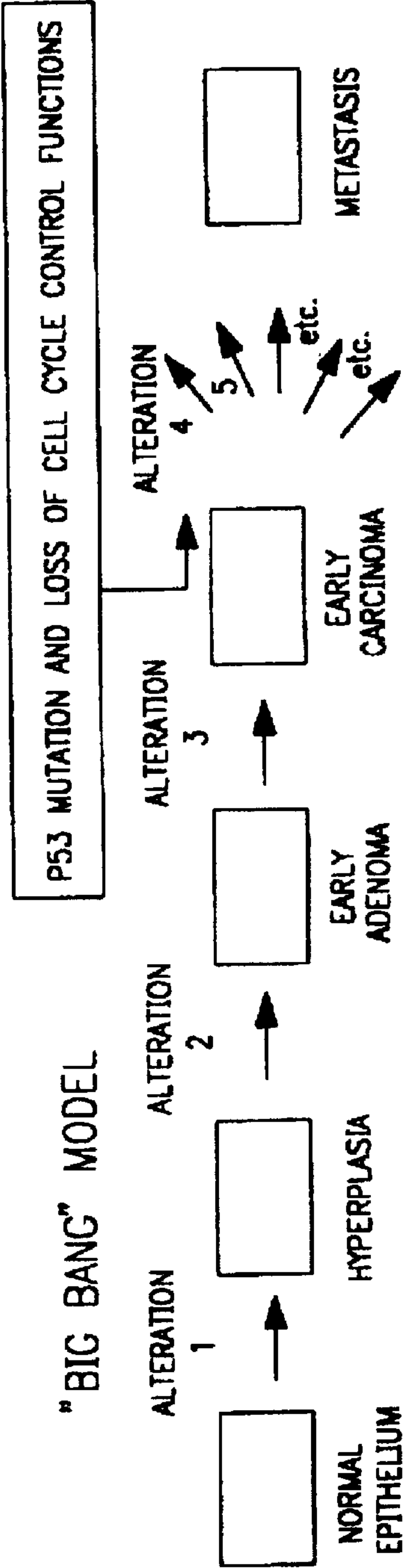


FIG. 1B

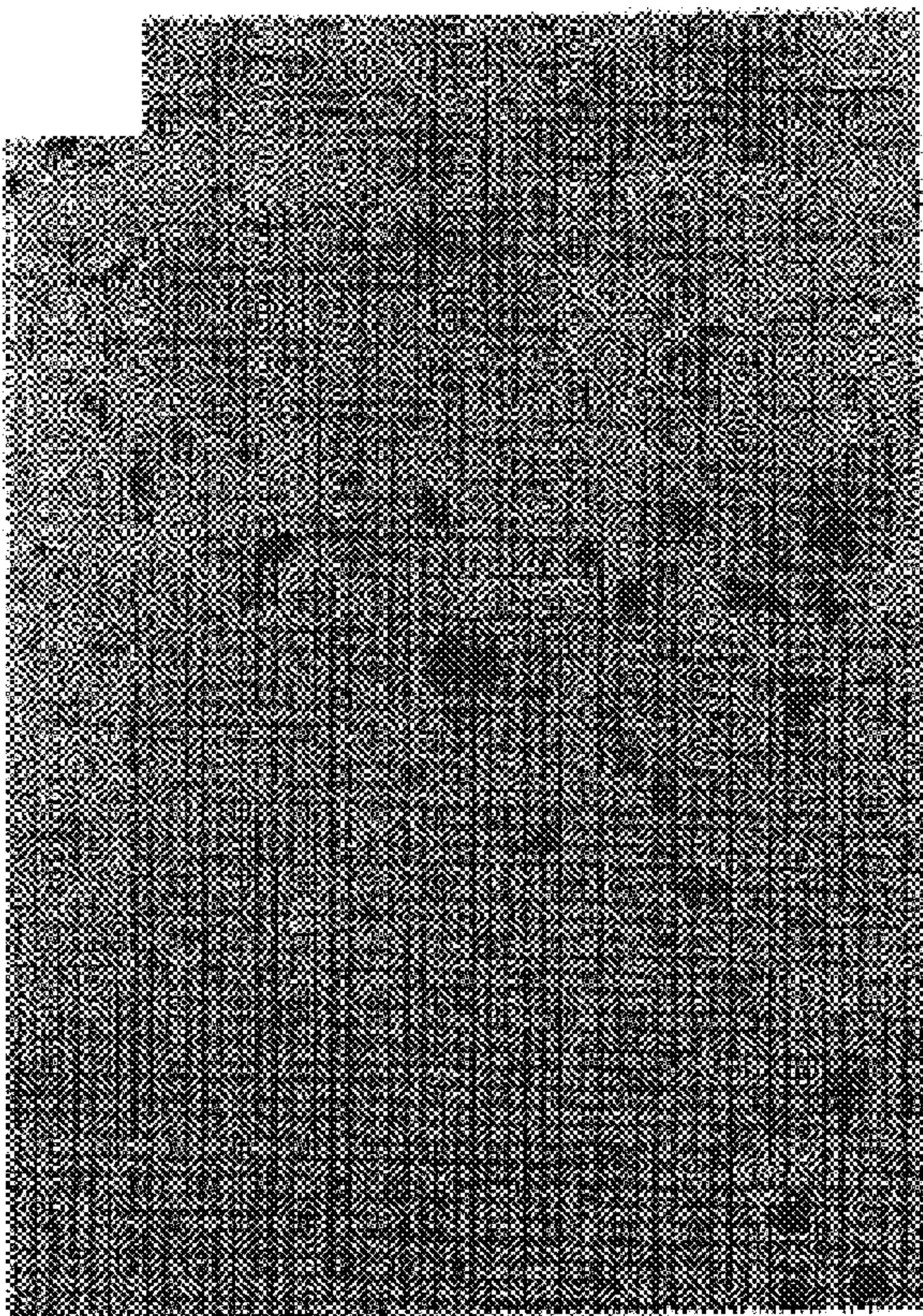


FIG. 2A

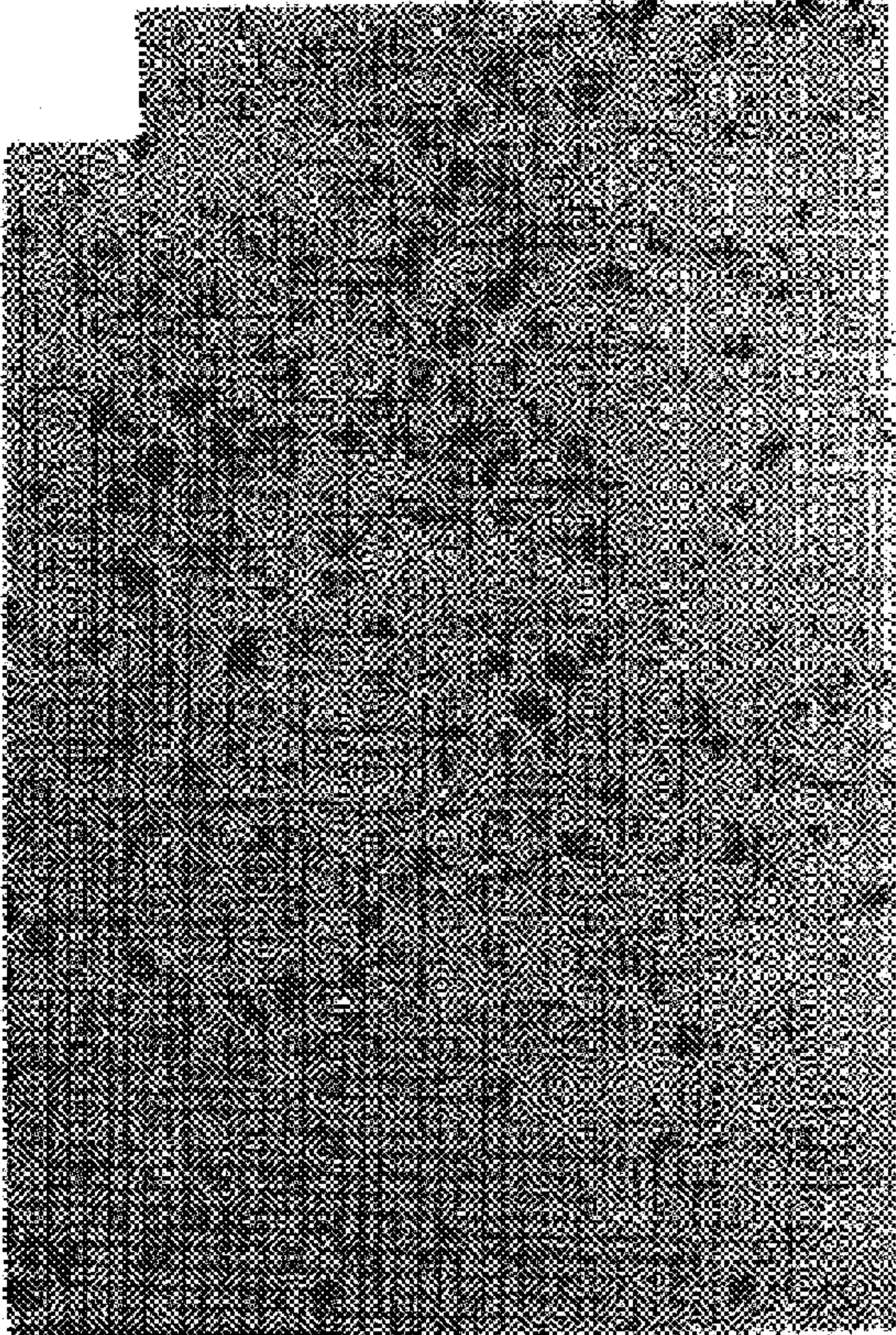


FIG. 2B

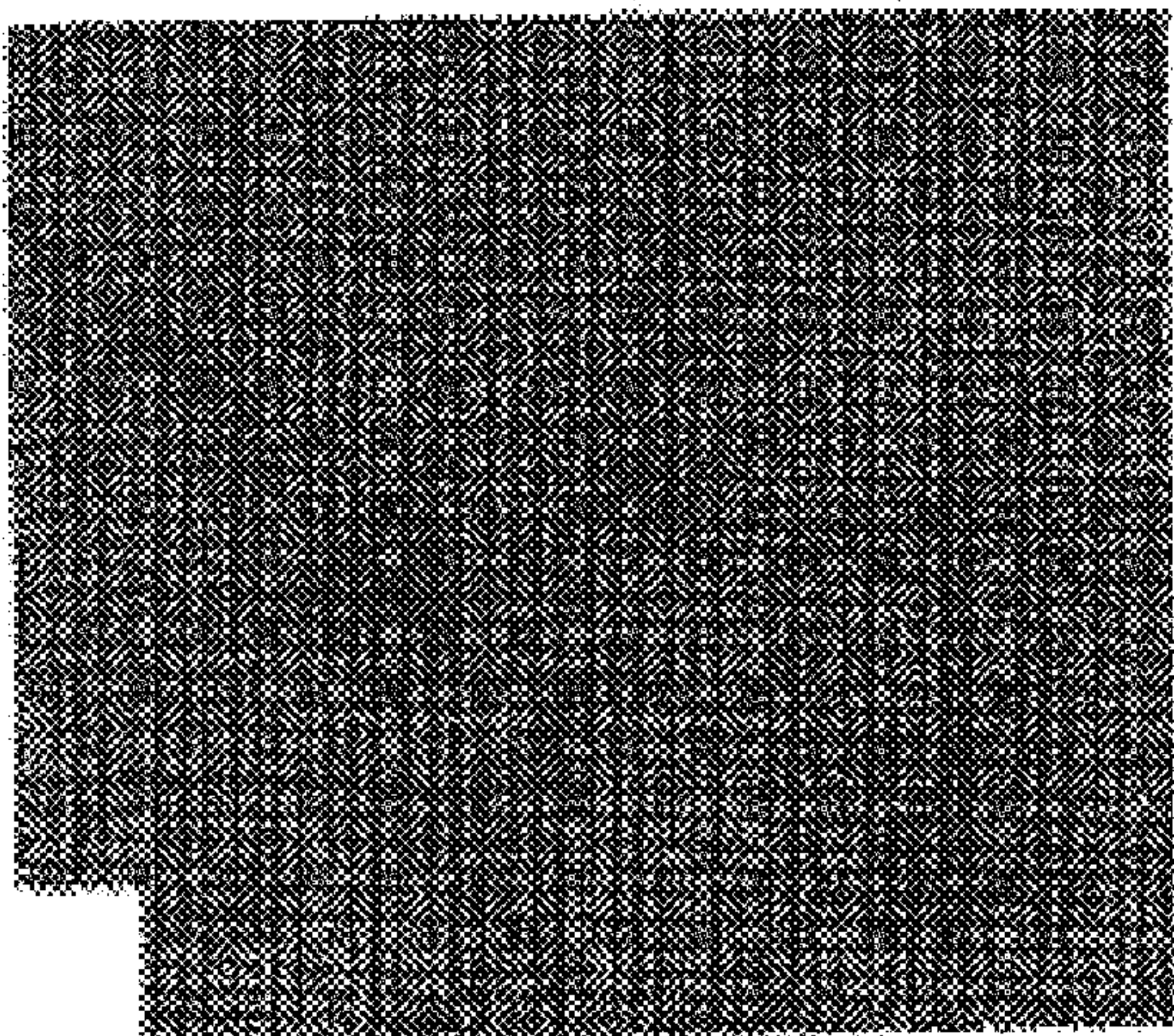


FIG. 3A

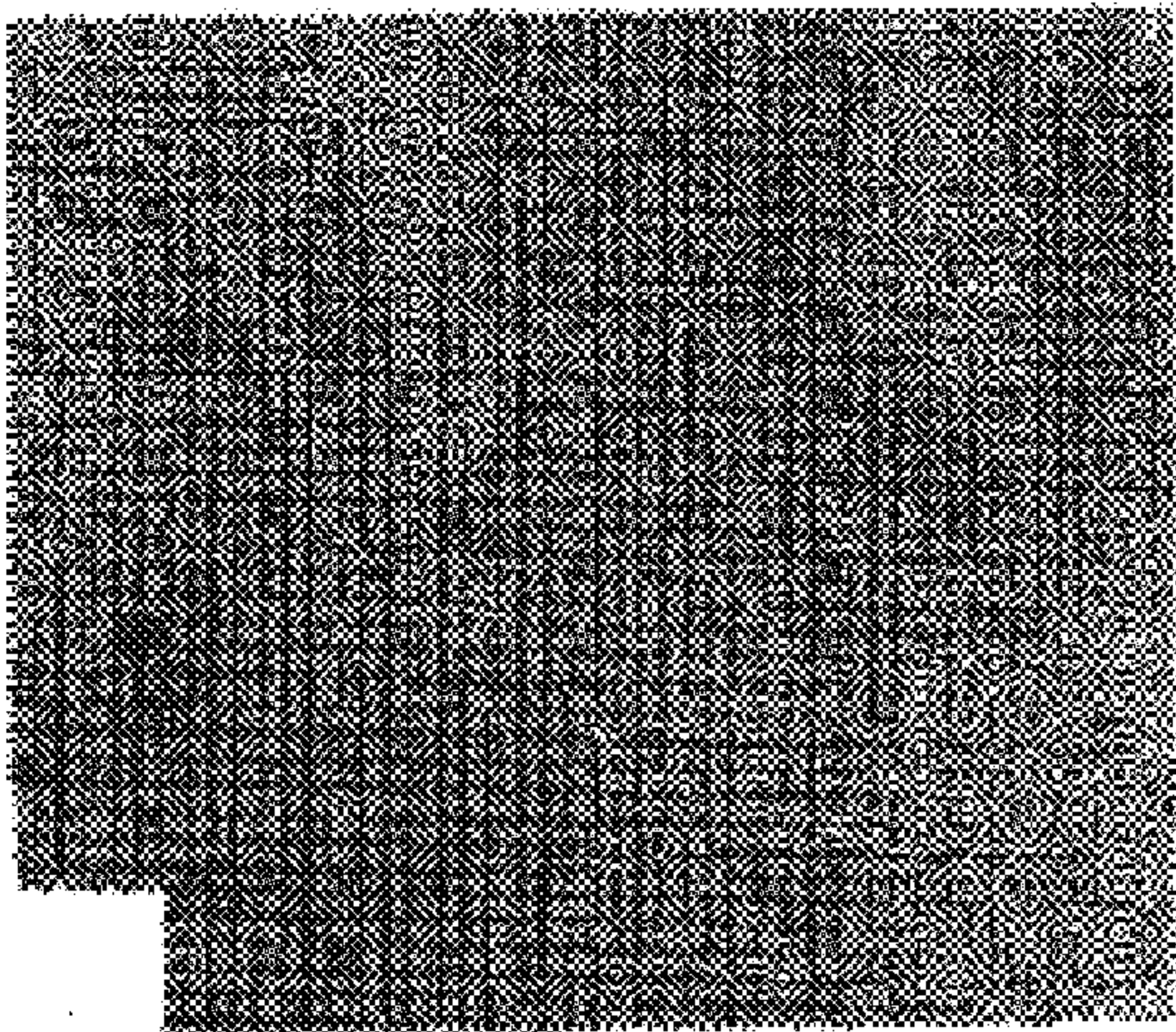


FIG. 3B

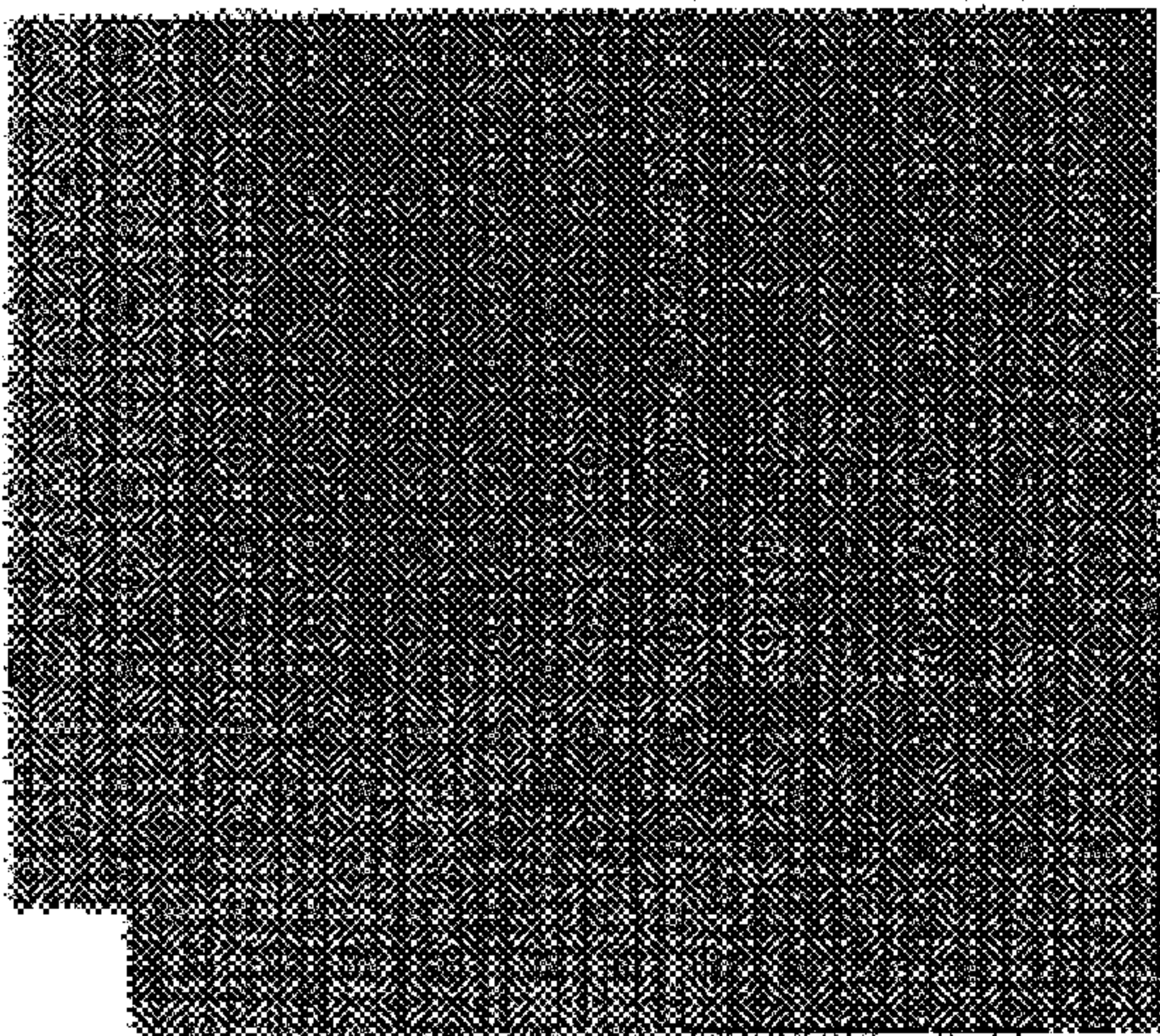


FIG. 3C

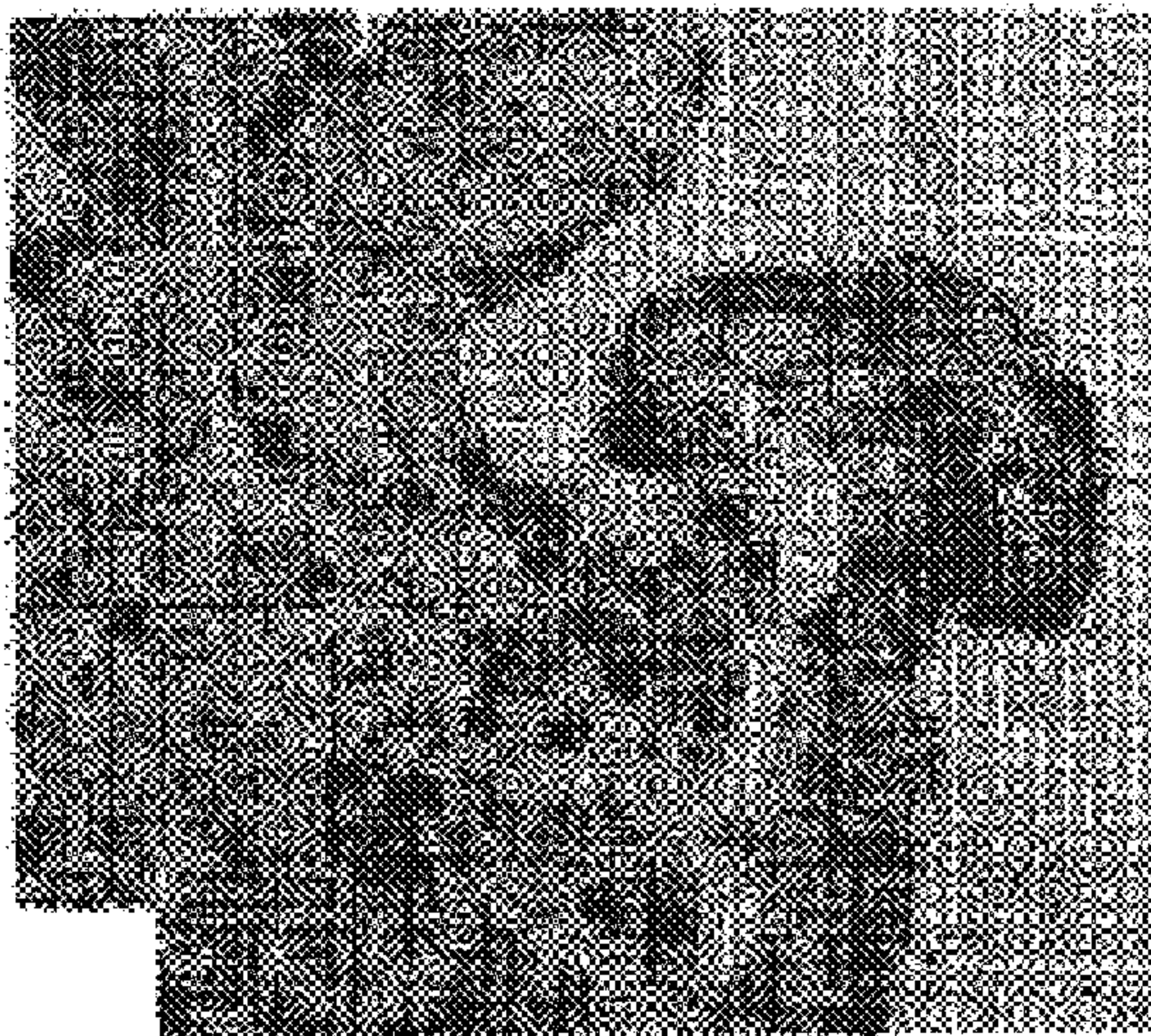


FIG. 3D

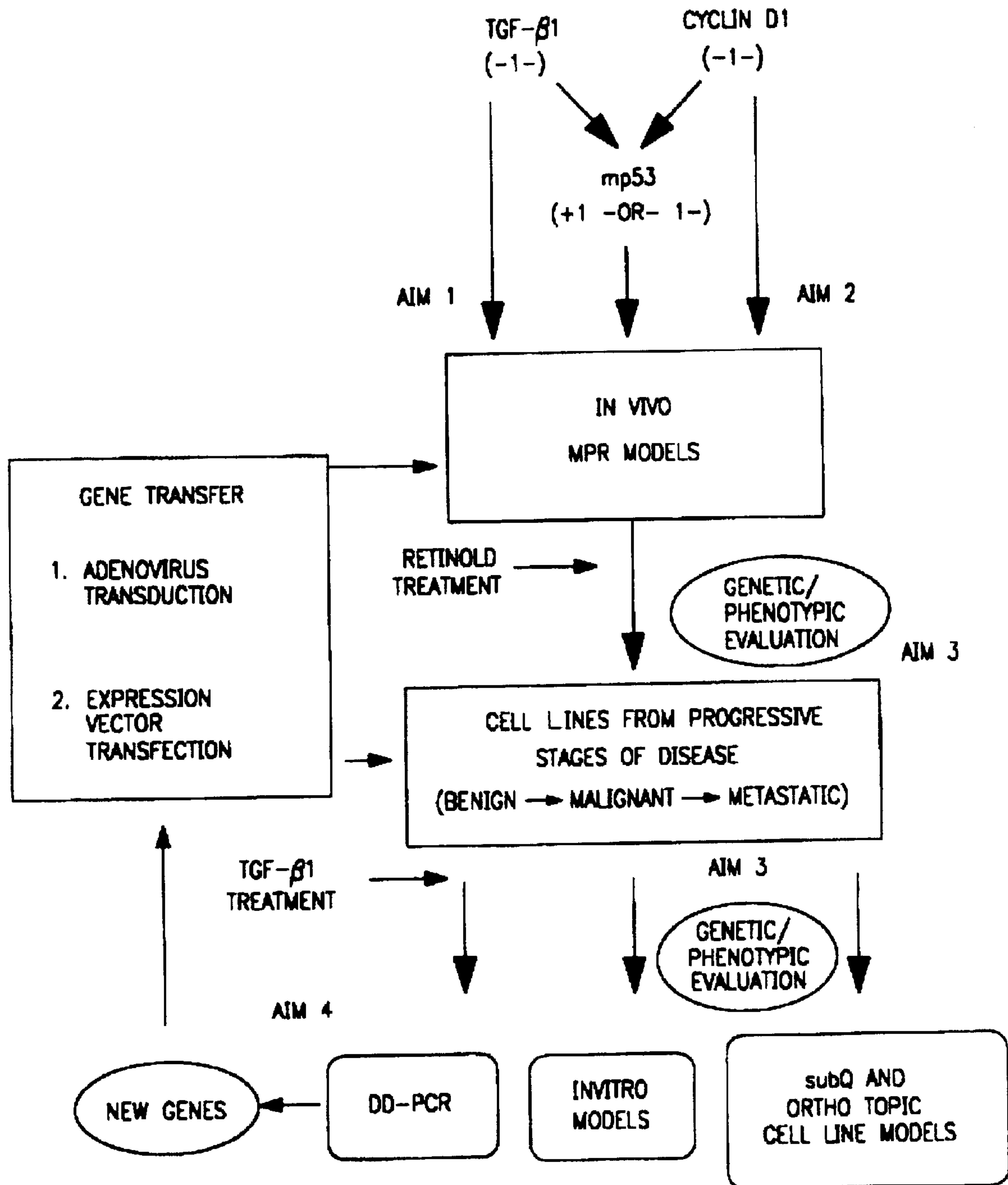


FIG. 4

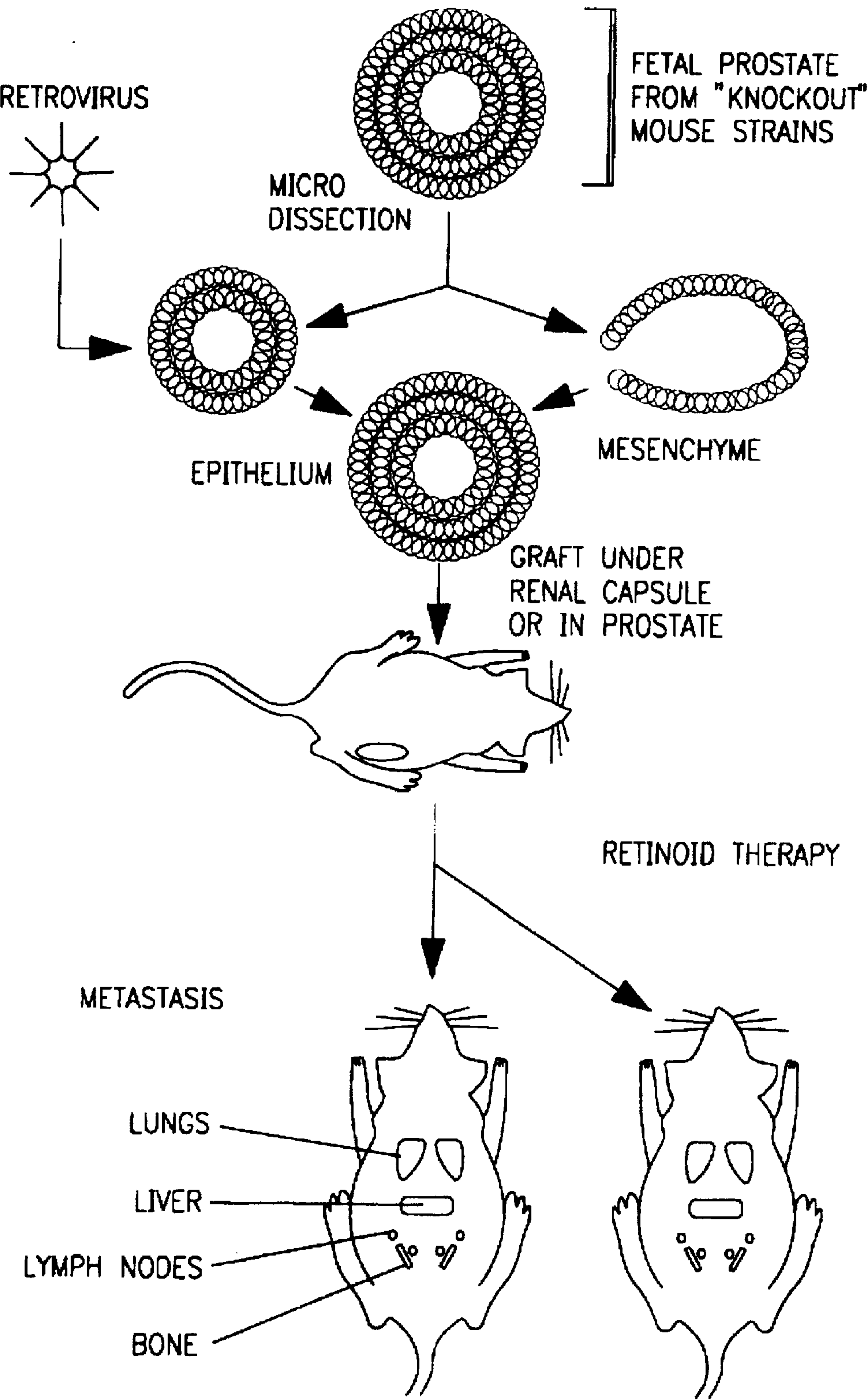


FIG. 5A

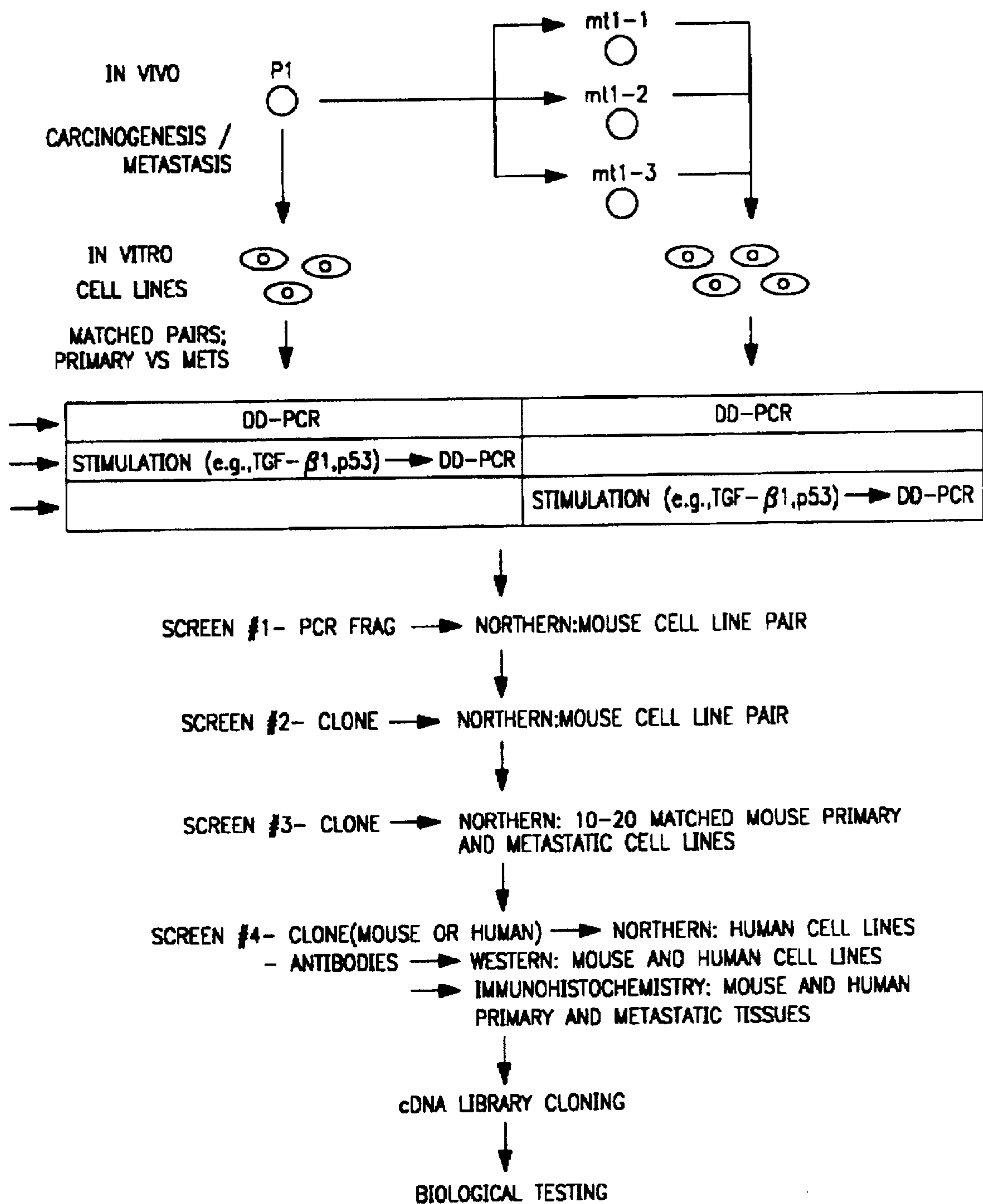


FIG. 5B

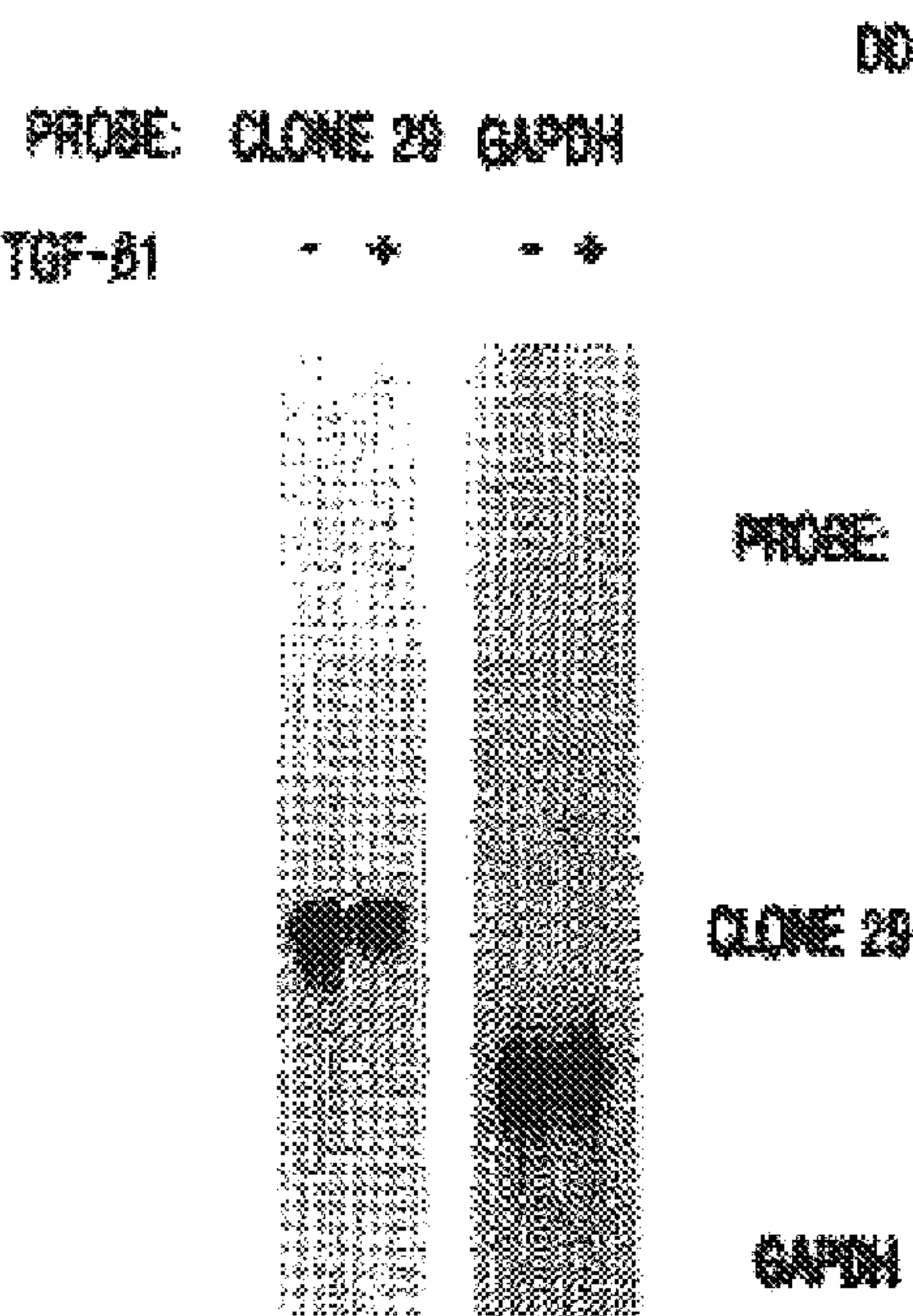


FIG. 6A

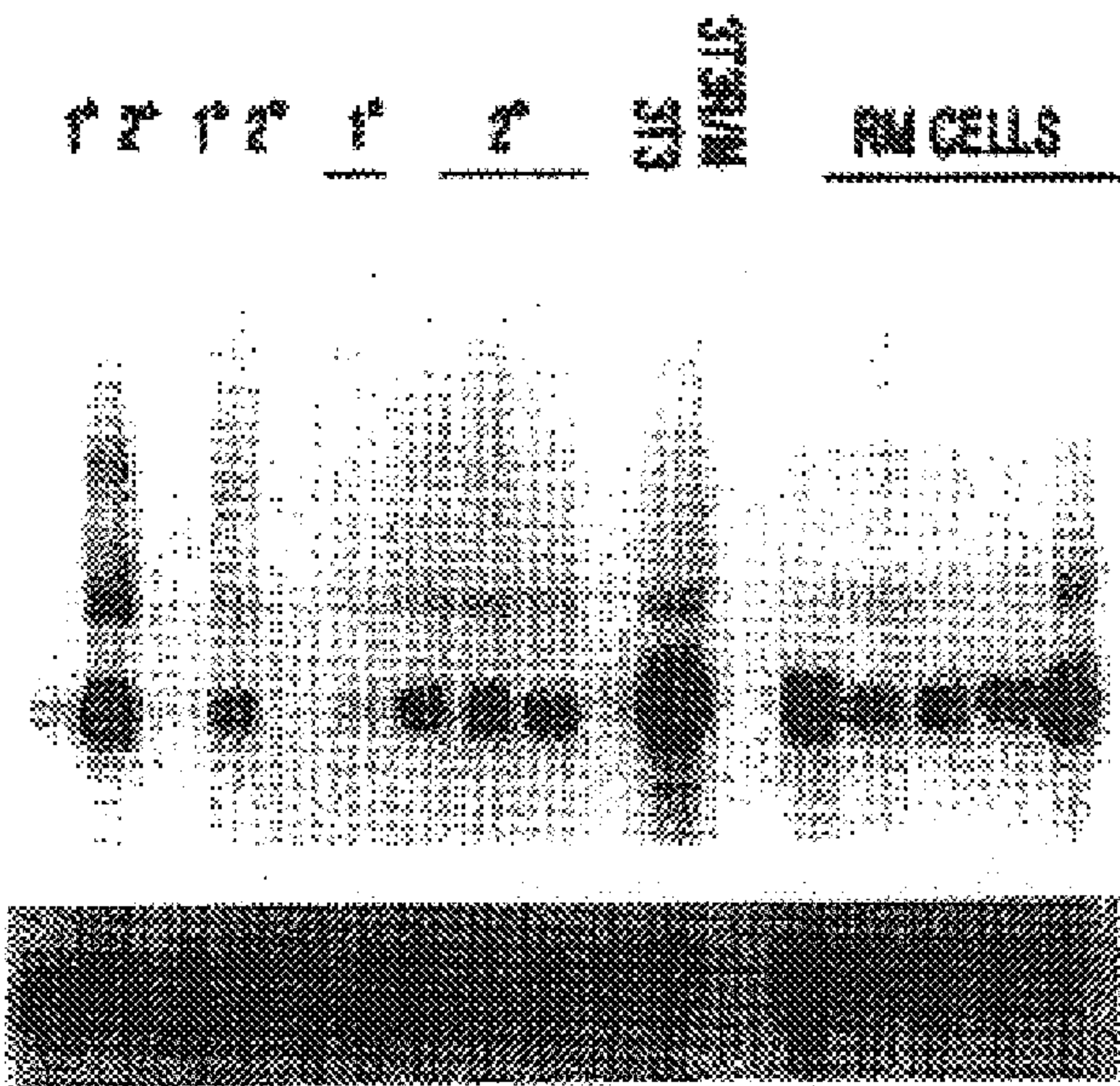
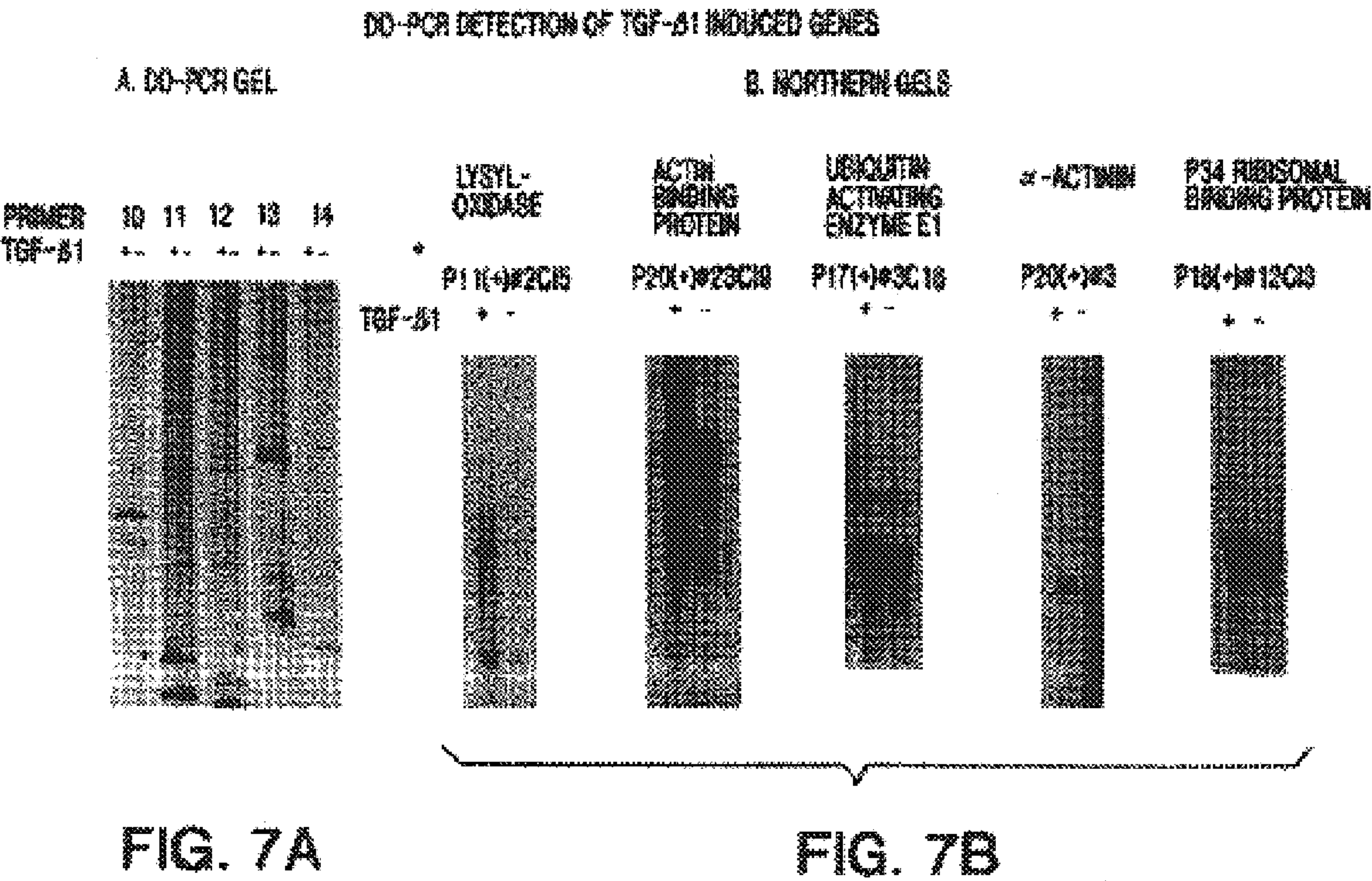


FIG. 6B



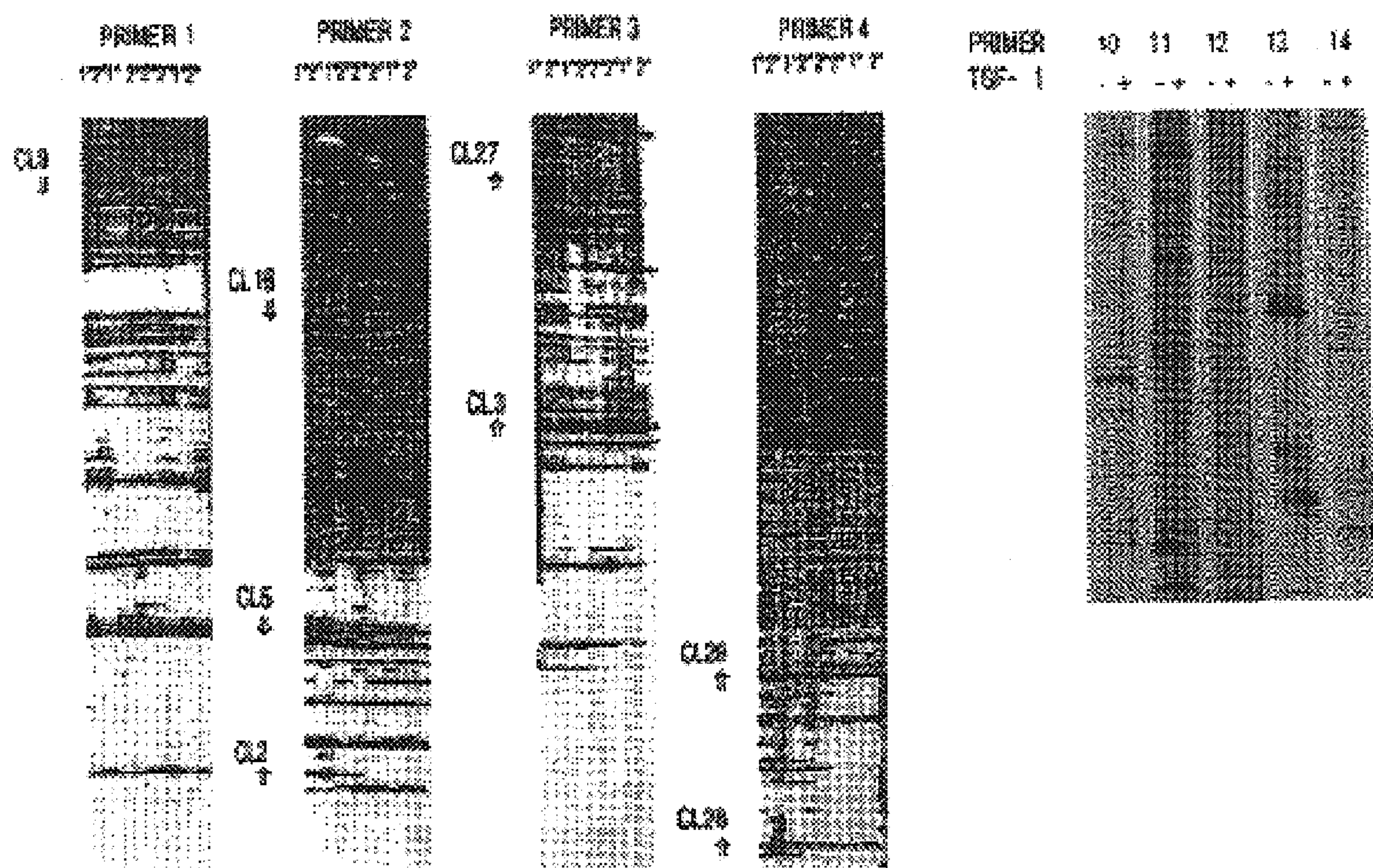


FIG. 8

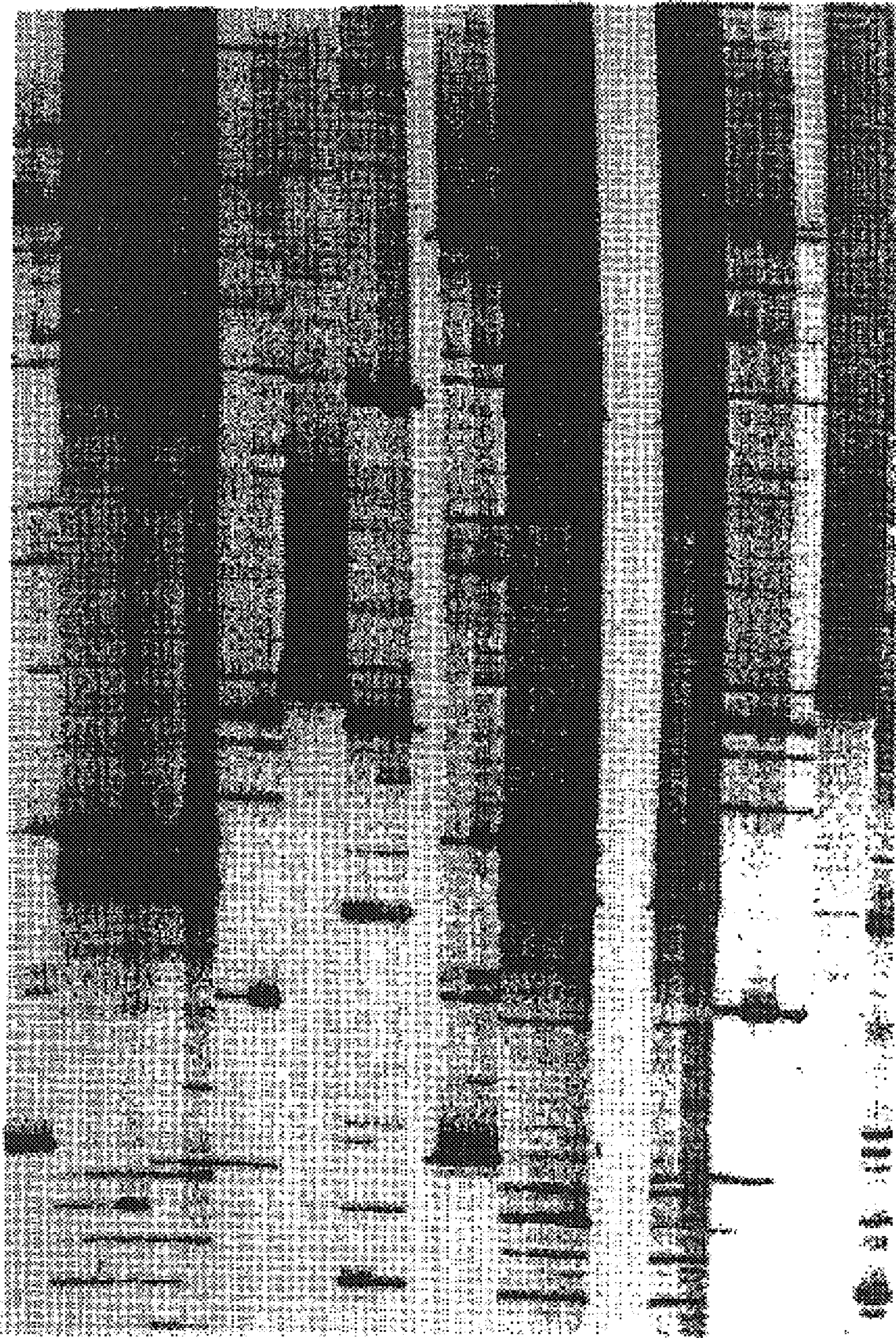


FIG. 9

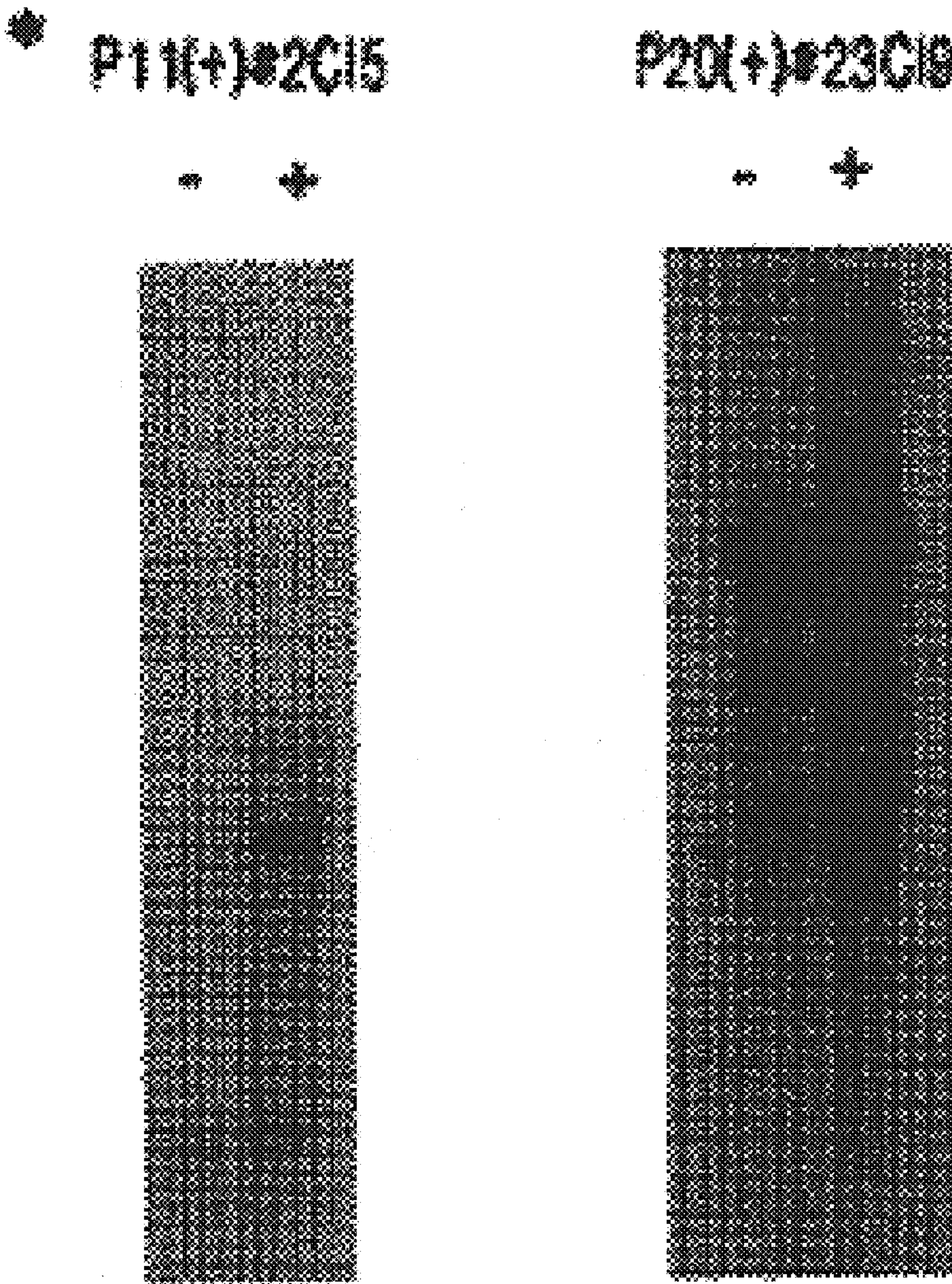


FIG. 10

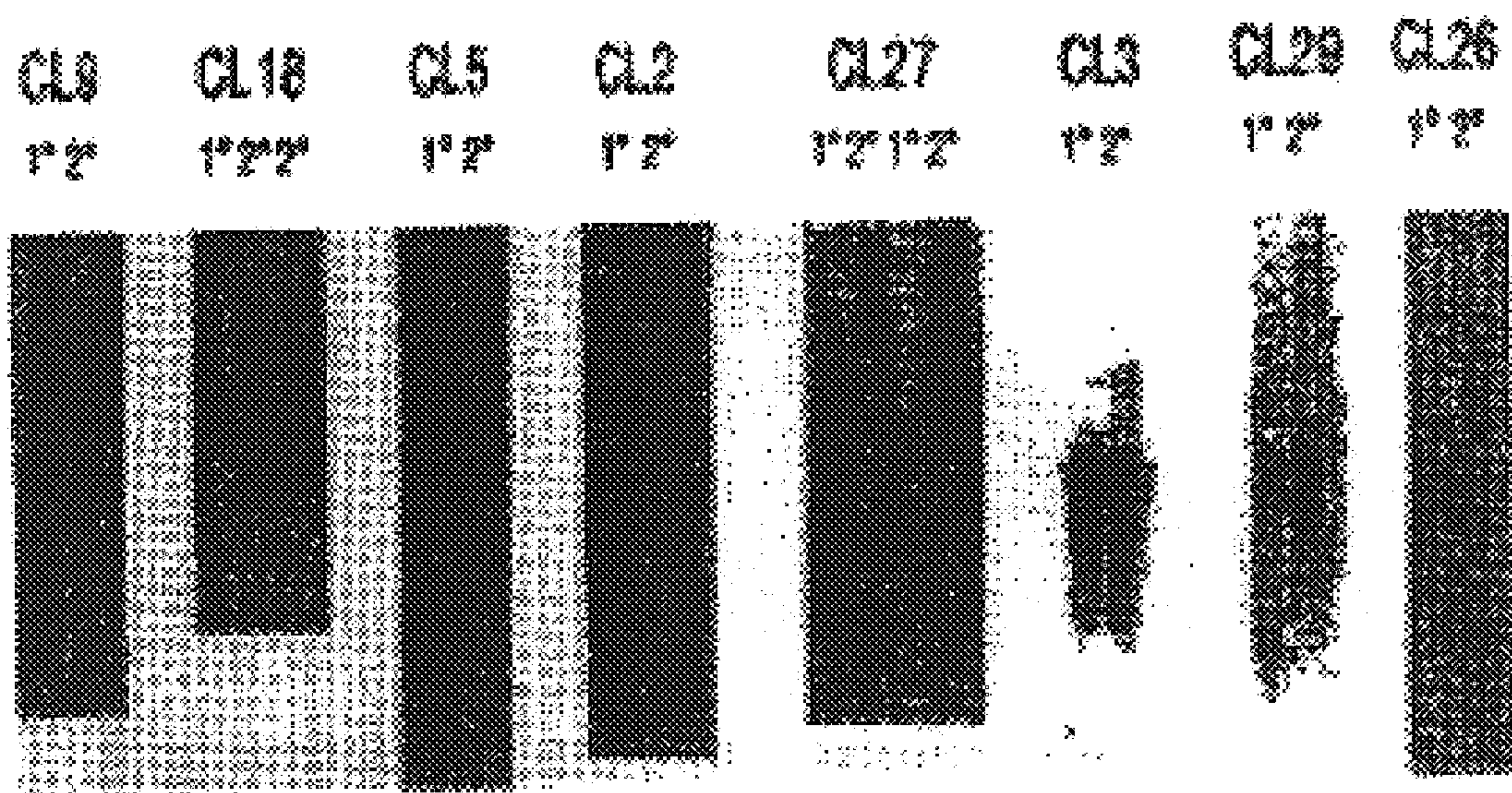


FIG. 11

CL-1#2

AATTTTTTTTTTCGACGGCCCAACGGAATTTTTTTTTTCGACGGCCCAACGGAATTTT
TTTTTCGACGGCCCAACGGGAATTCGGCTTAGCTAAGGTCACCCAGACTTCATGGACT
TGTCTATTTTCTTGCCCAAAGGGATAGTTCCTCAGGTATTTGGGGACAGCATTACCTC
TTGCAGGAGCTATGCCTGTGTGTTTGTGCTAAGTTGATACTTTCTGCGATGATCTCAC

(SEQ ID NO. 31)

CL-10#3

TACCATCGGAGAAAGAAGACCAAGCAAGGCTCAGGCAGCCACCGCCTGCTTCGCACT
GAGCCTCCTGACTCAGACTCAGAGTCCAGCACAGACGAAGAGGAATTTGGAGAATTG
GAAATCGCTCTCGTTTTGTCAAGGGAGACTATCCCGATGCTGCAAGATCTGCTGTCCCT
CTGGCCTTTGTCATCCTCGCGCCTGCGTTGTGGCCTCTGTGGGCTTGGTGTGGAGCAAA
TGGCTCTCAAGGAGGACTGAGTCTCAAGGAAATT

(SEQ ID NO. 32)

CL-11A#5

AGCTAAGGTCAGGAGGTGTCTGAAGAATTGGCTGATGCATGGCAGGGATGTTGTTGAC
CTGCTTTTAGAACAATACTTCCATTTAATTATAGCATATCTTATGTGTGTATTAAAGCA
GAGCCGATCTGGTGGGGCTCATTAAGTAAATGTACTTACTGCAAAAGGTTCAACTGGT
GACCCCAGTTTTCCCCAGAAGCAATATGATAGGACAGAGGCGACTCCTGCAAGTTGTC
TCAGACTTCACACATACATTGTGACATTCTCTGAGCATGTGCACTGTACATGATATGAC
ACTATCAA

(SEQ ID NO. 33)

CL-11C#2

AGCTAAGGTCCACTACCTTGTGAAGATGTATAAACACCTGAAATGTAGAAGCGATCCG
TATGTCAAGATCGAGGGGAAGGACGCTGACGACTGGCTGTGTGTGGACTTTGGGAGTA
TGGTGATCCATTTGATGCTTCCAGAAACCAGAGAAACCTATGAATTAGAGAAACTATG
GACTCTACGTTCTTTTGATGACCTTAGCTAAGCCGAATCAGCACACTGGCGGCGTTACT
AGTGGATCGAGCTCGTACAGCTGATGCATAGCTTGAGTATCTATAGGTTACTAATAGC
TGGCTATCATGTCAAGCGTTC

(SEQ ID NO. 34)

FIG. 12A

CL-12#1

AGCTAAGGTCAAAATAAAAGCTCAAGATGACATCAGTCCCATTGTGCTAAGTCCTGG
TGTTGTATGGATGGTAAGCAGCAGCCAATTATGGTGACAGGTGATAGATCCAATTTGT
TAACATTTCTCCATCTCTAAGCCATCCTTAAAGAAAATCATGAATGGAGTCACACCAT
CTTCACGGTAGTCCAGGAGAGCAACCATAACCATCTGGATTCATGTTTCACCAATAAAA
ACTGGTAGTTATTGAATTAGCAAGGATGTGCTACTCTCTGCAGCTCAGC

(SEQ ID NO. 35)

CL-13#1

AGCTAAGGTCTCATGCAATGGAAGTTAATTCTTAGAAGTGTGAAGAATTACATCAAACA
TAAAAGCCTCCCTATTAATGTAGTCCACAAAAGTGGCAGGTATATATGCCTTCTGAAT
TTGTCTCCAGTGACTTTGGTAAATCTAACTAAATTTTAAAAATTCTTAATGAATTTAT
CGTCAACAACAACCACCTCTTGGAATAAACCCTTGCAGTGTCTGTGTTAGACTCAG
AAGTCAA

(SEQ ID NO. 36)

CL-14#4

GAATTCGGCTTAGCTAAGGTCAGCGTGAAGTTTAAGCAGACATGAGTCTGAAACAGTC
TCATGACACATCTGATAGGATTTTTTAAGACTGCCTGGCTTAGTCTTACTGCTGTTAGT
GTATATTAGGTGTTGTACACATTATAAAGAAAATTATGTCTCATTATCTTGTTTAAGTC
AAGGAAAATAGAGAACTTTGGTCAAAT

(SEQ ID NO. 37)

CL-2#2

GAATTCGGCTTAGCTAAGGTCAGCGTGAAGTTTAAGCAGACATGAGTCTGAAACAGTC
TCATGACACATCTGATAGGATTTTTTAAGACTGCCTGGCTTAGTCTTACTGCTGTTAGT
GTATATTAGGTGTTGTACACATTATAAAGAAAATTATGTCTCATTATCTTGTTTAAGTC
AAGGAAAATAGAGAACTT

(SEQ ID NO. 38)

CL-2#3

GAATTCGGCTTAGCTAAGGTCAAAATACACGGATTGCAATCACTTTTCTAAACAAAAG
AAACAAAGTAACTGCTGAGGTAGCAAAGATGAGTTCTCGTCATACTGCCTTGTAAGT

FIG. 12B

TTTTGTGAACTGTGTTATTA AAAATCTGAGCTTAACAAAATCTTTACAAGTCACCTCAT
GAAACAGCATTG GCGCAATAAGAGTTTAATTCCACACCAGTGAGACCTTAGCCT

(SEQ ID NO. 39)

CL-2#4

GAATTCGGCTTTCTGCGATCCACTCTTTGAAGCTATTGGCAAGATATTCAGCAACATCC
GCATCAGCACGCAGAAAGAGATATGAGGGACATTTCAAGGATGAAAGGTTTTTTTCCC
CCCTTACTATTTCCCTTGGTGCCAATTCCAAGTTGCTCTCGCAGCAGCAAATTTATGAAT
GGTTTGTCTTGATCAAGAACAAAGAATTCATTCCCACCATTCTCATATATACTACTTTC
TCTTCTT

(SEQ ID NO. 40)

CL-3#1

GAATTCGGCTTTCTGCGATCCACTCTTTGAAGCTATTGGCAAGATATTCAGCAACATCC
GCATCAGCACGCAGAAAGAGATATGAGGGACATTTCAAGGATGAAAGGTTTTTTTCCC
CCCTTACTATTTCCCTTGGTGCCAATTCCAAGTTGCTCTCGCAGCAGCAAATTTATGAAT
GGTTTGTCTTGATCAAGAACAAAGAATTCATTCCACCATTCTCATATATCTACGTCTCT
TCTAG

(SEQ ID NO. 41)

CL-4#1

GAATTCGGCTTTCTGCGATCCTAGAGCAGGTAAGTGAAGAAGGCCAGTAAGTTTAAAG
GATGGCCTTGTTGCCTTCTATCAAGTTCTCTGGGACTTTGTAATTTTGATTACTACTATT
GATACATGGTTATGGTCAGAAGGCCTCTTCTCCCTT

(SEQ ID NO. 42)

CL-4#2

AGCTAAGGTCCGGACTCTATGGCATGACCCCAAAAACATTGGCTGGAAAGATTACACT
GCCTACAGGTGGCACCTGATTCACAGGCCTAAGACAGGCTACATGAGAGTCTTAGTGC
ATGAAGGAAAGCAAGTCATGGCTGACTCAGGACCAATTTATGACCAAACCTACGCTG
GTGGACGGCTGGGCTGTTTGTCTTCTCCAAGAGATGGTCTATTCTCGGACCTCAAGTAT
GAGTGCAGAGATGCTAGAGAGCAGGCTCAGTCTCAGCA

(SEQ ID NO. 43)

FIG. 12C

CL-5A#4

TGACCATCGAGTGCATCAGCCTCATCGGGCTGGCCGTCGGGAAGGAGAAATTCATGCA
GGATGCTTCAGATGTGATGCAGCTATTGTTGAAGACACAGACAGACTTCAATGATATG
GAAGATGACGACCCCCAGATTTCTTACATGATCTCAGCATGGGCCAGGATGTGCAAAA
TCTTGGGAAAGAATTCCAGCAGTACCTTCCCGTGGTTATGGGGCCGCTGATGAAGACT
GCTTCAATTAAGTCCTGAGTGCCTCTAGACACCAGGACATGAGATATGAGGTA

(SEQ ID NO. 44)

CL-6#2

TGACCATCGTGTAGTTGGTGTGCTTGTTGTCGAAGATGAGGGCCTCCTGGATGAGCTG
GTGCTGCTGCTCCAGCAGGTCCAGGCTGGGCTTGTAAGTCCACGATGCTGCGCTCGTAC
TGCTTCAGGTGGCTCAGCTGGTCTTCCAGAGTCCCGTTCATCTCAATGGAGATGCGCCC
GATCTCCTCCATCTTAGTCTGGATCCACGGCCCCACCATATTGGCTTGGCTGGCGAACT
GTCGGCGAAGGCTGCATTGGATTGCT

(SEQ ID NO. 45)

CL-7#4

TGACCATCGAACACCCCAACACTCTCCACTACCTGCCATTTCTTCCAGCCTTATCCACA
CCACCCCGTTTCTCCTGAAGACTGATTTGCTTAGCAACTGCACTGAGCCAACCCTGAA
GACACATGATTATTGGTTGGGCTCCATTAAACAACAAGCCTAGTGCTTGGGAAGGGGG
GTGGGGAGGGGAAGAGACGTGAGAAGCATGTTGGCGTAGACCTTGAGGCATGGATGA
AGCATCTGCCGGCCTGACCTGGTACAGGTGGCATCTGCACTGCAGCAAGGC

(SEQ ID NO. 46)

FIG. 12D

CL-8#2

TGACCATCGAAGTGCAAAGGAAATGACTTGATTTCATGAAGTATCTCCAGAAGTAACG
CTTTGTTTTCTGCATCCTGAACTTTATTCCCAGTGAAGAGCTGAAAATCTGGACGCTCA
AAAAATGGAAGCACTTTGGAGAGAGCCCTTA ACTCTATCAGGTACAGGAAGTACAAG
TTCCTCAGCCTTCGTGGGCCTTCTCCTTCAGTCAGAATCCATCAAAGGTGCTGGA ACTC
TGTGACATTGTGACCCATTCTTTCAGCCAGTATCTGTAAGATAC

(SEQ ID NO. 47)

CL-9#1

GGGAACGAATGATCTGGA ACTGTGGCTTGTAGACAACCCAAATATCTTAGGTAGGTAA
GAAATTCCAGCATCACACTATATAGGAAATACTGTGCGAA ACTGACAGTTAACTGTGC
ACAAAGTTCAATGGCTTCAAATAATGTATAAAGGATAAGAAGAA ACCAGTTTACCAT
TTTGGT ATTATTTTGGTTGCTTTGTATAACTTCAATAATTT

(SEQ ID NO. 48)

CL-54A#2.-SP

GGGAACGAATGATCTGGA ACTGTGGCTTGTAGACAACCCAAATATCTTAGGTAGGTAA
GAAATTCCAGCATCACACTATATAGGAAATACTGTGCGAA ACTGACAGTTAACTGTGC
ACAAAGTTCAATGGCTTCAAATAATGTATAAAGGATAAGAAGAA ACCAGTTTACCAT
TTTGGTATTATTTTGGTTGCTTTGTATAACTTCAATAATTT

(SEQ ID NO. 49)

CL-54A#2.-S0

GACGTAAGCC

(SEQ ID NO. 50)

CCACAAAGCAAGCTTCTGTCTGGAGTACAGCTCCTGTGACTATGGGTACCACAGGGCC
TTTGCGTGCACTGCACACACACAGGGATTGAGTCCTGGATGTTATGACACCTATGCGG
CAGACATAGACTGCCAGTGGATTGATATTACAGATGTACAACCTGGAA ACTACATTCT
AAAGGTCAGTGTA AA

(SEQ ID NO. 51)

FIG. 12E

CTATCAATGAAGGGGAGATCACTGGGTAAGTTCGAATGCCCTCAGGCAAGGTGGCC
CAGCCTTCCATTACTGAATTCAAAGATGGCACTGTTACTGTACGTTACTCACCCAGTGA
AGCTGGCCTGCATGAAATGGACATTGCTATGACAATATGCATATCCCAGGAAGCCCT
CTGCAGTTCTATGTTGATTATGTCAACTGTGGCCACATCACTGCTTATGGTCC

(SEQ ID NO. 52)

TTAGCACCTCGACCACGAAATGAGGAAGATGCAACAGACGTGGTGGGCCTGGCTCAG
GCTGTAAACGCTCGGTCCCCACCTTCAGTAAACAGAACAGCTTGGATGAAGACCTTA
TTCGGAAGCTAGCTTATGTTGCTGCTGGGGACCTGGCACCCATAAATGCTTTCATTGG
GGGCCTTGCTGCCCAGGAAGTCATGAAGGCCTGCTCTGGAAAGTTTATGCCCATCATG
CAGTGGTTGTACTTTGATGCTCTTGAATGTCTCCCAGAACGGACAAAGAGGCTCTGAC
AGAGGAGAGTGCCTCCACGTCAGAACCGTTACGATGGGCAGGTAGCTGTATTGGTCA
GACTTCAGGAGAAGCTGAGAAGCAAA

(SEQ ID NO. 53)

TTAGCACCTCCAATGGCTGGGTACCAGCCAGCCGCAATGTCCGCTCCACAAATTTGGA
GTCTGTGAGGTACTGATTAACATTTTCTGCTGGCTGCTTGAAAAGGCCTTCAAATTCAT
CCCGGGCCCACTGAAGAGTGTGTTTCGATGGCATTGGGAAAGTTTTTCAGGGTACAAAT
GGGGATGGATTTCTCTGGTGGATCCTGGCTAGACGTGATGGATTCTGTCAGGAAGGGG
ATTACCACCTGCACGTTGCCCTTT

(SEQ ID NO. 54)

TTAGCACCTCACACTCACATGCCCTTCTACATAGAGACTGGTTAAACAGCCCTCCCTCC
CTTGTCCCGACTTGACTTCCAGGCCCCCTCTGCTTTCCTCTCACAACCACACCAGGTCTG
ATGGAGTCCAGTGCCTGCAGTGACCCAACATAGACTGCACTTTCACCTACCTACTGGA
TGGTCCTGCAGCCCAGACGGCTGCTCTTCTTCTCATGGAGTTTCTCTCCTGCCTGAGA
TATGCTATCTGGTCTGCCCCCTGTGTAGCTCCCATGGGATCCCTTAAAATCGATCCTTTT
TTAA

(SEQ ID NO. 55)

FIG. 12F

TTAGCACCTCGTGAGGAGACTGTTGTCCACAGGCCAGCTAGTGGTACCCTACTGAGAA
GTTGGGTTTTGGTTTTGTTTCCCTTGAAGGGTCGCTGTTAGAGGATGGAAGTAACTTCT
AATTCTTGATCTGTTTGTGTTGGTCTTGTTTTTCAGTACTTTTTGCCAGTTGTATACACTTGG
AGAGGGAATTTGTATGCCTGTAATCTTGTTCTTGAGGTCAGAAATTCAAAACATTGGG
AGCTTTTGTGTAAGGTTAAACTGTGAATCCATATAGCAAATGCAGATCCTTTTACA
GTGTAAACCACATTTCCCTGCCTCAGCCTAAAGCACTGGTCATTT (SEQ ID NO. 56)

ACCTGCATGCCTAAAGGAGTAGGCTTAGGGGTGGGGAGAGAGAAGGCATAGGCTTTT
CTAGTTATACAAAGCTGTGTAAGGCAAGGTTCCCTTTCTACTAAATGGTCAGCTGTCACT
ACATTTATACTTTTGTATGTCATAAACCTTTCTTTTCATTCCTCCCTGGGTAACCAGGA
CAATCGGAGGGCAGTGTGTTACTGGGATTAGAGGACTAGCAATACTGGGTAACCCGCC
TAAGCTGGAAGGTGACGTAATACGTTTCTTTAAAGATTCAAGTCAGTCAAGCAGTTTAG
CAATATCAAAATGTCTGGCTGTTTGGTCCAGTGTACACTGTT (SEQ ID NO. 57)

GCTATCTGCGAAACTACAGAAAGGAAGACAGCTTGGCCCAGCGCGGTGAAGTTCAGA
ATTCAGTAGGTAGTTGTTGTTGGTTGACTTGGAGGTAGCTGGGTAATCAACAGCTTTCA
CTTTAGATTCAATGTGAACCGCAGAGTTACTCATGACCAAGAGTCTGGCAAACCTCATT
AATGCTGTTTAATACTTGTTTGATATTTTTTTCACCTTTTGAGCCCTTTTCCCAAAGAATT
CAATATCAGTTTAGTAGCAACAGTACAGTTGCCATTTAAATTGGTTTAGTTGCAGTATA
GCA (SEQ ID NO. 58)

GCTATCTGCGAAACTACAGAAAGGAAGACAGCTTGGCCCAGCGCGGTGAAGTTCAGA
ATTCAGTAGGTAGTTGTTGTTGGTTGACTTGGAGGTAGCTGGGTAATCAACAGCTTTCA
CTTTAGATTCAATGTGAACCGCAGAGTTACTCATGACCAAGAGTCTGGCAAACCTCATT
AATGCTGTTTAATACTTGTTTGATATTTTTTTCACCTTTTGAGCCCTTTTCCCAAAGAATT

FIG. 12G

CAATATCAGTTTAGTAGCAACAGTACAGTTGCCATTTAAATTGGTTTAGTTGCAGTATA
GCA (SEQ ID NO. 59)

GCTATACTGCAACTAAACCAATTTAAATGGCAACTGTACTGTTGCTACTAAACTGATA
TTGAATTCTTTGGGAAAAGGGCTCAAAAGGTGAAAAAATATCAAACAAGTATTAAAC
AGCATTAAATGAGTTTGCCAGACTCTTGGTCATGAGTAACTCTGCGGTTACATTGAATC
TAAAGTGAAAGCTGTTGATTACCCAGCTACCTCCAAGTCAACCAACAACAACCTACCTA
GTGAATTCTGAACTTCACCGCGCTGGGCCAAGCTGTCTTCC

(SEQ ID NO. 60)

GCTATACTGCCCACCACATTGCCACACTCGGAATGACATTTCTATATTTTCACCTCCCC
AGATTTCCATTTCTTCATCGTAACTTCCAATGTGCTCAAAATATTTTTTAGATATAGAA
AAAAGGCCTCCTGCAAAGGTGGGGGTCTTAATTGGGTAGGTTTCATCTTTCCTTCTTTG
CTTCTCATGATCAGGAAGTGACTCCCAGCCAAAGGAAAGGCTCCAGTCAAAATTTCCA
CGGTTATGGTTGCTTCCGTACGGAGAAGGCTTGTTGAATTCAAATGTGTTTAGATCTAT
GGATGCGATGTCTGGACTCACCACGGCA

(SEQ ID NO. 61)

GCTATACTGCTGAAGGAGATCATTTTGGTGGATGATGCTAGTGTAGACGACTACCTGC
ATGAAAAGCTGGAGGAATACATAAAACAGTTTTCTATTGTGAAAATAGTCAGGCAGC
AAGAAAGGAAAGGCCTGATCACCGCGCGGTTGCTAGGGGCAGCTGTAGCAACTGCCG
AGACGCTCACGTTCTTAGATGCTCACTGTGAGTGCTTCTATGGCTGGCTGGAACCTCTG
CTGGCCAGGATAGCTGAGAACTACACTGCCG

(SEQ ID NO. 62)

AGTTGCCAGGGGGCAGCTCACGGCGCAGCTCATCCTCTGTGATGTAATTCTTATCTCC
AGCCAGGATCTTGAAGGAAGCCATGACCTGATCTGCAGTATCAGTATCTGCCGTCTCT

FIG. 12H

CGGGACATAAAGTCGATGAAGGCCTGGAACGTCCTACCCCCAAGCGGTTGGGGTCT
ACAATGCTCATGATTCGGGCAAACCTCTGCCTCTCCCATGTTGTAACCCATGGAGATAA
GGCAGGCGCGGAAATCGTCTGTGTCCATCATGCCCGTCTTCTTCCGGTCAAAGTGGTT
GAAAGA (SEQ ID NO. 63)

AAGCCGTGTCGCTGAACTGGGAGGACACACTGCTCACCTAGAAGGCTCTGGCTGACC
CTCCGCCCCGGTTAAACAGGGACTTTGTGGCCATGTGCTGGCGACACAGGTCCTGGTAC
TCAAAGTAGTGTCACCATGGGGCCCCCTCCGGCCCCAGCGCTGCCAGGCGTCCTTATC
CCGCTGTCTCGAATGATGGCGCATACCAAGGCCACTGAAAGCCACTAGCAGCCCAGCG
ACGCCTGCCAGGGCCACTAGAGTAAGCAGCACTGAGCGCATGGGAGATATGCCAT
(SEQ ID NO. 64)

AAGCCGTGTCTGGACGTCCGTGTGTCCGGCTCTTGCTCACGCAGTCATGGCCTCCGGA
ACGCGCAAATCGGAAAGTCGGCTCCTGACTTCACGGCCACAGCGGTGGTGGATGGTGC
CTTCAAGGAAATCAAGCTTTCGGACTACAGAGGGAAGTACGTTGTCCTCTTTTTCTACC
CACTGGACTTCACTTTTGTGTTGCCCCACGGAGATCATCGCTTTTAGCGACCATGCTGAG
GACTTCCGAAAGCTAGGCTGCGAGGTGCTGGGAGTGTCTGTGGACTCTCAGTTCACCC
ACCTGGCGTGGATCAATACCCACGGAAAGAGGGAGGCTT (SEQ ID NO. 65)

AAGCCGTGTCGGAGGGCACCAAGGCTGTCACCAAGTACACCAGCTCCAAGTGAGTGC
TCAAGACTCAGCTCTTAACCCAAAGGCTCTTTTCAGAGCCACTCAAGACTTCAAAT
GGAGCTTTAATGCTGACTTAGTGACTACCGGGAAAATAACTGACTTCATCTGCAGGAT
TGTGTACAAACACTTATGGTTTAGTAAATCGAAAAGATAGACATTGCCCATCAGTTCT
GTCTGGTCCACTTAAATATGCTTTTTTCTTAGAAGTTCTAAGAACCCTGTCAATAACCT
ATCTAGGTCCAGTCCTTGAGTTCAAAGGCCAAATACCAATG (SEQ ID NO. 66)

FIG. 12I

CAACGCTCAGGATGTAAGCTGTTTCCAGCACCTGGTTCAAGCGAATGTAAGAAATAAG
AAGGTGTTGAAAGATGCCGTGAATAACATTACAGCAAAGGGGATCACAGATTACAAG
AAAGGCTTTAGCTTTGCCTTCGAACAGCTACTTAATTATAATGTTTCCAGAGCTAATTG
CAATAAGATTATCATGTTATTCACGGATGGAGGAGAAGAGAGAGCCCAGGAGATATT
TGCCAAATACAATAAAGACAAAAAAGTCCGTGTGTTTACATTTTCCGTCGGTCAACAT
AATTATGACAGAGGACCTATTCAGTGGATGGCTTGTGAAATAAAGGTTACTATTATGA
GATTCCTCCATT

(SEQ ID NO. 67)

TCAACGCTCATCACACCAAGAATCAACTGGTTCTTCAAGTTTGTCTTATTTTCAGATTG
GCCAGTGACGTTGAAGACTGGTAGAGTTCCAGTAATGACAAGTCCCAGTTCCAGGGCA
TCCAAATACACATTTGTCCATTGAACTTGCTTCGCTTTGTCACCAGCTAAAACCATTGG
TCTTCCCAGAACATCTAGATATTCCTGAGTATTGATTCTTATTGCACCAATGGAGGGAA
TCTCATAATAGTAACCTTTATTTTCACAAGCCATCCACTGAATAGGTCTCTGTCATAAT
TATGTTGACCGACGGAAATGTAA

(SEQ ID NO. 68)

TAACGCTCAGGAGAAGAATAGGAATGCAGAGAACTCTGCCACAGCCCCACGCTCCC
GGGCAGCACCTCAGCCACCACCGCAACCACCACCCCTGCTGTAGATGAAAGCAAGCCT
TGGAACCAGTATCGCTTGCCTAAGACTCTTATACCTGACTCCTACCGGGTGATCTTGAG
ACCCTACCTCACCCCCAACAATCAGGGCCTGTACATCTTCCAAGGCAACAGTACTGTT
CGCTTTACCTGCAACCAGACCACGGATGTCATTATCATCCACAGCAAAAAGCTCAACT
ACACCCTCAAAGGAAACCACAGGGTGG

(SEQ ID NO. 69)

CGAGTCAGACGGCTTCAGCATCGAGACCTGTAAGATCATGGTGGACATGCTGGATGAA
GATGGGAGTGGCAAGCTTGGCCTGAAGGAGTTCTACATCCTCTGGACGAAGATTCAGA
AATACCAAAAAATCTACCGGGAAATCGATGTGGACAGGTCTGGAACATGAATTCCTA

FIG. 12J

CGAGATGCGGAAAGCACTGGAAGAAGCAGGTTTCAAGCTGCCCTGTCAACTCCATCA
AGTCATCGTTGCCCCGGTTTGCAGACGACGAGCTAATCATCGACTTTGACAATTTTG

(SEQ ID NO. 70)

CGAGTCAGACAACCTGTTCAAGTGGGGTGGGGACCATCCACGGAGCAGCCGGCACCG
TATATGAAGACCTGAGGTACAACTCTCCCTAGAGTTCCCCAGCGGCTACCCTTACAA
CGCACCCACAGTGAAGTTCCTCACACCCTGCTACCACCCCAACGTGGACACCCAGGGC
AACATCTGCCTGGACATCCTCAAGGATAAGTGGTCTGCACTATATGATGTCAGGACTA
TCTTGCTCTCTATCCAGAGCCTGCTAGGAGAACCCAACATCGATAGCCTTTGAACACA
CACGCTGCGGAACTCTGGAAAA

(SEQ ID NO. 71)

TATGAGTCCGGAGCGACGGCTACGAGTGTGAACTGTTCCAGCCCCGAGCGACACACCA
GAAGTTATGACTACATGGAAGGAGGGGATATAAGGGTGAGAAGACTGTTCTGTCGCA
CCCAGTGGTACCTGAGGATTGACAAACGAGGCAAAGTGAAAGGGACCCAGGAGATGA
AGAACAGCTACAACATCATGGAAATCAGGACCGTGGCAGTTGGAATTGTGGCAATCA
AAGGGGTGGAAAGTGAATACTATCTTGCCATGAACAAGGAAGGGAACTCTATGCAA
AGAAAGAATGCAATGAGGATTGCAACTTCAAAGAACTGATTCTGGAAAACCATTTATA
ACACCTATG

(SEQ ID NO. 72)

TATGAGTCCGAGGAGGAGCACAATGCTGGGAGTGTGGAAAGCCAGGTTGTCCCCAGC
ACACACCGAGTGACCGATTCCAAGTTCCATCCACTCCATGCCAAGATGGATGTCATCA
AAAAAGGCCACGCCAGGGACAGCCAGCGCTACAAAGTTGACTATGAGTCTCAAAGCA
CAGACACCCAGAACTTCTCCTCCGAGTCTAAGCGGGAGACAGAATACGGTCCCTGCCG
CAGAGAAATGGAGGACACACTGAATCATCTGAAGTTCCTCAATGTGCTGAGTCCAGAG
TCTCACATCCAACTGTGACAAGAAGGGG

(SEQ ID NO. 73)

FIG. 12K

TCGCCCCGGGACTTCATGCGATTGAGAAGATTGTCTACCAAATATAGAACAGAAAAGAT
TTATCCCACAGCCACTGGAGAAAAAGAAGAAAATGTTAAAAAGAACAGATATAAGGA
CATACTGCCATTTGATCACAGCCGAGTTAAGTTGACTTTGAAGACTCCATCCCAAGAT
TCAGATTATATCAATGCAAATTTTATTAAGGGTGTGTATGGGCCAAAAGCATATGTGG
CAACCCAAGGGCCTTT

(SEQ ID NO. 74)

TGTGGAAAGCCAGGTTGTCCCCAGCACACACCGAGTGACCGATTCCAAGTTCCATCCA
CTCCATGCCAAGATGGATGTCATCAAAAAAGGCCACGCCAGGGACAGCCAGCGCTAC
AAAGTTGACTATGAGTCTCAAAGCACAGACACCCAGAACTTCTCCTCCGAGTCTAAGC
GGGAGACAGAATACGGTCCCTGCCGCAGAGAAATGGAGGACACACTGAATCATCTGA
AGTTCCTCAATGTGCTGAGTCCAGAG

(SEQ ID NO. 75)

TGACCATCGAAGTGCAAAGGAAATGACTTGATTTCATGAAGTATCTCCAGAAGTAACG
CTTTGTTTTCTGCATCCTGAACTTTATTCCCAGTGAAGAGCTGAAAATCTGGACGCTCA
AAAAATGGAAGCACTTTGGAGAGAGCCCTTAACCTCTATCAGGTACAGGAAGTACAAG
TTCCTCAGCCTTCGTGGGCCTTCTCCTTCAGTCAGAATCCCATCAAAGCGCTGCTGGAA
CTCTGTGACATTGTGACCCCATTTCTTTTCCAGCCAAGTATCTTGTAAGATACTTG
CACTCAAATGCACATTAATGCTTGCGTGCAGGCCAGATATAAGTCTGTAGAATCGCTC
TTTCTACACAGAGGCCTTCTAGCCAGTTGTAAA

(SEQ ID NO. 76)

CTGCTTGATGCTAAGCCCCGGCAGCCTGTGTTTCATCTACAGGATGCACAACATAAAAG
AAAAGATCTGATTCCCGCAGGTTCTCTTCTGACCTACACACACACACACTAAAATAAC
ATTTAAAAATATGTGCCAAATTATATTTGTTTCGGGTGCCACCTTCCACCAGCTTACCAC
TACGGTAGAACTGTCAAATTCATCTCCCTGAATTTGTCTTAAAGGGGTGTCCATGCAC
AGGCCCAAGAGTCACCTCCAATGAAATAAATGTAATACTGAAGTATGCCATGATGTTT

FIG. 12L

AGCTAAGGTCCAGGGGGCAAAGCGGTGACGTGTGCACATCGATATGAGAAACGGCAG
CACGTCAACACGAAGCAGGAGTCGCGGGATATCTTTGGAAGATGTTATGTCCTAAGTC
AGAATCTCAGAATTGAAGATGATATGGACGGAGGAGACTGGAGTTTCTGCGATGGCC
GGTTGAGAGGCCATGAAAAGTTTGGCTCCTGTCAGCAAGGAGTAGCGGCTACTTTCAC
TAAGGACTTTCATTACATTGTTTTTGGAGCCCCAGGGACTTACAACCTGGAAAGGGATC
GTCGTGTAGAACAAAAGAATAACACTTTTTT

(SEQ ID NO. 81)

AAGCCGTGTCTGTGCTCAAGGAAGAAACCCACTGGACCAACTTCTGTCAGAAAGGAA
AACCTTGTTCAAAGTTTCAGGACCCTGTTCTTTGCTTATTTGCACATGGTCACCTTGGT
CTGAGCTAGCCACCATTGTCACCCACAGCTGCAAAGAAAGCAGACCTTAGGAAACACT
GTCACGGCTGAGTGTGACTGCCTTGTTTCATCCCCTGGACTGGTACTGTGTTGCCTGCAG
TACCATTGGGATCCCATAGCAAGAGAGGGAGAGGGAGATGTTAGTTAGCCTTTGCTAC
GAACCAAGCTGTCCCAAGTCTCAACAGCTAAACAGGTATTCATTTACCATGATTCTAT
GGTTAGCTAAGCTCTTGAG

(SEQ ID NO. 82)

CTTTCTACCCTGGAGGATGTGCTTGAGGCACACTGCTCCTGTGCTCTCCACTTGAGGCA
TAAGCCCAGTCAGTTGTGCATAGATGATTAACCTCTGACCCCTAAAGATGGTAAGTTG
CTCTGGAGAAAGCATTTTAACAGACAAACCAGGAGGCAAATCCCAACTTAGAGAGAT
GTTATCCACTGCACACTGTAGAGCAAACCTTGAGAGACCCAAGAGCCTTGGTCTGCATC
CTGTCCTTGCCCTGTGATAAACACTCGAGTACCCCTGATACCGGGCGATATTTTTGATT
AACTGGTCGAGGCTCCTTGTCOAATTCCAAAAGAGAACATCTGTGTTTC

(SEQ ID NO. 83)

FIG. 12N

TGGTAAAGGGCATCTGTAAATACACTCTATGAGGAAATTAAACTTGAACATGGCAGT
CTGACATTGCAAAACAAAACAAAACAAAACCTGACCCTCCAATAGCAGCGAAAACAAC
GTGAAAGATACAAAGCAATGAGAATCTGGTTCTGAACGCCTGGGATCCTGGGAGTCAT
CGGTAGCAGCGCCATGAGAGGAGCCGTGGCCTGTCCCATGTGGTCCCACCTTCACCTC
TTCCTCACATCCCTCTTAAG

(SEQ ID NO. 84)

TGGTAAAGGGGGCAAGGGCAAAGGCACGGGAGACAGAGGCCACTGCATCTGTACCCA
CATCAGACATGTTTGTCCATTTTCTCTCATTTGGCCTTAGACCATTGGCAAGAGTAAAT
GCTCTTAGTCCCGTTATCTAGAAATTTCTTCCTTTGGGGAGAACCCTTATAGACAATA
TCAGCTCTCTACAAATAACACGAAAGGTCGTAACAC
AGCAAGTGACCAGAAAGTGCCCGTCCTTGCGGCTCTGATCCACGTGGCTCTCCGTAGA
CAAATTGTTTTTTCTTGTAGGGATACTGTTTTGCTTCTGAACTTTCTTACAAGTGTTTG
GGACTCTTCGGGTGGCGTT

(SEQ ID NO. 85)

TGGTAAAGGGTCAAGTGTTTCGATCAGAGTGGAGCTCCATTACCGAATGTAATCGTGGA
AGTCCAAGACAGAAAGCATATCTGCCCGTTTAGAACCAACAAGCTTGGAGAATACTAT
CTGCTTCTGCTGCCCCGGGTCCTACGTGATCAATGTTACAGTCCCTGGACACGACTCCTA
CCTCACGAAGCTTACTATTCCAGGGAAATCCCAGCCCTTCAGTGCTCTTAAAAAGGAT
TTTACCTCCCGCTGCGATGGCAGCCGGATTCCATCTCCGTATCCAATCCTTCGTGCCG
ATGATTCCGCTGTACAAATTCATGCCAAGCCACTCGGCTGCCACAAAGCCTAGTCTGG
G

(SEQ ID NO. 86)

GAATTCGGCTTTCTGCGATCCACTCTTTGAAGCTATTGGCAAGATATTCAGCAACATCC
GCATCAGCACGCAGAAAGAGATATGAGGGACATTTCAAGGATGAAAGGTTTTTTTCCC
CCCTTACTATTTCTTGGTGCCAATTCCAAGTTGCTCTCGCAGCAGCAAATTTATGAAT

FIG. 120

GGTTTGTCTTGATCAAGAACAAGAATTCATTCCCACCATTCATATATACTACTTTC
TCTTCTT

(SEQ ID NO. 87)

GAATTCGGCTTTCTGCGATCCACTCTTTGAAGCTATTGGCAAGATATTCAGCAACATCC
GCATCAGCACGCAGAAAGAGATATGAGGGACATTTCAAGGATGAAAGGTTTTTTTCCC
CCCTTACTATTTCTTGGTGCCAATTCCAAGTTGCTCTCGCAGCAGCAAATTTATGAAT
GGTTTGTCTTGATCAAGAACAAGAATTCATTCCACCATTCATATATCTACGTCTCT
TCTAG

(SEQ ID NO. 88)

ACGAGGGGAAACCTCCTCAGAGCCTGCAGCCAGCCACGCGCCAGCATGTCTGGGGGC
AAATACGTAGACTCCGAGGGACATCTCTACACTGTTCCCATCCGGGAACAGGGCAACA
TCTACAAGCCCAACAACAAGGCCATGGCAGACGAGGTGACTGAGAAGCAAGTGTATG
ACGCGCACACCAAGGAGATTGACCTGGTCAACCGCGACCCCAAGCATCTCAACGACG
ACGTGGTCAAGATTGACTTTGAAGATGTGATTGCAGAACCAGAAGGGACACACAGTTT
CGACGGCATCTGGAAGGCCAGCTTCACCACCTTCACTGTGACAAAATATTGGTTTTAC
CGCTTGTTGTCTACGATCTTCGGCATCCCAATGGCACTCATCTGGGGCATTACTTTGC
CATTCTCTCCTTCCTGCACATCTGGGCGGTTGTACCGTGCATCAAGAGCTTCCTGATTG
AGATTCAGTGCATCAGCCGCGTCTACTCCATCTACGTCCATACCTTCTGCGATCCACTC
TTTGAAGCTATTGGCAAGATATTCAGCAACATCCGCATCAGCACGCAGAAAGAGATAT
GAGGGACATTTCAAGGATGAAAGGTTTTTTTCCCCCCTTACTATTTCTTGGTGCCAAT
TCCAAGTTGCTCTCGCAGCAGCAAATTTATGAATGGTTTGTCTTGATC

(SEQ ID NO. 89)

MECLYYFLGFLLLAARLPLDAAKRFHDVLGNERPSAYMREHNQLNGWSSDENDWNEKL
YPVWKRGD MRWKNSWKGRVQAVLTSDSPALVGSNITFAVNLIF
PRCQKEDANGNIVYEKNCRNEAGLSADPYVYNWTAWSESDGENGTGQSHHNVFPDGK

FIG. 12P

PFPHHPGWRRWNFIYVFHTLGQYFQKLGRCSVRVSVNTANVTLG PQLMEVTVYRRHGRA
YVPIAQVKDVYVVTDQIPVFVTMFQKNDRNSSDETFLKDL PIMFDVLIHDPSHFLNYSTIN
YKWSFGDNTGLFVSTNHTVNHTYVLNGTFSNLTVKAAAPGPCPPPPPPRPSKPTPSLGP
AGDNPLELSRIPDENCQINRYGHFQATTIVEGILEVNIIQMTDVLMPVPWP ESSLIDFVVTC
QGSIPTEVCTIISDPTCEITQNTVCSPVDVDEMCLLTVRRTFNGSGTYCVNLT LGDDTSLAL
TSTLISVPDRDPASPLRMANSALISVGCLAIFVTVISLLVYKKHKEYNPIENSPGNVVR SKGL
SVFLNRAKAVFFPGNQEKDPLLKNQEFKGVS

(SEQ ID NO. 90)

1 CAGATGCCAG AAGAACACTG TTGCTCTTGG TGGACGGGCC CAGAGGAATT
CAGAGTTAAA
61 CCTTGAGTGC CTGCGTCCGT GAGAATTCAG CATGGAATGT CTCTACTATT
TCCTGGGATT
121 TCTGCTCCTG GCTGCAAGAT TGCCACTTGA TGCCGCCAAA CGATTTTCATG
ATGTGCTGGG
181 CAATGAAAGA CCTTCTGCTT ACATGAGGGA GCACAATCAA TTAAATGGCT
GGTCTTCTGA
241 TGAAAATGAC TGGAATGAAA AACTCTACCC AGTGTGGAAG CGGGGAGACA
TGAGGTGGAA
301 AAATCCTGG AAGGGAGGCC GTGTGCAGGC GGTCCTGACC AGTGA CTCAC
CAGCCCTCGT
361 GGGCTCAAAT ATAACATTTG CGGTGAACT GATATTCCT AGATGCCAAA
AGGAAGATGC
421 CAATGGCAAC ATAGTCTATG AGAAGAACTG CAGAAATGAG GCTGGTTTAT
CTGCTGATCC
481 ATATGTTTAC AACTGGACAG CATGGTCAGA GGACAGTGAC GGGGAAAATG
GCACCGGCCA
541 AAGCCATCAT AACGTCTTCC CTGATGGGAA ACCTTTTCCT CACCACCCCG
GATGGAGAAG

FIG. 12Q

601 ATGGAATTTC ATCTACGTCT TCCACACACT TGGTCAGTAT TTCCAGAAAT
TGGGACGATG

661 TTCAGTGAGA GTTTCTGTGA ACACAGCCAA TGTGACACTT GGGCCTCAAC
TCATGGAAGT

721 GACTGTCTAC AGAAGACATG GACGGGCATA TGTTCCCATC GCACAAGTGA
AAGATGTGTA

781 CGTGGTAACA GATCAGATTC CTGTGTTTGT GACTATGTTC CAGAAGAACG
ATCGAAATTC

841 ATCCGACGAA ACCTTCCTCA AAGATCTCCC CATTATGTTT GATGTCCTGA
TTCATGATCC

901 TAGCCACTTC CTCAATTATT CTACCATTAA CTACAAGTGG AGCTTCGGGG
ATAATACTGG

961 CCTGTTTGTT TCCACCAATC ATACTGTGAA TCACACGTAT GTGCTCAATG
GAACCTTCAG

1021 CCTTAACCTC ACTGTGAAAG CTGCAGCACC AGGACCTTGT CCGCCACCGC
CACCACCACC

1081 CAGACCTTCA AAACCCACCC CTTCTTTAGG ACCTGCTGGT GACAACCCCC
TGGAGCTGAG

1141 TAGGATTCCT GATGAAAAC TCCAGATTAA CAGATATGGC CACTTTCAAG
CCACCATCAC

1201 AATTGTAGAG GGAATCTTAG AGGTAAACAT CATCCAGATG ACAGACGTCC
TGATGCCGGT

1261 GCCATGGCCT GAAAGCTCCC TAATAGACTT TGTCGTGACC TGCCAAGGGA
GCATTCCCAC

1321 GGAGGTCTGT ACCATCATTT CTGACCCCAC CTGCGAGATC ACCCAGAACA
CAGTCTGCAG

1381 CCCTGTGGAT GTGGATGAGA TGTGTCTGCT GACTGTGAGA CGAACCTTCA
ATGGGTCTGG

1441 GACGTACTGT GTGAACCTCA CCCTGGGGGA TGACACAAGC CTGGCTCTCA
CGAGCACCT

FIG. 12R

1501 GATTTCTGTT CCTGACAGAG ACCCAGCCTC GCCTTTAAGG ATGGCAAACA
GTGCCCTGAT
1561 CTC CGTTGGC TGCTTGGCCA TATTTGTCAC TGTGATCTCC CTCTTGGTGT
ACAAAAACA
1621 CAAGGAATAC AACCCAATAG AAAATAGTCC TGGGAATGTG GTCAGAAGCA
AAGGCCTGAG
1681 TGTCTTTCTC AACCGTGCAA AAGCCGTGTT CTCCCGGGA AACCAGGAAA
AGGATCCGCT
1741 ACTCAAAAAC CAAGAATTGA AAGGAGTTTC TTAAATTTTCG ACCTTGTTTC
TGAAGCTCAC
1801 TTTTCAGTGC CATTGATGTG AGATGTGCTG GAGTGGCTAT TAACCTTTTT
TTCCTAAAGA
1861 TTATTGTTAA ATAGATATTG TGGTTTGGGG AAGTTGAATT TTTTATAGGT
TAAATGTCAT
1921 TTTAGAGATG GGGAGAGGGA TTATACTGCA GGCAGCTTCA GCCATGTTGT
GAAACTGATA
1981 AAAGCAACTT AGCAAGGCTT CTTTTCATTA TTTTTATGT TTCACTTATA
AAGTCTTAGG
2041 TAACTAGTAG GATAGAAACA CTGTGTCCCG AGAGTAAGGA GAGAAGCTAC
TATTGATTAG
2101 AGCCTAACCC AGGTAACTG CAAGAAGAGG CGGGATACTT TCAGCTTTCC
ATGTAAGTGT
2161 ATGCATAAAG CCAATGTAGT CCAGTTTCTA AGATCATGTT CCAAGCTAAC
TGAATCCAC
2221 TTCAATACAC ACTCATGAAC TCCTGATGGA ACAATAACAG GCCCAAGCCT
GTGGTATGAT
2281 GTGCACACTT GCTAGACTCA GAAAAAATAC TACTCTCATA AATGGGTGGG
AGTATTTTGG
2341 TGACAACCTA CTTTGCTTGG CTGAGTGAAG GAATGATATT CATATATTCA
TTTATTCCAT

FIG. 12S

2401 GGACATTTAG TTAGTGCTTT TTATATACCA GGCATGATGC TGAGTGACAC
TCTTGTGTAT
2461 ATTTCCAAAT TTTTGTATAG TCGCTGCACA TATTTGAAAT CATATATTAA
GACTTTCCAA
2521 AGATGAGGTC CCTGGTTTTT CATGGCAACT TGATCAGTAA GGATTTCACC
TCTGTTTGTA
2581 ACTAAAACCA TCTACTATAT GTTAGACATG ACATTCTTTT TCTCTCCTTC
CTGAAAAATA
2641 AAGTGTGGGA AGAGACAAAA AAAAAAAAAA //

(SEQ ID NO. 91)

AAGGTGAAAGATGTGTATGTGATAACAGATCAGATCCCTGTATTCGTGACCATGTCCC
AGAAGAATGACAGGAACTTGTCTGATGAGATCTTCCTCAGAGACCTCCCCATCGTCTT
CGATGTCCTCATTGATGCCAGCCACTTCCTCAACGACTCTGCCATTCCTACAAGT
GGAACCTTGGGGACAACACTGGCCTGTTTGTCTCCAACAATCACACTTTGAATCACAC
TTATGTGCTCAATGGAACCTTCAACCTTAACCTCACCGTGCAAACCTGCAGTGCCCGGG
CCATGCCCTCCCCCTTCGCCTTCGACTCCGCCTCCACCTTCGTA

(SEQ ID NO. 92)

AAGGTGAAAGATGTGTATGTGATAACAGATCAGATCCCTGTATTCGTGACCATGTCCC
AGAAGAATGACAGGAACTTGTCTGATGAGATCTTCCTCAGAGACCTCCCCATCGTCTT
CGATGTCCTCATTGATGCCAGCCACTTCCTCAACGACTCTGCCATTCCTACAAGT
GGAACCTTGGGGACAACACTGGCCTGTTTGTCTCCAACAATCACACTTTGAATCACAC
TTATGTGCTCAATGGAACCTTCAACCTTA

(SEQ ID NO. 93)

AAGGTGAAAGATGTGTATGTGATAACAGATCAGATCCCTGTATTCGTGACCATGTCCC
AGAAGAATGACAGGAACTTGTCTGATGAGATCTTCCTCAGAGACCTCCCCATCGTCTT

FIG. 12T

CGATGTCCTCATTCATGATCCCAGCCACTTCCTCAACGACTCTGCCATTTCTACAAGT
GGAAC TTTGGGGACAACACTGGCCTGTTTGTCTCCAACAATCACACTTTGAATCACAC
TTATGTGCTCAATGGAACCTTCAACCTTAACCTCACCGTGCAAACCTGCAGTGCCCGGG
CCATGCCCTCCCCCTTCGCCTTCGACTCCGCCTCCACCTTCGTA (SEQ ID NO. 94)

TACGAAGGTGGAGGCGGAGTCGAAGGCGAAGGGGGAGGGCATGGCCCGGGCACTGCA
GTTTGCACGGTGAGGTTAAGGTTGAAGGTTCCATTGAGCACATAAGTGTGATTCAAAG
TGTGATTGTTGGAGACAAACAGGCCAGTGTTGTCCCCAAAGTTCCACTTGTAGGAAAT
GGCAGAGTCGTTGAGGA

(SEQ ID NO. 95)

AAGGTGAAAGATGTGTATGTGATAACAGATCAGATCCCTGTATTCGTGACCATGTCCC
AGAAGAATGACAGGAACTTGTCTGATGAGATCTTCCTCAGAGACCTCCCCATCGTCTT
CGATGTCCTCATTCATGATCCCAGCCACTTCCTCAACGACTCTGCCATTTCTACAAGT
GGAAC TTTGGGGACAACACTGGCCTGTTTGTCTCCAACAATCACACTTTGAATCACAC
TTATGTGCTCAATGGAACCTTCAACCTTAACCTCACCGTGCAAACCTGCAGTGCCCGGG
CCATGCCCTCCCCCTTCGCCTTCGACTCCGCCTCCACCTTCGTA

(SEQ ID NO. 96)

RRWRRSRRRRGRAWPGHCSLHGEVKVEGSIEHISVIQSVIVGDKQASVVPKVPLVGNGRV
VEEVAGIMNEDIEDDGEVSEEDLIRQVPVILLGHGHEYRDLICYHHIFHL

(SEQ ID NO. 97)

KVKDVYVITDQIPVFVTMSQKNDRNLSDEIFLRDLPIVFDVLHDP SHFLNDS AISYKWNFG
DNTGLFVSNNHTLNHTYVLNGTFNLNLTVQTA VPGPCPPPS PSTPPPPS (SEQ ID NO. 98)

FIG. 12U

YEGGGGVEGEGGGHGP GTAVCTVRLRLKVPLST*V*FKV*LLETNRPVLSPKFHL*EMAES
LRKWLGS*MRTSKTMGRSLRKISSDKFLSFFWDMVTNTGI*SVITYTSFT (SEQ ID NO. 99)

MECLYYFLGFLLLAARLPLDAAKRFHDVLGNERPSAYMREHNQLNGWSSDENDWNEKL
YPVWKRGD MRWKNSWKGRVQAVLTSDSPALVGSNITFAVNLIFFRCQKEDANGNIVYE
KNCRNEAGLSADPYVYNWTAWSEDS DGENGTGQSHHNVPD GK
PFPHPGWRRWNFIYVFHTLGQYFQKLGRCSVRVSVNTANVT LGPQLMEVTVYRRHGRA
YVPIAQVKDVYVVT DQIPVFVTMFQKNDRNSSDETFLKDLPIMFDVLIHDPSHFLNYSTIN
YKWSFGDNTGLFVSTNHTVNHTYVLNGTFSNLTVKAAAPGPCPPPPPPRPSKPTPSLGP
AGDNPLELSRIPDENCQINRYGHFQATITIVEGILEVNIIQMTDVLMPVPWPPESSLIDFVVT C
QGSIPTEVCTIISDPTCEITQNTVCSPVDVDEMCLLTVRRTFN GSGTYCVNLT LGDDTSLAL
TSTLISVPDRDPASPLRMANSALISVGCLAIFVTVISLLVYKKHKEYNPIENSPGNVVR SKGL
SVFLNRAKAVFFPGNQEKDPLLKNQEFKGVS (SEQ ID NO. 100)

1 CAGATGCCAG AAGAACACTG TTGCTCTTGG TGGACGGGCC CAGAGGAATT
CAGAGTTAAA
61 CCTTGAGTGC CTGCGTCCGT GAGAATTCAG CATGGAATGT CTCTACTATT
TCCTGGGATT
121 TCTGCTCCTG GCTGCAAGAT TGCCACTTGA TGCCGCCAAA CGATTTCATG
ATGTGCTGGG
181 CAATGAAAGA CCTTCTGCTT ACATGAGGGA GCACAATCAA TTAAATGGCT
GGTCTTCTGA
241 TGAAAATGAC TGGAATGAAA AACTCTACCC AGTGTGGAAG CGGGGAGACA
TGAGGTGGAA
301 AAATCCTGG AAGGGAGGCC GTGTGCAGGC GGTCTTGACC AGTGACTCAC
CAGCCCTCGT
361 GGGCTCAAAT ATAACATTTG CGGTGAACCT GATATTCCT AGATGCCAAA
AGGAAGATGC

FIG. 12V

421 CAATGGCAAC ATAGTCTATG AGAAGAACTG CAGAAATGAG GCTGGTTTAT
CTGCTGATCC
481 ATATGTTTAC AACTGGACAG CATGGTCAGA GGACAGTGAC GGGGAAAATG
GCACCGGCCA
541 AAGCCATCAT AACGTCTTCC CTGATGGGAA ACCTTTTCCT CACCACCCCG
GATGGAGAAG
601 ATGGAATTTC ATCTACGTCT TCCACACACT TGGTCAGTAT TTCCAGAAAT
TGGGACGATG
661 TTCAGTGAGA GTTTCTGTGA ACACAGCCAA TGTGACACTT GGGCCTCAAC
TCATGGAAGT
721 GACTGTCTAC AGAAGACATG GACGGGCAIA TGTTCCCATC GCACAAGTGA
AAGATGTGTA
781 CGTGGTAACA GATCAGATTC CTGTGTTTGT GACTATGTTT CAGAAGAACG
ATCGAAATTC
841 ATCCGACGAA ACCTTCCTCA AAGATCTCCC CATTATGTTT GATGTCCTGA
TTCATGATCC
901 TAGCCACTTC CTCAATTATT CTACCATTAA CTACAAGTGG AGCTTCGGGG
ATAATACTGG
961 CCTGTTTGTT TCCACCAATC AACTGTGAA TCACAUGTAT GTGCTCAATG
GAACCTTCAG
1021 CCTTAACCTC ACTGTGAAAG CTGCAGCAAC AGGACCTTGT CCGCCACCGC
CACCACCACC
1081 CAGACCTTCA AAACCCACCC CTTCTTTAGG ACCTGCTGGT GACAACCCCC
TGGAGCTGAG
1141 TAGGATTCCT GATGAAAAC TCCAGATTAA CAGATATGGC CACTTTCAAG
CCACCATCAC
1201 AATTGTAGAG GGAATCTTAG AGGTAAACAT CATCCAGATG ACAGACGTCC
TGATGCCGGT
1261 GCCATGGCCT GAAAGCTCCC TAATAGACTT TGTCGTGACC TGCCAAGGGA
GCATTCCCAC

FIG. 12W

1321 GGAGGTCTGT ACCATCATT CTGACCCAC CTGCGAGATC ACCCAGAACA
CAGTCTGCAG
1381 CCCTGTGGAT GTGGATGAGA TGTGTCTGCT GACTGTGAGA CGAACCTTCA
ATGGGTCTGG
1441 GACGTACTGT GTGAACCTCA CCCTGGGGGA TGACACAAGC CTGGCTCTCA
CGAGCACCT
1501 GATTTCTGTT CCTGACAGAG ACCCAGCTC GCCTTTAAGG ATGGCAAACA
GTGCCCTGAT
1561 CTCCGTTGGC TGCTTGGCCA TATTTGTCAC TGTGATCTCC CTCTTGGTGT
ACAAAAACA
1621 CAAGGAATAC AACCCAATAG AAAATAGTCC TGGGAATGTG GTCAGAAGCA
AAGGCCTGAG
1681 TGTCTTTCTC AACCGTGCAA AAGCCGTCTT CTCCCGGGA AACCAGGAAA
AGGATCCGCT
1741 ACTCAAAAAC CAAGAATTTA AAGGAGTTC TTAAATTTCG ACCTTGTTTC
TGAAGCTCAC
1801 TTTTCAGTGC CATTGATGTG AGATGTCCTG GAGTGGCTAT TAACCTTTT
TTCCTAAAGA
1861 TTATIGTTAA ATAGATATTG TGGTTTGGGG AAGTTGAATT TTTTATAGGT
TAAATGTCAT
1921 TTTAGAGATG GGGAGAGGGA TTATACTGCA GGCAGCTTCA GCCATGTTGT
GAAACTGATA
1981 AAAGCAACTT AGCAAGGCTT CTTTTCATTA TTTTTATGT TTCACTTATA
AAGTCTTAGG
2041 TAACTAGTAG GATAGAAACA CTGTGTCCCG AGAGTAAGGA GAGAAGCTAC
TATTGATTAG
2101 AGCCTAACCC AGGTAACTG CAAGAAGAGG CGGGATACTT TCAGCTTTCC
ATGTAAGTGT
2161 ATGCATAAAG CCAATGTAGT CCAGTTTCTA AGATCATGTT CCAAGCTAAC
TGAATCCCAC

FIG. 12X

2221 TTCAATACAC ACTCATGAAC TCCTGATGGA ACAATAACAG GCCCAAGCCT
GTGGTATGAT
2281 GTGCACACTT GCTAGACTCA GAAAAAATAC TACTCTCATA AATGGGTGGG
AGTATTTTGG
2341 TGACAACCTA CTTTGCTTGG CTGAGTGAAG GAATGATATT CATATATTCA
TTTATTCCAT
2401 GGACATTTAG TTAGTGCTTT TTATATACCA GGCATGATGC TGAGTGACAC
TCTTGTGTAT
2461 ATTTCCAAAT TTTTGTATAG TCGCTGCACA TATTTGAAAT CATATATTAA
GACTTTCCAA
2521 AGATGAGGTC CCTGGTTTTT CATGGCAACT TGATCAGTAA GGATTTCAACC
TCTGTTTGTA
2581 ACTAAAACCA TCTACTATAT GTTAGACATG ACATTCTTTT TCTCTCCTTC
CTGAAAAATA
2641 AAGTGTGGGA AGAGACAAAA AAAAAAAAAA // (SEQ ID NO. 101)

MECLYYFLGFLLLAARLPLDAAKRFHDLGNERPSAYMREHNQLNGWSSDENDWNEKL
YPVWKRGMRWKNSWKGRVQAVLTSDSPALVGSNTFAVNLIFFRCQKEDANGNIVYE
KNCRNEAGLSADPYVYNWTAWSESDGENG TGQSHHNVFPDGKPFPHHPGWRRWNFIY
VFHTLGQYFQKLGRCSVRVSVNTANVT LGPQLMEVTVYRRHGRAYVPLAQVKDVYVVT
DQIPVFVTMFQKNDRNSSDETFLKDLPMFDVLHDP SHFLNYSTINYKWSFGDNTGLFVS
TNHTVNHTYVLNGTFSLNLT VKAAAPGPCPPPPPPRPSKPTPSLGPAGDNP LELSRIPDEN
CQINRYGHFQATITIVEGILEVN I QMTDVLMPVPWPESLIDFVVTCQGSPT EVCTIISDPT
CEITQNTVCSPVDVDEMCLLT VRRTFNGSGTYCVNLTLGDDTSLALTSTLISVPDRDPASP
LRMANSALISVGCLAIFVTVISLLVYKKHKEYNPIENSPGNVVR SKGLSVFLNRAKAVFFPG
NQEKDPLLKNQEFGKVS* (SEQ ID NO. 102)

FIG. 12Y

CTGACCAGGAACCCACTCTTCTGTGCATGTATGTGAGCTGTGCAGAAGTATGTGGCTG
GGAAGTGTGTTCTCTAAGGATTATTGTAAAATGTATATCGTGGCTTAGGGAGTGTGG
TTAAATAGCATTTTAGAGAAGAAAAAAAAAAAAAAAAAACTCGAGAGTACTTCTAG
AGCGGCCGCGGCCATCGATTTTCCACCCGGGTGGGGTACCAGGTAAGTGTACCCAA
TTCGCCTATAGTGAGT (SEQ ID NO. 103)

AGGACAAGCCAAGGACACTCTAAGTCTTTGGCCTTCCCTCTGACCAGGAACCCACTCT
TCTGTGCATGTATGTGAGCTGTGCAGAAGTATGTGGCTGGGAAGTGTGTTCTCTAAG
GATTATTGTAAAATGTATATCGTGGCTTAGGGAGTGTGGTTAAATAGCATTTTAGAGA
AGACATGGGAAGACTTAGTGTTTCTTCCCATCTGTATTGTGGTTTTTACACTGTTCTG
GGGTGGACACGCTGTGTCTGAAGGGGAGGTGGGGGTCAGTCTACTTAAGGTCCTAGG
TTAACTGGGGGAGATACCACAGATGCTCAGCTTCCACATAACATGGGCATGAACCAG
CTAATCACACTGAA (SEQ ID NO. 104)

GGATCCTTCTCCTGGTCTCCTCGGAAGAACGGGGCTTTCGCGTGAAGGAGAACAC
TCAGGCCCTTGCCCTTGACCGTGTTCTGGGGCAGTTTCCTATTGGCTTGACGCCTTG
TGTTTTTTGTACAGCAAGATGGTAACCATGGTGACAAGCACAGCCAGGCAGCCGATGG
AGATCAGGACACCATTCACTGCTCTCAGAGGGAGTCTGGGTCTTTGCCAGGGATAGAG
ATCAGGGTGCTGGTGAGGGCCAGGCTTCGATCATCTCCAGAGTGAAATTCACACAGT
AGGTGCCAGACCCATTGAAGGCTCTTCTCACAGACAGCAGCACAGCCCATCCACAGCC
ACAGGGCTGCAGACCCGGTTCTGGGCGATCTGGCAGGTGGGGTCCGAGATGATCGTA
CAGGCTTCATGGGGGTGGCCCCTTTGCAGGTCACAGTGAAGTCCATCAGGGAGTTGG
CAGGCTGCGGTGTGGGCATGGGGACATCTGCTATCTGCATGATGCTGACTTCCAGGATCC
(SEQ ID NO. 105)

TAGCAGATGTCCCATGCCACACCGCAGCCTGCCAACTCCCTGATGGACTTCACTGT
GACCTGCAAAGGGGCCACCCCATGGAAGCCTGTACGATCATCTCCGACCCACCTGC
CAGATCGCCAGAACCGGGTCTGCAGCCCTGTGGCTGTGGATGGGCTGTGCTGCTGTC

FIG. 12Z

TGTGAGAAGAGCCTTCAATGGGTCTGGCACCTACTGTGTGAATTTCACTCTGGGAGAT
GATCGAAGCCTGGCCCTCACCAGCACCCCTGATCTCTATCCCTGGCAAAGACCCAGACT
CCCTCTGAGAGCAGTGAAT (SEQ ID NO. 106)

GGATCCTTCTCCTGGTCTCCTCGGAAGAACGGGGCTTTCGCGTGACTGAGGAGAACAC
TCAGGCCCTTGCCCTTGACCGTGTTCCCTGGGGCAGTTTCCTATTGGCTTGTACGCCTTG
TGTTTTTTGTACAGCAAGATGGTAACCATGGTGACAAGCACAGCCAGGCAGCCGATGG
AGATCAGGACACCATTCACTGCTCTCAGAGGGAGTCTGGGTCTTTGCCAGGGATAGAG
ATCAGGGTGCTGGTGAGGGCCAGGCTTCGATCATCTCCCAGAGTGAAATTCACACAGTA
(SEQ ID NO. 107)

TTTTTTTTTTTTTTTTTTAGACTGCCTTTTAAATGAGTAGAATATGTACACACACGCACC
ATACACAAAGCCCGGGCCCATTAATAATTTGTCAGGAGCTCAGGCATGCTCAGTGAGT
TGGAAGGCAGATGAAGCATG
CCTTCAGGTGGTGATTAGCTGGGTTCATGCCCATGTTATCGTGGAAAGCTGAGGCATC
TGTGGTATCTCCCCCAGTTAACCTAGGACCTTAAGTAGCAGTGACCCACCTCCCTTCAG
ACACAGCG

(SEQ ID NO. 108)

GGATCCTGGAAGTCAGCATCATGCAGATAGCAGATGTCCCCATGCCACACCGCAGCC
TGCCAACTCCCTGATGGACTTCACTGTGACCTGCAAAGGGGGCCACCCCCATGGAAGCC
TGTACGATCATCTCCGACCCACCTGCCAGATCGCCCAGAACCGGGTCTGCAGCCCTG
TGGCTGTGGATGGGCTGTGCTGCTGTCTGTGAGAAGAGCCTTCAATGGGTCTGGCACC
TACTGTGTGAATTTCACTCTGGGAGATGATCGAAGCCT

(SEQ ID NO. 109)

FIG. 12AA

TTTTTTTTTTTTTTTTTTTTCTTCTCTAAAATGCTATTTAACCACACTCCCTAAGCCACGA
TATACATTTTACAATAATCCTTAGAGAACAACAGTTCCCAGCCACATACTTCTGCACA
GCTCACATACATGCACAGAAGAGTGGGTTCCTGGTCAGAGGGAAGGCCAAAGACTTA
GAGTGTCTTGGCTTGTCTGGAGCAATGGATCCTTCTCCTGGTCTCCTCGGAAGAACG
GGCTTT (SEQ ID NO. 110)

AAACTGCAGTGCCCGGGCCATGCCCTCCCCCTTCGCCTTCGACTCCGCCTCCACCTTCA
ACTCCGCCCTCACCTCCGCCCTCACCTCTGCCCACATTATCAACACCTAGCCCCCTCTTT
AATGCCTACTGGTTACAAATCCATGGAGCTGAGTGACATTTCCAATGAAAAGTGCCGA
ATAAACAGATATGGCTACTTCAGAGCCACCATCACAATTGTAGAGGGGATCCTGGACG
CAGCATCATGCAGATAGCAGATGTCCCATGCCACACCGCAGCCGTCCAACCTCCTGAT
GGACTTCACTGTGACCTCAAGGGCACCCATGGAAGCTGTCAGA (SEQ ID NO. 111)

CCTCAACGACTCTGCCATTTCTTACAAGTGGAACCTTTGGGGACAACACTGGCCTGTTT
GTCTCCAACAATCACACTTTGAATCACACTTATGTGCTCAATGGAACCTTCAACCTTAA
CCTCACCGTGCAAAGTGCAGTGCCCGGGCCATGCCCTCCCCCTTCGCCTTCGACTCCGC
CTCCACCTTCAACTCCGCCCTCACCTCCGCCCTCACCTCTG (SEQ ID NO. 112)

CCTCAACGACTCTGCCATTTCTTACAAGTGGAACCTTTGGGGACAACACTGGCCTGTTT
GTCTCCAACAATCACACTTTGAATCACACTTATGTGCTCAATGGAACCTTCAACCTTAA
CCTCACCGTGCAAAGTGCAGTGCCCGGGCCATGCCCTCCCCCTTCGCCTTCGACTCCGC
CTCCACCTTCAACTCCGCCCTCACCTCCGCCCTCACCTCTGCCCACATTATCAACACCT
AGCCCCCTCTTTAATGCCTACTGGTTACAAATCCATGGAGCTGAGTGACATTTCCAATG
AAAAGTGCCGAATAAACAGATATGGCTACTTCAGAGCCACCATCACAATTGTAGAGG
GGATCCTGGAAGTCAGCATCATGCAGATAGCAGATGTCCCATGCCACACCGCAGCC
TGCCAACTCCCTGATGGACTTCACTGTGACCTGCAAAGGGGGCCACCCCCATGGAAGCC
TGTACGATCATCTCCGACCCACCTGCCAGATCGCCCAGAACCGGGTCTGCAGCCCTG

FIG. 12BB

GAATTCGCACGAGGGGAGTCAGAGTCAAGCCCTGACTGGTTGCAGGCGCTCGGAGTC
AGCATGGAAAGTCTCTGCGGGGTCCTGGGATTTCTGCTGCTGGCTGCAGGACTGCCTC
TCCAGGCTGCCAAGCGATTTTCGTGATGTGCTGGGCCATGAACAGTATCCCGATCACAT
GAGAGAGCACAACCAATTACGTGGCTGGTCTTCGGATGAAAATGAATGGGTTC AATA
TCACTTTTGTGGTGAA (SEQ ID NO. 117)

GAATTCGGCACGAGGAAGGAGGCCGTGTGCAGGCAGTCCTGACCAGTGACTCACCGG
CTCTGGTGGGTTC AATATCACTTTTGTGGTGAACCTGGTGTTC C C C CAGATGCCAGAAG
GAAGATGCTAATGGCAATATCGTCTATGAGAAGAACTGCAGGAATGATTTGGGACTG
ACATCTGACCTGCATGTCTACA A CTGGACTGCAGGGGCAGATGATGGTGACTGGGAAG
ATGGCACCT (SEQ ID NO. 118)

GAAGGTGGAGGCGGAGTCGAAGGCGAAGGGGGAGGGCATGGCCCGGGCACTGCAGTT
TGCACGGTGAGGTTAAGGTTGAAGGTTCCATTGAGCACATAAGTGTGATTCAAAGTGT
GATTGTTGGAGACAAACAGGCCAGTGTTGT C C C CAAAGTTCCACTTGTAGGAAATGGC
AGAGTCGTTGAGGAAGTGGCTGGGATCATGAATGAGGACATCGAAGACGATGGGGAG
GTCTCTGAGGAAGATCTCATCAGACAAGTT (SEQ ID NO. 119)

GAATTCGGCACGAGGTCAAGCCCTGACTGGTTGCAGGCGCTCGGAGTCAGCATGGAA
AGTCTCTGCGGGGTCCTGGGATTTCTGCTGCTGGCTGCAGGACTGCCTCTCCAGGCTGC
CAAGCGATTTTCGTGATGTGCTGGGCCATGAACAGTATCCCGATCACATGAGAGAGCAC
AACCAATTACGTGGCTGGTCTTCGGATGAAAATGAATGGATGAACACCTTGTATCCA
(SEQ ID NO. 120)

FIG. 12DD

AAGGGGGAGGGGCATGGCCCGGGCACTGCAGTTTGCACGGTGAGGTTAAGGTTGAAGG
TTCCATTGAGCACATAAGTGTGATTCAAAGTGTGATTGTTGGAGACAAACAGGCCAGT
GTTGTCCCCAAAGTTCCACTTGTAGGAAATGGCAGAGTCGTTGAGGAAGTGGCTGGGA
TCATGAATGAGGACATCGAAGACGATGGGGAGGTCTCTGAGGAAGATCTCATCAGAC
AAGTTCCTGTCATTCTTCTGGGACATGGTCACGAATACAGGGATCTGATCTGTTAT

(SEQ ID NO. 121)

GAATTCGGCACGAGCCGACACTGTGACTCCTGGTGGATGGGACTGGGGAGTCAGAGT
CAAGCCCTGACTGGTTGCAGGCGCTCGGAGTCAGCATGGAAAGTCTCTGCGGGGTCCT
GGGATTTCTGCTGCTGGCTGCAGGACTGCCTCTCCAGGCTGCCAAGCGATTTCGTGAT
GTGCTGGGCCATGAACAGTATCCCGATCACATGAGAGAGCACAACCAATTA

(SEQ ID NO. 122)

AAGGTGAAAGATGTGTATGTGATAACAGATCAGATCCCTGTATTCGTGACCATGTCCC
AGAAGAATGACAGGAACTTGTCTGATGAGATCTTCCTCAGAGACCTCCCCATCGTCTT
CGATGTCCTCATTCATGATCCCAGCCACTTCCTCAACGACTCTGCCATTTCTTACAAGT
GGAACTTTGGGGACAACACTGGCCTGTTTGTCTCCAACAATCACACTTTGAATCACAC
TTATGTGCTCAATGGAACCTTCAACCTTAACCTCACCGTGCAAACCTGCAGTGCCCGGG
CCATGCCCTCCCCCTTCGCCTTCGACTCCGCCTCCACCTTCGTA

(SEQ ID NO. 123)

TACCATCGGAGAAAGAAGACCAAGCAAGGCTCAGGCAGCCACCGCCTGCTTCGCACT
GAGCCTCCTGACTCAGACTCAGAGTCCAGCACAGACGAAGAGGAATTTGGAGAATTG
GAAATCGCTCTCGTTTTGTCAAGGGAGACTATCCCGATGCTGCAAGATCTGCTGTCCCT
CTGGCCTTTGTCATCCTCGCGCCTGCGTTGTGGCCTCTGTGGGCTTGGTGTGGAGCAAA
TGGCTCTCAAGGAGGACTGAGTCTCAAGGAAATT

(SEQ ID NO. 124)

FIG. 12EE

AGCTAAGGTCAGGAGGTGTCTGAAGAATTGGCTGATGCATGGCAGGGATGTTGTTGAC
CTGCTTTTAGAACAATACTTCCATTTAATTATAGCATATCTTATGTGTGTATTAAAGCA
GAGCCGATCTGGTGGGGCTCATTAAGTAAATGTACTTACTGCAAAAGGTTCAACTGGT
GACCCCAGTTTTCCCCAGAAGCAATATGATAGGACAGAGGCGACTCCTGCAAGTTGTC
TCAGACTTCACACATACATTGTGACATTCTCTGAGCATGTGCACTGTACATGATATGAC
ACTATCAA (SEQ ID NO. 125)

AGCTAAGGTCCACTACCTTGTGAAGATGTATAAACACCTGAAATGTAGAAGCGATCCG
TATGTCAAGATCGAGGGGAAGGACGCTGACGACTGGCTGTGTGTGGACTTTGGGAGTA
TGGTGATCCATTTGATGCTTCCAGAAACCAGAGAAACCTATGAATTAGAGAAACTATG
GACTCTACGTTCTTTTGATGACCTTAGCTAAGCCGAATCAGCACACTGGCGGCGTTACT
AGTGGATCGAGCTCGTACAGCTGATGCATAGCTTGAGTATCTATAGGTTACTAATAGC
TGGCTATCATGTCAAGCGTTC (SEQ ID NO. 126)

GCTGAGCTGCAGAGAGTAGCACATCCTTGCTAATTCAATAACTACCAGTTTTTATTGGT
GAAACATGAATCCAGATGGTATGGTTGCTCTCCTGGACTACCGTGAAGATGGTGTGAC
TCCATTCATGATTTTCTTTAAGGATGGCTTAGAGATGGAGAAATGTTAACAAATTGGA
TCTATCACCTGTCACCATAATTGGCTGCTGCTTACCATCCATAACAACACCAGGACTTAG
GACAAATGGGACTGATGTCATCTTGAGCTTTTATTTTGACCTTAGCT
(SEQ ID NO. 127)

AGCTAAGGTCAGAGCCAATAGTATCATGAGAACTGAAGAAGTAATAAAGCAACTTCT
CCAGAAATTTAAGATTGAGAATAGCCCTCGGGATTTGCTCTTTACATTATTTTGGGA
CAGGAGAGCAGAGAAAGCTAAAGAAGACCGATGTCCACTGCTGCAGAGGTTACTACA
AGGACCATCCAAAAGCAATGCTCGGATCTCTCATGGATAAAGATGCAGAAGAATCAC
GAGAGATGTGGCTCGTACATTATTTCACTTTCTTCTGATCATACTCAAGATAGATGAGA
GAGAAT (SEQ ID NO. 128)

FIG. 12FF

TTGACTTCTGAGTCTAACACAGACACTGCAAGGGTTAATTTTCCAAGAGGTGGTTGTT
GTTGACGATAAATTCATTAAGAATTTTAAAAATTTAGTTAGATTTACCAAAGTCACTG
GAGACAAATTCAGAAGGCATATATACCTGCCAGTTTTGTGGACTACATTAATAGGGAG
GCTTTTATGTTTGATGTAATTCTTACAGTTCTAAGAATTAAGTTCCATTGCATGAGACC
TTAGCT (SEQ ID NO. 129)

AAGGTGAATCCCCGACGGCTCTGGGCCCCGAGGAGAAGCGTCGCCGTGGCAAATTGGC
ACTGCAGGAGAAGCCCTCCACAGGTACTTGGA AAAACTGGTCTCTGAGGCCAAGGCC
AGCTCCGAGACATTCAGGACTTCTGGATCAGCCTCCAGGGACACTGTGCAGTGAGAAG
ATGGCCATGAGTCCTGCCAGTGAG (SEQ ID NO. 130)

AATTTTTTTTTTCGACGGCCCAACGGGGGGCTTGGTGGATGGAAATATGGTTTTGTGAGT
TATTGCACTACCTGGAATATCTATGCCTCTTATTTGCGTGTACTGTTGCTGCTGATCGT
TTGGTGCTGTGTGAGTGAACCTATGGCTTAGAAAAACGACTTTGTCTTAAACTGAGTG
GGTGTTCAAGG (SEQ ID NO. 131)

CACCTGATTTAAAGGAAAAGCATTCTGACGTAAGAAGCTGAAAGGCGGCCCTTGCGTG
CTTTGAACTTTCTTATACAGCACAGTCATCTGAAGCTTCCTGTGTGACCAAGACAAGA
ACGCGTGCACAAGACTGAGAAACAGCAAGAAACAACCCGGCATTCTACTTTCTCAAC
ACTATCATACTTTAAACCTTTCAC (SEQ ID NO. 132)

FIG. 12GG

CTAGCTTACGCTAGTCCCCCATGCATAAAGACTGATCGCTTTTCCTTAGAAAGGTGAG
AGGGTTAGGACAAGGCCGTGTGGTAACAACACCCGCAGCTCGAAAAACCAATGGCTT
GTTAACGTGTCAGTGAGGCACTGTACGGACGTCCATAGTCCACATCTTCAAATTCCCG
CAGAAGGCTTCCTATTCTTAAACTCTA

(SEQ ID NO. 133)

CTACATTTCTGTATCCATTCCTCTGTTGAAGGCTCTGGTTCTTTCCAGCTTCTGGCTATT
ATAAATAAGGCTGCTATAAACACAGTGGAGGCATGTGTCCTTGTTATATTTTGGAGCA
TCTTTTGGGTATATGCCCAGAAGTGCTATAGCTGGTTCCTCAGGTAGTACTATGTCGAA
TTTTCTGAGGAACTGCCAGACTGATTTCCAGAGTGGTTGTACCAGCTTGCAATCCCACC
AGCAATAGAGGAGTGTTTCCTCTTTCTCTATATTCTTGCCAACATCTGCTGTCACCTGAG
TGTTT

(SEQ ID NO. 134)

TGGTAAAGGGGGAATGATGTCGAGGCCATCCTGGGCTGTAGAGCCAGGCCCTGGCTTG
GGGAGTGGGCATTGTAACTTGTTGCTGACTTTGTGTTGACCCCTGCATCAGCAACTAT
TTCCTTAAATCCAGGATACAACCTTGTTAAGTGTGACAGCTTTCCTTTACACACCATTTT
TGTGGGTGTATATATATATTTGACTTGGGGAGAATTATTTTTTACAAAAATACAAAAT
AGCTTTTAA

(SEQ ID NO. 135)

AGCTAAGGTCCGGACTCTATGGCATGACCCCAAAAACATTGGCTGGAAAGATTACACT
GCCTACAGGTGGCACCTGATTCACAGGCCTAAGACAGGCTACATGAGAGTCTTAGTGC
ATGAAGGAAAGCAAGTCATGGCTGACTCAGGACCAATTTATGACCAAACCTACGCTG
GTGGACGGCTGGGCTGTTTGTCTTCTCCAAGAGATGGTCTATTCTCGGACCTCAAGTAT
GAGTGCAGAGATGCTAGAGAGCAGGCTCAGTCTCAGCA

(SEQ ID NO. 136)

FIG. 12HH

TGACCTACGTGTAGTTGGTGTGCTTGTTGTCTGAAGATGAGGGCCTCCTGGATGAGCTG
GTGCTGCTGCTCCAGCAGGTCCAGGCTGGGCTTGTAGTCCACGAGTCTGCGCTCGTAC
TGCTTCAGGTGGCTCAGCTGGTCTTCCAGAGTCCCGTTCATCTCAATGGAGATGCGCCC
GATCTCCTCCATCTTAGTCTGGATCCACGGCCCCACCATATTGGCTTGGCTGGCGAACT
GTCGGCGAAGGCTGCATTGGATTGCT

(SEQ ID NO. 137)

AATTTTTTTTTTCGACGGCCCAACGGGGGCTTGGTGGATGGAAATATGGTTTTGTGAGT
TATTGCACTACCTGGAATATCTATGCCTCTTATTTGCGTGTACTGTTGCTGCTGATCGT
TTGGTGCTGTGTGAGTGAACCTATGGCTTAGAAAAACGACTTTGTCTTAACTGAGTG
GGTGTTCAAGG

(SEQ ID NO. 138)

CACCTGATTTAAAGGAAAAGCATTCTGACGTAAGAAGCTGAAAGGCGGCCCTTGCGTG
CTTTGAACTTTCTTATACAGCACAGTCATCTGAAGCTTCCTGTGTGACCAAGACAAGA
ACGCGTGCAACAAGACTGAGAAACAGCAAGAAACAACCCGGCATTCTACTTTCTCAAC
ACTATCATACTTTAAACCTTTCAC

(SEQ ID NO. 139)

CTAGCTTACGCTAGTCCCCCATGCATAAAGACTGATCGCTTTTCCTTAGAAAGGTGAG
AGGGTTAGGACAAGGCCGTGTGGTAACAACACCCGCAGCTCGAAAAACCAATGGCTT
GTTAACGTGTCAGTGAGGCACTGTACGGACGTCCATAGTCCACATCTTCAAATTCCCG
CAGAAGGCTTCCTATTCTTAAACTCTA

(SEQ ID NO. 140)

CTACATTTCTGTATCCATTCTCTGTTGAAGGCTCTGGTTCTTCCAGCTTCTGGCTATT
ATAAATAAGGCTGCTATAAACACAGTGGAGGCATGTGTCCTTGTTATATTTTGGAGCA
TCTTTTGGGTATATGCCCAGAAGTGCTATAGCTGGTTCCTCAGGTAGTACTATGTCGAA

FIG. 12II

TTTTCTGAGGAACTGCCAGACTGATTCCAGAGTGGTTGTACCAGCTTGCAATCCCACC
AGCAATAGAGGAGTGTTCTCTTTCTCTATATTCTTGCCAACATCTGCTGTCACCTGAG
TGTTT (SEQ ID NO. 141)

TGGTAAAGGGGGAATGATGTCGAGGCCATCCTGGGCTGTAGAGCCAGGCCCTGGCTTG
GGGAGTGGGCATTGTAACTTGTTGCTGACTTTGTGTTGACCCCTGCATCAGCAACTAT
TTCCTTAAATCCAGGATACAACTTGTTAAGTGTGACAGCTTTCCTTTACACACCATTTT
TGTGGGTGTATATATATATTTGACTTGGGGAGAATTATTTTTTACAAAAATACAAAAT
AGCTTTTAA (SEQ ID NO. 142)

AGCTAAGGTCCGGACTCTATGGCATGACCCCAAAAACATTGGCTGGAAAGATTACACT
GCCTACAGGTGGCACCTGATTCACAGGCCTAAGACAGGCTACATGAGAGTCTTAGTGC
ATGAAGGAAAGCAAGTCATGGCTGACTCAGGACCAATTTATGACCAAACCTACGCTG
GTGGACGGCTGGGCTGTTTGTCTTCTCCAAGAGATGGTCTATTCTCGGACCTCAAGTAT
GAGTGCAGAGATGCTAGAGAGCAGGCTCAGTCTCAGCA

(SEQ ID NO. 143)

TGACCTACGTGTAGTTGGTGTGCTTGTTGTCGAAGATGAGGGCCTCCTGGATGAGCTG
GTGCTGCTGCTCCAGCAGGTCCAGGCTGGGCTTGTAAGTCCACGAGTCTGCGCTCGTAC
TGCTTCAGGTGGCTCAGCTGGTCTTCCAGAGTCCCGTTCACTCAATGGAGATGCGCCC
GATCTCCTCCATCTTAGTCTGGATCCACGGCCCCACCATATTGGCTTGGCTGGCGAACT
GTCGGCGAAGGCTGCATTGGATTGCT

(SEQ ID NO. 144)

TGACCATCGATAAGTTTAATAACTACAGACTTTTCCCAAGACTACAAAAGCTTCTTGA
AAGTGACTACTTTAGATATTACAAGGTGAACTTGAAGAAGCCTTGTCCTTTCTGGAAT

FIG. 12JJ

GACATCAACCAGTGTGGAAGAAGAGACTGTGCCGTCAAACCCTGCCATTCTGATGAAG
TTCCTGATGGAATTAAGTCTGCCGAGCTACAAGTATTCTG
AGGAAGCCCAACCGCATTGAAGAATGTGAGCAAGCTGAGCG (SEQ ID NO. 145)

AACTCTGTGAACCGTGCCTTTCTCTGTGGAGGTGGAGGTGTCGGTTGAAGACAAGCGA
GGTCCTCCAAGGGGCTGTGTCTTATGTTGCCATCTCCCCTTG TAGCTTGGCTGCCCACC
CTCCAGACTGTGCGCCATGGCTCCAAGGCTGTGACCCGCCACTGGAGTCATGCACTTC
CAGCGGCAGAAGCTGATGCTATAACTGAGTATATTCCTCCAAACCTGCCATCAACCCG
AGA (SEQ ID NO. 146)

ACTTCTCCAGAGAATTTAAGATTGAGAATAGCCCTCGGGATTTGCTCTTTACATTATT
TTTGGGACAGGAGAGCAGAGAAAGCTAAAGAAGACCGATGTCCCACTGCTGCAGAGG
TTACTACAAGGACCATCCAAAAGCAATGCTCGGATCTTCCTCATGGATAAAGATGCAG
AAGAAATCAGCAGAGATGTGGCTCCGTACATTAATTTCACTTTTCTTTCTTGGATCCAT
CCTTCAAGATTAGATGAAGAAGAGAAATGGAGATTGAGAGAATATGCAATCATACCGA
(SEQ ID NO. 147)

AGGGTTACTTCAGGCTAAGGCAATAGAAATCCATTTTAAGATGGTGTGCTAAAGGCTT
GATGGATGTTTCATCGTCTGTCTAAAGGAGAATGAAGTCATCAACAGGATGTCAGGGGA
AAGTGAGATCATCGCAGAAAGTATCAACTTAGCACAAACACACAGGCATAGCTCCTG
CAAGAGGTGAATGCTGTCCCCAAATACCTGAGGAACTATCCCTTTGGGCAAGAAAATA
GACAAGTCCATGAAGTCTGGGTGA
(SEQ ID NO. 148)

GACCAGGTACACTTGAGCAAAGCACCCAGTATTTAATTCCTTACAGAAAGGAGAGGA
AAGGTCTGCAGTTGGACTGATGGTATGCTAACACCGCAAATGACTGTCATTTGATCTC

FIG. 12KK

AGAAGTTCAGGATTGATTGCTATGTTTTAGCTCTAATTGTGAGAAACAGTAGTCATTTT
AGTCTTAAATTTTGCCCTCAGGAAATTCAGGGAGACTGAGCCTTCCTTCCCCCACCTTC
GTAAAGCCGAATTCAGCACACGGCGGCCGTTACTAGTGGATCCGAGCTCG

(SEQ ID NO. 149)

TACAAGGTGGGATGGCAGGAACTGAAGGCTTCTGTAAATCCAGTTTTGGCTCTCTCTC
TGGTCTTTCTTTCTTTCTGTTCTGTTTGGAAGGGTTTCTGGTCTTTCAGGAGGTATTTT
TTTAATTTTCATGTTTTCTCTCTGTGGTACCTGCCCCCTTGTTTGACGACAGGAGCTGATG
GAGGTGGCGGTTTCTTGGGTCTATTCCCTTCCTTGTCAAAGTCCGATGGAAGTAACTTC
ACGAAGTTGTCAGGAAACACGCCTCGTCTGCCATTGAGTTCTCCTTCCCACCAGCCTA
CGCGATGCAGTCTTATTGATGAGAGTCACTATATCTCCTTA

(SEQ ID NO. 150)

TCACCCATGACTTCTATGGACTTGTCTATTTTCTTGCCCAAAGGGATAGTTCCTCAGGT
ATTTGGGGACAGCATTACCTCTTGACAGGAGCTATGCCTGTGTGTTTGTGCTAAGTTGA
TACTTTCTGCGATGATCTCACTTTCCCCTGACATCCTGTTGATGACTTCATTCTCCTTTA
GACAGACGATGAACATCCATCAGGCCTTTATGCACACCATCTTAAAATGGATTTCTAT
TGCTTAGCCTGAAGTCC

(SEQ ID NO. 151)

CCCATAGAGATAGGTTTGCTCCAGAACCTGCAGCATTGTCACATCACAGGGAACAAGG
TGGACATTCTGCCAAAACAGTTGTTTAAGTGCGTGAAGTTGAGGACTTTGAACCTGGG
GCAGAACTGTATCGCCTCCCTGCCTGAGAAAATCAGTCAGCTCACCCAGCTCACTCAG
CTGGAGCTGAAGGGCAACTGCCTAGACCGCCTGCCAGCCCAGCTGGCAGTGTCGATGC
TCAAGAAGA

(SEQ ID NO. 152)

CAATAATCCAGGTAAAATAGAGTAAAATAGTCTGCTAGCAGCAAGTTCCTACCATACT
TTCAACAACACTCACGAGATACGGAATGATTACAGCATTAGAATATTTTCAGAAATGA
CAGGTAGGTGTGGTGGACAGGTGGCTCACATTCAAGACTCAAGTCTACTTAAAAAAGA

FIG. 12LL

AAATCTCACTAGCACTAGATTCTAGCTCCTTTGTTTCCCCCTTTCTTTTGGTTTCAAAG
GCGTTTCTACAACCCATAAGAGG

(SEQ ID NO. 153)

GCCAAGCTATTATGACACTATAGATACTCAACGTATCGATCAACGTTGGTACCGAGCT
CGGATCCACTAGTAACGGCCGCCAGTGTGCTGGAATTCGGCTTGGATTGGTCAGAGCA
GTGTGCAATATGATCCAATAAGTCTCCTCCCTTGGCCCCCTCCCCAAAATGTTTGCAGT
GTTATTTTTGTGGGTTTTTTTTTAACACCCTGACACCTGTTGTGGACATTGTCAACCTTT
GTAAGAAAACCCAAATAAAAATTGAAAAATAAAATAAAAAGAAACCCATGAACATTC
GCACCACTTGTGGCTTCTGACTATCTTCCACAGAGGGAAGTTTAAAACCCAAACTTCC
AAAGGTTTGAACCTCAAGACACTTTCGCAGTGGAGTCGTAGACCAATCCCA

(SEQ ID NO. 154)

TAAATAAATTAAAAAACTATTAAACCTAAAAACGTCCACCAAACCCTAAAACCATTA
ACAACCAACAAACCCACTACAATTAAACCTAAACCTCCATAAATAGGTGAAGGCTTT
AATGCTAACCCAAGACAACCAACCAAAAAATAATGAACTTAAAACAAAAATA

(SEQ ID NO. 155)

GGTAAAGGGGACCTGGAGAACGCCTTCCTGAACCTGGTCCAGTGCATCCAGAACAAG
CCCCTGTACTTCGCTGACCGGCTGTACGACTCCATGAAGGGCAAGGGGACTCGAGACA
AGGTCTGATTAGAATCATGGTCTCTCGCAGTGAAGTGGACATGCTGAAAATCAGATCT
GAATTCAAGAGGAATATGGCAAGTCCTGTACTACTACAT

(SEQ ID NO. 156)

AGAGCAGCAGGCCAGCTGTACTTGGTTTGGCAAGAAAAAGAAGCAGTACAAAGATAA
ATATTTGGCAAAGCACACGCAGTGTTTGATCAATTAGATCTTGTACATATGAAGAA
GTAGTCAAACCTGCCAGCATTCAAAGGAAAACATTAGTCTTATTAGGTGCACATGGTG
TTGGAAGAAGACACATAAAAAATACCCTCATCACAAAGCAC

(SEQ ID NO. 157)

FIG. 12MM

TCGGTCATAGTAGTAAGGGAAATCTCCCAGGTAAGATGAATACTGCGGTAGGACGAA
CAATCCTCCAGGATGTTTGTTCATATTAAACTGTTACGTGATATGTGCTTGAATATTC
TGTCTGAATAATCTCTAGTGTAGTTAATACAATCTTCTCAACTGAAGAAAAATAAGC
CTCCCACAAGAACTGTGTCTGCTGTCTAAGTGCTAGGATTTTATCCTGATGAATAGACC
TGATTGTAGAAGGAATCTGTAATAGCAATCTCTCATCGCCTATGACCGAAAGCCGAAT
TCTGCAGATATCCATCACACTGGCCGGCCGCTCGAGCATCGATCTAGAGGG

(SEQ ID NO. 158)

CTGCTTGATGACAAAGGGTGTAGTCTTCATCTTTTCCTGGATTATTTTGGAAAGTGACAG
GTGGAAATTCCATCGTCACGTTTATGTGGTCTGTAAAGCCAACGATCTCAAATTCTGG
CGGCTCAAGAGGAGCGTTTGCAGGCACGATGTAGTCTGAGCAGCGGCACACGGTCAA
GTCCCCTCTGTGCACTATGACGATGGCGACGACGTAGCTCTCCATGCCCTCCAACCAC
TTATCTGTCACGTCACATGATGACTTCGTGGTATCTGAACAGTTCTTAACCTTCGTCAG
ATTTTCGTCTTT

(SEQ ID NO. 159)

AAATCGTTGCTTCAGAAAGACTCAATAACACTTACTTGTGCCTGGCTGTGCTGACAGT
ACATTCTGTGTCATTTTCCTTCATGGGCGGAACAGTCCACAGAGCTCACCAACAAGTA
CTCCAAAAGTGAAGAGTTTAAGCTTCGAGATGCAACCAGATGAGCTTCTAGAAAA
GCCCATGTCTCCCATGCAGTACGCACGGTCTGGACTAGGGACAGCAGAGATGAATGGC
AACTCATAGCTGCAGGTGGTTATAACAGAGAGGAATGTCTTCGAACAGTTGAATGCT
ATGATCCACATACAGATCACTGGTCCTTCCTTGCTCCCATGAGAACATCAAGCAG

(SEQ ID NO. 160)

CTTTCCGAAGAGCACACCCTCCTCTCAATGAGCTTGTGAGGTCTCTTTCTTCTCTTCCT
TCCAACGTGGTGCTAGCTCCAGGCGAGCGACGTGAGAGTGCCACCTGAGACAGACAC
CTTGGTCTCAGTTAGAAGGAAGATGCAGGTCTAAGAGGAATCCCCGCAGGTCTGTCTG
AGCTGTGATCAAGAATATTCCGCAATGTGCCTTTTCTGAGATCGTGTTAGCTCCAAAG

FIG. 12NN

CTTTTTCCTATCGCAGAGTGTTTCAGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTTC
CCTTGGCGGATTTCCTCGTGTGT (SEQ ID NO. 161)

CCTATTGAACGGTCTTGCAATGACGAGCATTTCAGATGCTTAAGGAAAGCATTGCTGCT
ACAAATATTTCTATTTTATAGAAAGGGTTTTATGGACCAATGCCCCAGTTGTCAGTCAA
AGCCGTTGGTGTGTTTTCATTGTTTAAAATGTCACCTATAAAACGGGCATTATTTATGTTT
TTTTTCCCTTTGTTTCATATTCTTTTGCATTCTGATTATTGTATGTATCGTGTAAGGAA
GTCTGTA (SEQ ID NO. 162)

CCTATTGAACGGTCTTGCAATGACGAGCATTTCAGATGCTTAAGGAAAGCATTGCTGCT
ACAAATATTTCTATTTTATAGAAAGGGTTTTATGGACCAATGCCCCAGTTGTCAGTCAA
AGCCGTTGGTGTGTTTTCATTGTTTAAAATGTCACCTATAAAACGGGCATTATTTATGTTT
TTTTTCCCTTTGTTTCATATTCTTTTGCATTCTGATTATTGTATGTATCGTGTAAGGAA
GTCTGTA (SEQ ID NO. 163)

CCTGGGTCCGTCCTCCAACCCCTCACGCCCAAACCCTCCGACTTTCACCTCTTGAAGTG
ATCGGAAAGGGCAGTTTTGGAAAGGTTCTTCTGGCTAGGCACAAGGCAGAAGAAGTA
TTCTATGCAGTCAAAGTTTTACAGAAGAAGCCATCCTGAAGAAGAAAGGAAGGAAGC
ATATTATGTCAGAGCGGAATGTTCTGTTGAAGAATGTGAAGCACCCCTTTCCTGGTGGG
CCTTCACTTCTCATTCCAGACCGCTGACAAGCTCT (SEQ ID NO. 164)

GATGCTGAACACAAAAAGAAAGAAAGAAAGGAAGAGGAGCAAGAGAAGCTGAA
GGGAGGGAGCCTTGGCGAAAATCAGATCAAAGATGAGAAGATTAAAAAGGACAAAG
AGCCCAAAGAAGAGTCAAGAGCTTCTTGGATAGAAAGAAAGGATTTACAGAGTGAGG
CGCAGAATGGAGATTCATGACCCACAACTTAAAC

FIG. 1200

(SEQ ID NO. 165)

AAAGCCAATTGGTAGAGAAATTGAAGACACAAATGCTGGATCAGGAAGAGCTTCTGG
CATCAACCAGAAGGGATCAAGATAATATGCAAGCTGAACTGAATCGCCTCCAAGCAG
AAAATGATGCTTCTAAAGAAGAGTAAAGAGTTTTACAGGCCTTAGAGGACTGCTGTTA
ATTATGATCAGAGTTCAGGAGTTAAGAC

(SEQ ID NO. 166)

CTGCTTGATGTCCTGTGTAGCGAATGTCACAGCGTACAACATTGTTAGTGTAGTCTGAT
TCAGGCACCAGGTAGCTGGGGTTTACACTGACCTTTAGAATGTAGTTTCCAGGTTGTA
CATCTGTAATATCAATCCACTGGCAGTCTATGTCTGCCGCATAGGTGTCATAACATCCA
GGA CTCAATCCCTGTGTGTGTGCAGTGCACGCAAAGGCCCTGTGGTACCCATAGTCAC
AGGACGTGTCCTCCAGACAGAAGCTTGCTTTGTGGCCTTCAGCCACTCTCCTCTGTGTG
TTGGCATCAACGAGAAGCCGAATTCTCGAGATATCCATCACACT (SEQ ID NO. 167)

CTGCTTGATGTCCTGTGTAGCGAATGTCACAGCGTACAACATTGTTAGTGTAGTCTGAT
TCAGGCACCAGGTAGCTGGGGTTTACACTGACCTTTAGAATGTAGTTTCCAGGTTGTA
CATCTGTAATATCAATCCACTGGCAGTCTATGTCTGCCGCATAGGTGTCATAACATCCA
GGA CTCAATCCCTGTGTGTGTGCAGTGCACGCAAAGGCCCTGTGGTACCCATAGTCAC
AGGACGTGTCCTCCAGACAGAAGCTTGCTTTGTGGCCTTCAGCCACTCTCCTCTGTGTG
TTGGCATCAACGAGAAGCCGAATTCTCGAGATATCCATCACACT (SEQ ID NO. 168)

GATCTGACACTACAGCATGAGCGTTAGATTTATAAAATTATTTTTCTTCTAAATGCTG
GAAACTCTAAGGGTTTATTCAGAAAAAACTGGCCAATTTTCAAATGGCTTAGAAGC
AGGGTTAATTAAGTATTGAATGAGCCACTGTGATATCCTGATGACACCCAGTCACAAT
GACAGTTTTGAAGCATACAACCAAAACAATTGAGATCTCAAACTATTTTACATCACT
TATGGTAATGTTATGTAAAAATGAAAATGCTTTCTGTGGAAGTTACATTCTTTACCAGG
TCTTTAACATAAATTAACACGACGTCGAGTAAGCCTTTGTTTCGGAAGACAACTAGTT
TGTGAGTTCAGTCAGATCCCAGCT (SEQ ID NO. 169)

FIG. 12PP

AGTTGCCAGGACCACCACCATAGTTGCCAGGTTCATCATAAACAAATCCAACATCAAT
CTTAAATTCCCCCATCAGACAATCTGCCCTCAAAGAATGGGAATTATAAACCCGGATA
CTGATGATCTCATCCATGAGCTCAGAGGGTGTGATGTGCACATTGTAGAAAAATAACT
CGTCAAAAAACGGATTGTTCCCTCTCTTGATTCTCGTGCGATGCGTCTGACCACAGATG
TGAACTTTCACCACGGGCCTTATGTTGTTGCCGCATAACTGACGGCCCTCGATCACTCT
GACACGGATCTGGAAATCTGTGGCTTGTTGGACAGCATCCTT (SEQ ID NO. 170)

AAGCCGTGTCCCAAAGAATGGATAGAGACGCGATCAGATGCGACAGTGCTGTGGAGA
AAGCCCAGGAACCTGCACAATTGCCCTGGTCCAATGGCTCGTGGATCAGGTTGGGCCA
CTTCTCTGAAGCTTCAAAGGCAGTGGGTAGCACTTCCCCTTGGCCCAGCACCGTATAA
ATCTCATTTCATATTCATGACAGTGGAGGATGGGCGGATTGTGCCCAGGCGGTACGGAA
TGCCCTCATCCAGGGTCATGCCCCAGAAGGCACTGTGGTTCCCAGCCTGCCACCCGTA
GTTGCCTCGGTTGATGGCTTTAATCATGTCTGGTCACTAGACACGGCTTAAGCGAATCT
CGAGATATCCATCACACTGGCGGCGTCGAGAT (SEQ ID NO. 171)

AAGCCGTGTCTGATGATGGAGGTAGTGGTGGGGGAGGAGGGACTGAGGGTCCTGAGG
TGGTGGCCCCTGGAACTGATCCCACATAGTTACCCACTGCTAGTTCTGACCCCGTGGA
CAACGTGCCAGAGGCCATGACTGGCAGTATGGCAATGTCCCCATCCCCTTTCTTCTTA
ATTTTAATGGTCCCTTGTTTCTCCAGTTCGTGAATCTTTTTTTCCAGGGTAGACTGTCTT
TGAATGGCTTCTTCCTTTTCTTTGACCATTTTTCTTAACGTGTGAACTTGGGTATTTGCA
TCTTTGTAGATTTCCGGACAACATCAGTTCCTTATTCCTCTGCATAAGTTGCTTTCAGTT

(SEQ ID NO. 172)

CGAGTCAGACACATGAAAGCAAAACGCGGGCAGATAAAACGATCGCCTTACCTTCTA
GCAAAAATCTGAAGCTTGTGTCAGAAACAAAGACTCAGAAAGGTTTGTTTTCAGATGA
AGAAGACTCTGAGGATTTGTTTTCTTCTCAAAGTTCAAGTAAGCCAAAAAGTGCATCA

FIG. 12QQ

CTTTCATCCAGCCAGCCCCAACATCAGTCTCCCTTTTTGGTGATGAAGATGAAGAGG
ACAGTCTTTTTGGGAGTGCAGCAGCTAAGAAGCAGACTTCATCTCTACAACCTCAGAG
TCAAGAGAAAGCAAAGCCTTCCGAGCAGCCCTCAAAGAAGACATCTGCCTTGTTGTTT
AGA

(SEQ ID NO. 173)

CGAGTCAGACTTAATTTAAAAACGAAACAAAACAAAAATAACATAGTTTAGAAATCA
AGGAGAAAGGACAGATAGTCTAAGAAAAAAGACAACACAAAAGAGGGGCAGGGCGG
CCAGCTTGCATCAGGGATCTTGGCTGGAGACCTGCTTTGAATAGGTTTCTTGCAGGTAT
TTCTTAAATGCTGTGGGGTTTTTCCAGAGTTCCGCAGCGTGTGTGTTCAAAGGGCTATC
GATGTTGGGTTCTCCTAGCAGGCTCTGGATAGAGAGCAAGATAGTCCTGACATCATAT
AGTGCAGACCACTTATCCTTGAGGATGTCCGGCAGATGTTGCCTGGGTGTCACGTTGG
GGTGGTAGCAGGGTGTGAGGAACTTCACTG

(SEQ ID NO. 174)

CGAGTCAGACACTCCTGGCTCCTGGATTCTTTAGATGCCTCCATCAGACTGGGTACTTT
AGATGCCTCCATCAGACTACTTCGTCATTGTATTTCTCAGTTTCGCTCAGGGCAAGCGGC
AGTCTCTGGGCTGCTGTGGCAGGTGCCACCACTGCATTTAAAAGTTAAAATTTCTTCA
AATATTCCCATCAAGGCCTTGTAGCCTCTGAGATTGGTTTACTATTTGCCCAGTTATTT
AAAGCTCTCTGCATTCCTTCCTGATTTAATATTGCTATGGCCAGGACAATGTGTAGAAG
TAAAAAGGATATCATATTTACAGGTGTAACGC

(SEQ ID NO. 175)

FIG. 12RR

DD-PCR PRIMER AND PCR SIZE (nt)	cDNA FROM CELL LINE	MOUSE HOMOLOGY (%nt)	HUMAN HOMOLOGY (%nt)	NORTHERN (P-MT) (SCREEN 1)	NORTHERN-CLONED DNA (P-MT) (SCREEN 2)
P17-6 cl10 (1100)	151-1 LM1	MUSCLE NICOTINIC ACETYLCHOLINE RECEPTOR APLHA (54.3%)		NO	151-1LM1 UP, 151-1LMA DOWN
P19-6 cl2 (500)	151-2 PA		LYMPHOCYTE IgE RECEPTOR (52.6%)	NO	151-2LMA DOWN,DOWN
P21-6 cl3 (450)	151-2 PA	HISTON H2b (94.2%)		151-1LM1 DOWN,DOWN	151-1LM1 DOWN,DOWN
P21-9 cl6 (500)	151-1 PB	RATTUS NORVEGICUS THIOL- SPECIFIC ANTIOXIDANT mRNA(94.4%)		151-1LM1 DOWN,DOWN 151-2LMA UP,UP	151-1LM1 DOWN,DOWN 151-2LMA UP,UP
P21-17 cl9 (1000)	148-1 LMD	MUS MUSCULUS PUTATIVE PROTEIN TYROSIN PHOSPHATASE mRNA(98.3%)		148-1LMD UP,UP 151-1LM1 UP,UP	148-1LMD UP,UP 151-1LM1 UP,UP
P22-5 cl3 (600)	148-1 LMD	RAT DIHYDROPYRIDINE- SENSITIVE L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT GENE (92.5%)		148-1LMD UP,UP	148-1LMD UP,UP

FIG. 13A-I

P22-6 c14 (600)	148-1 LMD	SAME AS P22-5 C13		148-1LMD UP 151-1LM1 UP	148-1LMD UP,UP
P22-9 c13 (800)	148-1 LMD	RAT KIDNEY ZN- PEPTIDASE AMINOPEPTIDASE N mRNA (90.5%)		148-1LMD UP,UP,UP	148-1LMD UP,UP,UP
P24-6 c13 (550)	151-1 PB		UBIQUITIN CARRIER PROTEIN (E2-EPF) mRNA (53.3%)	151-1LM1 DOWN 151-2LMA UP 151-2LMB UP	151-2LMA UP
P24-10 c13 (1400)	151-1 LM1	RATTUS NORVEGICUS CALPAIN I1 80 kDa SUBUNIT mRNA (93%)		151-1LM1 UP,UP	151-1LM1 UP,UP
P25-1 c13 (400)	148-1 PA	M. MUSCULUS KERATINOCYTE GROWTH FACTOR Fgf-7 (99.4%)		148-1LMD DOWN 151-1LM1 DOWN,DOWN 151-2LMB UP,UP 151-2LMA UP	148-1LMD DOWN 151-1LM1 DOWN 151-2LMB UP 151-2LMA UP
P25-9 c18 (1300)	151-1 PB	M. MUSCULUS mRNA FOR INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN-3(98.1%)		148-1LMD UP 151-1LM1 DOWN,DOWN,DOWN 151-2LMA UP,UP,UP	148-1LMD UP 151-1LM1 DOWN,DOWN,DOWN 151-2LMA UP,UP,UP
P2-27 (c118- 3)	148-1 PA	RATTUS NORVEGLUS GLYPICAN mRNA (93.4%)			148-1LMD DOWN P53(+)12 DOWN

FIG. 13A-2

CLONE #	cDNA FROM CELL LINES	DD PRIMER	PCR SIZE (nt)	MOUSE HOMOLOGY	HUMAN HOMOLOGY	NORTHERN BLOT #	REGULATION TYPE	SEQUENCING PRIMER	SEQUENCING LENGTH
CI 3#1 CI 4#1 (SAME FRAG & ORIENTATION)	151-2 LMB	P3		TYROSINE KINASE? VIP2	CAVEOLIN (70%)	N123 148-1 UP 151-1 UP 151-2 UP	UP	-40	241 156
CI 5A#4	148-1 PA	P2		THROMBO-SPONDIN 100%	THROMBO-SPONDIN	N124 148-1 DOWN 151-1 DOWN 151-2 UP	DOWN	-40	233
CI 25#3	151-2 LMA	P5			53BP2 P53-BINDING PROTEIN (53.3%)	148-1 DOWN 151-1 DOWN 151-2 UP	DOWN		
CI 29#3 CI 28#1 (SAME FRAG; DIFFERENT ORIENTATION)	148-1 LMD	P5	335 332		TGF-BETA 2 (53.0%) Kvi-1 nmIs(53.0%)	N119 148-1 UP 151-1 UP 151-2 UP	UP	T7	335 332
CI 54A#2	141-1 PA	P8		MUSCULUS RECEPTOR TYROSIN KINASE CYCLIN G	PROTO-ONCOGENE TYROSINE PROTEIN KINASE GENE	N126 148-1 DOWN (WEAK) 151-1 DOWN (WEAK) 151-2 UP (WEAK)	DOWN	Sp6	220

FIG. 13B-I

FIG. 13B-2

CI 63#4	151-2 LMA	P10			Y316 GENE (53.8%) 1AC GENE (53.8%) Rb SUSCEPTIBILITY GENE (50%)	N127	UP	Sp6	340
CI 74#2	151-2 LMA	P11#3		86.8% SERUM & GLUCOCORTICOID REGULATED KINASE (sgk)		N120 148-1 UP 151-1 DOWN 151-2 UP		Sp6	320
CI 75#1	151-2 LMA	P11#10		87% MATCH sgk			UP	Sp6	250
CI 78B#4 MATCH THE SAME GENE BUT DIFF. FRAG.	148-1 LMD	P12		92.2% MATCH sgk	PROTEIN KINASE C-L (57%)			Sp6	270

DD-PCR PRIMER AND PCR SIZE (nt)	MOUSE HOMOLOGY(%nt)	HUMAN HOMOLOGY (%nt)	IGF-BETA STIMULATORY RESPONSE (12 hr.)	NORTHERN (P-MT)	CELL LINE
P11-2 c15 (310)	LYSYL OXIDASE (100%)		↑↑↑↑	↓↓	N132: 148-1 LMD, 151-1 LM1 DOWN, 151-2 LMB, 151-2 LMC UP
P20-23 c19 (850)	ACTIN BINDING PROTEIN(100%)		↑↑	↑↑	N142: 148-1 LMD, 151-2 LMA,LMB,MMA UP, 151-1 LM1 UNCHANGED
C129-3 (P5) (335)		NMB(79.8%)	↓↓	↑↑	N119: 148-1 LMD 151-1 LM1, 151-2 LMA,LMB,LMC,MMA UP
P17-3 c18 (1000)	UBIQUITIN ACTIVATING ENZYME E1(100%)		↑	↓↓	N142: 151-2 LMA DOWN
P20-3 (400)		ALPHA ACTININ 3 mRNA (77.5%)	↑↑		
P18-12 c13 (1000)	RAT mRNA FOR P34 PROTEIN (89.6%)		↑		
P25-7 c13 (1000)	M.MUSCULUS mRNA FOR P19-PROTEIN TYROSINE PHOSPHATASE (100%)		↑	↑↑	148-1IMD UP
P19-1 c13 (310)		POLYMORPHIC LOCI IN Xq28 (30%)	↑		

FIG. 13C

DD-PCR PRIMER AND PCR SIZE (nt)	MOUSE (RODENT) HOMOLOGY (%nt)	HUMAN HOMOLOGY (%nt)	SCREEN 1 P53 STIMULATORY RESPONSE (12h. OR 24h.)	SCREEN 2 CLONED DNA
P1-8 cl10 (1000)		DYSTROPHIN GENE (50.4%)	P53(+)24 DOWN,DOWN	P53(+)24 DOWN,DOWN
P1-9 cl10 (500)	M.MUSCULUS mRNA FOR CYCLIN G (96.5%)		P53(+)12 UP,UP P53(+)24 UP,UP,UP	P53(+)12 UP,UP,UP P53(+)24 UP,UP,UP
P7-4 cl1 (600)	RATTUS NORVEGLOUS SGK mRNA (51.3%), RAT LUNG DERIVED L01 C-ros-1 PROTO-ONCOGENE mRNA (48.4%)	NITRIC OXIDE SYNTHASE (47.1%)	148-1LMD DOWN P53(+)12 UP,UP P53(+)24 UP,UP,UP	P53(+)12 UP P53(+)24 UP
P9-17 cl9 (500)	RAT mRNA FOR CYCLIN D1 (79.1%)		P53(+)24 UP	P53(+)24 UP
P9-20 cl3 (850)		H. SAPIENS LDLC mRNA (51.8%)	P53(+)12 DOWN P53(+)24 DOWN,DOWN	P53(+)24 DOWN
P11-23 cl2 (800)	SYRIAN HAMSTER GENE FOR CYTOCHROME P-4 (52.5%), RAT CARBOHYDRATE BINDING RECEPTOR GENE (50.6%)		P53(+)24 UP,UP	P53(+)24 UP
P15-9 cl1 (600)	MOUSE (CLONE BALB11N) mRNA (47.2%)	PTGS2 GENE FOR PROSTAGLANDIN ENDOPEROXIDE SYNTHASE-2 (46.6%)	P53(+)24 DOWN	P53(+)24 DOWN,DOWN
P15-14 cl5 (500)			P53(+)12 UP P53(+)24 UP	P53(+)24 UP
P18-23 cl10 (500)			148-1LMD DOWN P53(+)12 DOWN P53(+)24 DOWN	148-1LMD DOWN P53(+)12 DOWN P53(+)24 DOWN

FIG. 13D

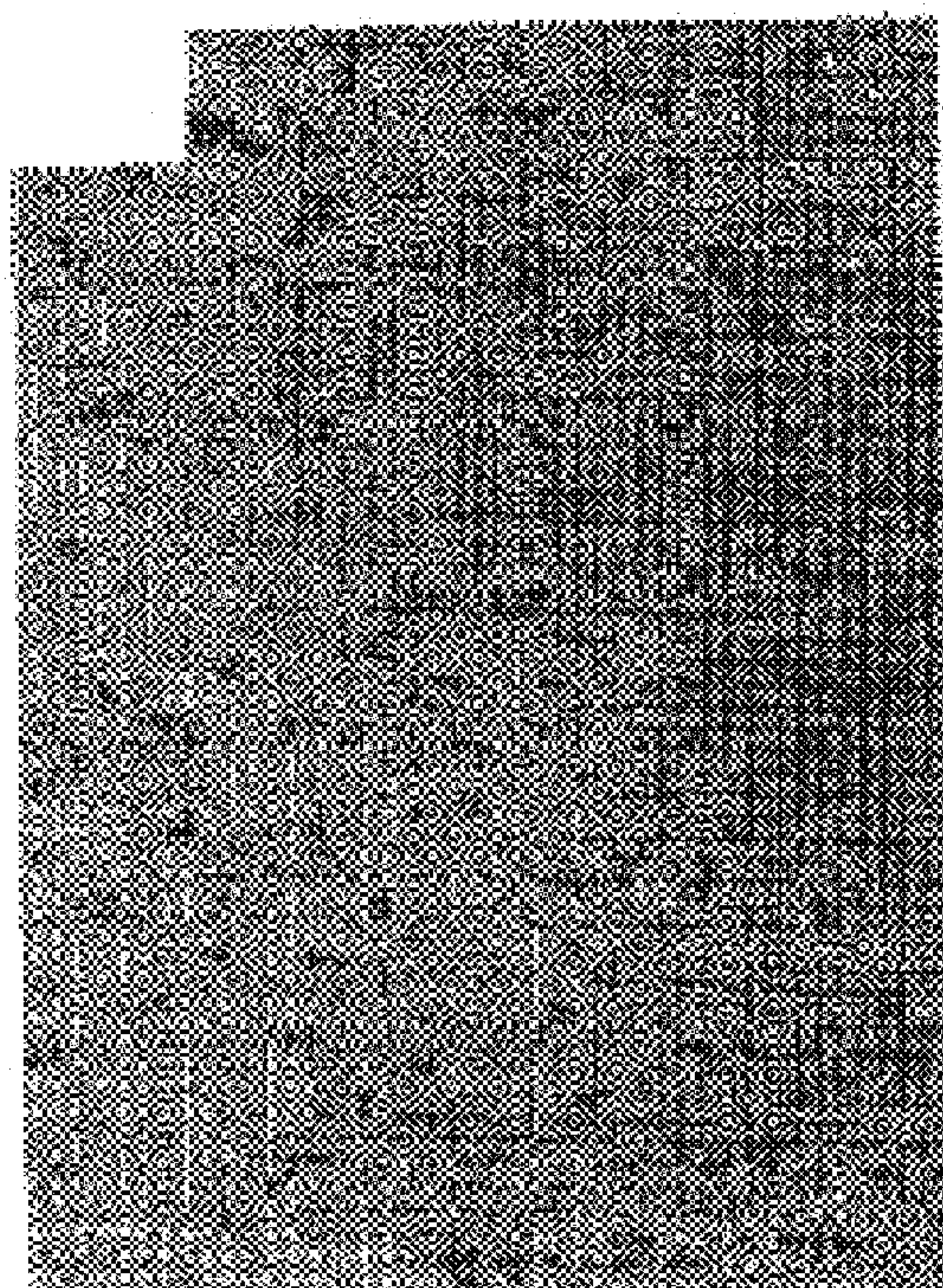


FIG. 14A

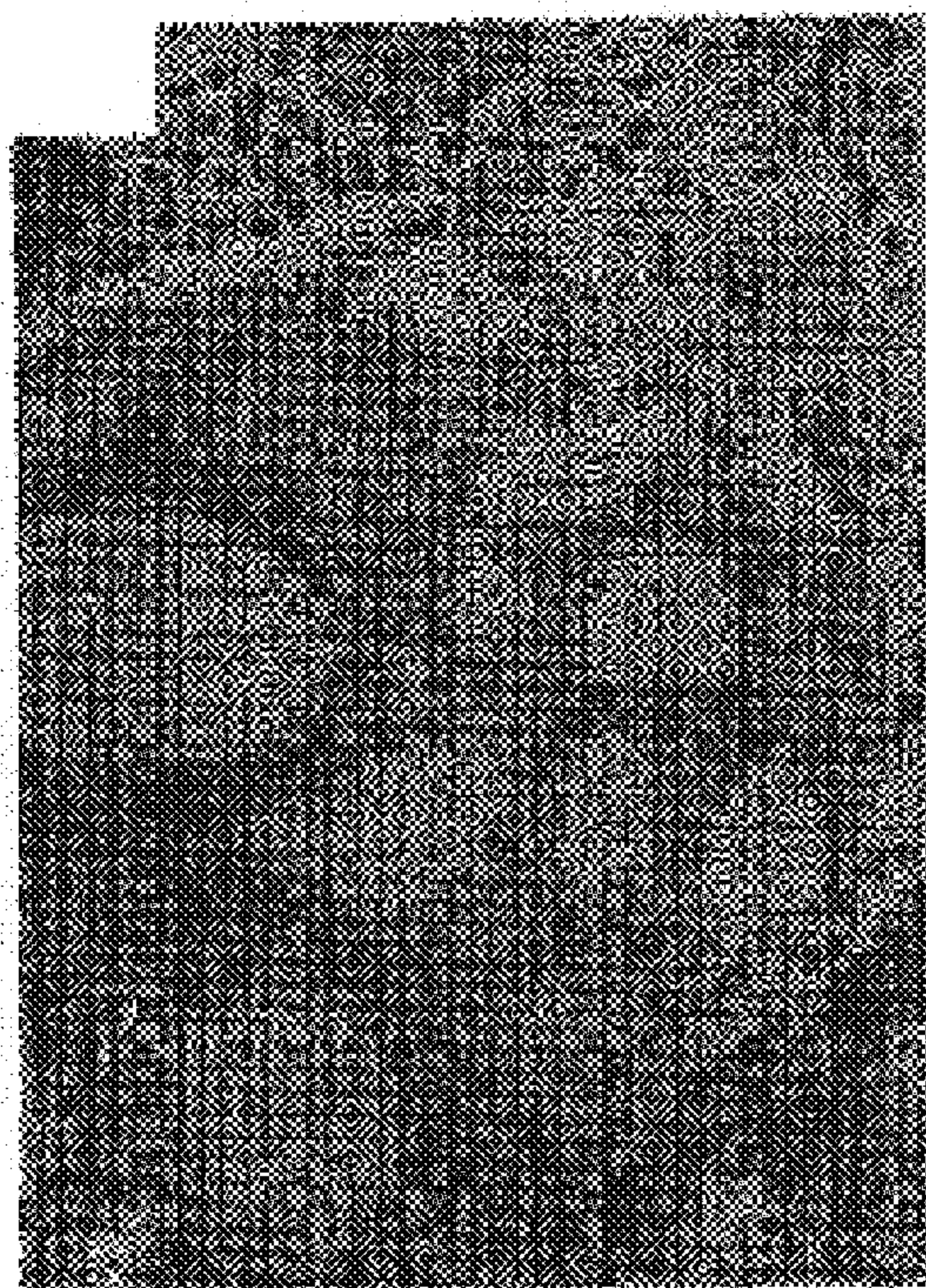


FIG. 14B

METHOD FOR IDENTIFYING METASTATIC SEQUENCES

Matter enclosed in heavy brackets [] appears in the original patent but forms no part of this reissue specification; matter printed in italics indicates the additions made by reissue.

More than one reissue application has been filed for the reissue of U.S. Pat. No. 5,783,182. Application Ser. No. 09/469,316, filed Dec. 22, 1999, now abandoned, is a reissue application of U.S. Pat. No. 5,783,182. Application Ser. No. 09/977,371, filed Oct. 16, 2001 is a continuation (and a reissue) of Ser. No. 09/469,316. Application Ser. No. 09/985,799, filed Nov. 16, 2001, is a continuation (and a reissue) of Ser. No. 09/977,371.

REFERENCE TO RELATED APPLICATION

[This patent application is a continuation of] *This patent application is a Continuation of U.S. application Ser. No. 09/977,371 filed Oct. 16, 2001, which is a Continuation of U.S. application Ser. No. 09/469,316, filed Dec. 22, 1999, abandoned, which is a broadening Reissue Application of U.S. Pat. No. 5,783,182, issued Jul. 21, 1998. The patent application issuing as U.S. Pat. No. 5,783,182 claims priority on United States provisional patent application, serial number 60/006,838, filed Nov. 16, 1995.*

RIGHTS IN THE INVENTION

This invention was made in part with United States Government support under grant number CA350129, awarded by the National Cancer Institute, National Institute of Health and the United States Government has certain rights in the invention.

BACKGROUND

1. Field of the Invention

The present invention relates to methods for the identification and isolation of metastatic sequences, to diagnostic probes and kits which contain metastatic sequences and to therapeutic treatments for neoplastic disorders based on metastatic sequences.

2. Description of the Background

The development of higher organisms is characterized by an exquisite pattern of temporal and spatially regulated cell division. Disruption in the normal physiology of cell division are almost invariably detrimental. One such type of disruption is cancer, a disease that can arise from a series of genetic events.

Cancer cells are defined by two heritable properties, uncontrolled growth and uncontrolled invasion of normal tissue. A cancerous cell can divide in defiance of the normal growth constraints in a cell leading to a localized growth or tumor. In addition, some cancer cells also gain the ability to migrate away from their initial site and invade other healthy tissues in a patient. It is the combination of these two features that make a cancer cell especially dangerous.

An isolated abnormal cell population that grows uncontrollably will give rise to a tumor or neoplasm. As long as the neoplasm remains in a single location, it is said to be benign, and a complete cure may be expected by removing the mass surgically. A tumor or neoplasm is counted as a cancer if it is malignant, that is, if its cells have the ability to invade surrounding tissue. True malignancy begins when the cells cross the basal lamina and begin to invade the underlying connective tissue. Malignancy occurs when the cells gain

the ability to detach from the main tumor mass, enter the bloodstream or lymphatic vessels, and form secondary tumors or metastases at other sites in the body. The more widely a tumor metastasizes, the harder it is to eradicate and treat.

As determined from epidemiological and clinical studies, most cancers develop in slow stages from mildly benign into malignant neoplasms. Malignant cancer usually begins as a benign localized cell population with abnormal growth characteristic called a dysplasia. The abnormal cells acquire abnormal growth characteristic resulting in a neoplasia characterized as a cell population of localized growth and swelling. If untreated, the neoplasia in situ may progress into a malignant neoplasia. Several years, or tens of years may elapse from the first sign of dysplasia to the onset of full blown malignant cancer. This characteristic process is observed in a number of cancers. Prostate cancer provides one of the more clear examples of the progression of normal tissue to benign neoplasm to malignant neoplasm.

The walnut-sized prostate is an encapsulated organ of the mammalian male urogenital system. Located at the base of the bladder, the prostate is partitioned into zones referred to as the central, peripheral and transitional zones, all of which surround the urethra. Histologically, the prostate is a highly microvascularized gland comprising fairly large glandular spaces lined with epithelium which, along with the seminal vesicles, supply the majority of fluid to the male ejaculate. As an endocrine-dependent organ, the prostate responds to both the major hormone, testosterone, and the major female hormones, estrogen and progesterone. Testicular androgen is considered important for prostate growth and development because, in both humans and other animals, castration leads to prostate atrophy and, in most cases, an absence of any incidence of prostatic carcinoma.

The major neoplastic disorders of the prostate are benign enlargement of the prostate, also called benign prostatic hyperplasia (BPH), and prostatic carcinoma; a type of neoplasia. BPH is very common in men over the age of 50. It is characterized by the presence of a number of large distinct nodules in the periurethral area of the prostate. Although benign and not malignant, these nodules can produce obstruction of the urethra causing nocturia, hesitancy to void, and difficulty in starting and stopping a urine stream upon voiding the bladder. Left untreated, a percentage of these prostate hyperplasia and neoplasias may develop into malignant prostate carcinoma.

In its more aggressive form, transformed prostatic tissues escape from the prostate capsule and metastasize invading locally and throughout the bloodstream and lymphatic system. Metastasis, defined as tumor implants which are discontinuous with the primary tumor, can occur through direct seeding, lymphatic spread and hematogenous spread. All three routes have been found to occur with prostatic carcinoma. Local invasions typically involve the seminal vesicles, the base of the urinary bladder, and the urethra. Direct seeding occurs when a malignant neoplasm penetrates a natural open field such as the peritoneal, pleural or pericardial cavities. Cells seed along the surfaces of various organs and tissues within the cavity or can simply fill the cavity spaces. Hematogenous spread is typical of sarcomas and carcinomas. Hematogenous spread of prostatic carcinoma occurs primarily to the bones, but can include massive visceral invasion as well. It has been estimated that about 60% of newly diagnosed prostate cancer patients will have metastases at the time of initial diagnosis.

Surgery or radiotherapy is the treatment of choice for early prostatic neoplasia. Surgery involves complete

removal of the entire (radical prostatectomy), and often removal of the surrounding lymph nodes, lymphadenectomy. Radiotherapy, occasionally used as adjuvant therapy, may be either external or interstitial using ^{125}I . Endocrine therapy is the treatment of choice for more advanced forms. The aim of this therapy is to deprive the prostate cells, and presumably the transformed prostate cells as well, of testosterone. This is accomplished by orchiectomy (castration) or administration of estrogens or synthetic hormones which are agonists of luteinizing hormone-releasing hormone. These cellular messengers directly inhibit testicular and organ synthesis and suppress luteinizing hormone secretion which in turn leads to reduced testosterone secretion by the testes. Despite the advances made in achieving a pharmacologic orchiectomy, the survival rates for those with late stage carcinomas are rather bleak.

SUMMARY OF THE INVENTION

The present invention overcomes the problems and disadvantages associated with current strategies and designs and provides new methods for the identification of sequences related to metastasis.

One embodiment of the invention is directed to methods for the identification of a metastatic sequence. One or more oncogenic sequences are transfected into a cell to form a transfected cell. The transfected cell is introduced into a primary site of a host animal to establish a colony which is incubated in the animal for a period of time sufficient to develop both a primary tumor and a metastatic tumor. Expressed sequences are harvested from the primary tumor and the metastasis. Harvested sequences are compared to each other and to non-metastatic cells to identify sequences related to metastasis. Dominant metastatic genes are genes whose expression leads to metastasis. Such genes are typically expressed at high levels in metastatic cells and not significantly expressed in normal or nonmetastatic cells. Recessive metastatic genes, genes whose expression prevents metastasis, may be selectively expressed in normal and nonmetastatic cells and absent in metastatic cells. Dominant and recessive metastatic genes may act directly or act pleiotropically by enhancing or inhibiting the expression or function of other dominant and recessive metastatic genes.

Another embodiment of the invention is directed to methods for identifying metastatic sequences. A mammalian cell is treated with a metastatic agent and the treated cell is implanted into a primary site of a host mammal. The host animal is maintained for a period of time sufficient for the cells to proliferate and to develop a [metastasis] *metastasis* at a secondary [cite] *site*. Expressed sequences from cells of the primary site and cells of the secondary site are reverse transcribed into cDNA by differential display polymerase chain reaction to identify differentially expressed sequences.

Another embodiment of the invention is directed to sequences isolated by the methods of the invention. Sequences may be in the form of DNA, RNA or PNA. The nucleic acid may be single-stranded or double-stranded. Single stranded nucleic acid may be in the form of a sense strand or an antisense strand. In addition, the sequence may be part of a homologous recombination vector designed to recombine with another metastatic sequence.

Another embodiment of the invention is directed to a method for treating a neoplastic disorder comprising administering a pharmaceutically effective amount of a metastatic nucleic acid to a patient. The nucleic acid may be single-stranded in the sense or the antisense direction. Alternatively, the nucleic acid may be packaged in a viral

vector such as, for example, a retroviral, a vaccinia or an adenoviral vector. Administration may be performed by injection, pulmonary absorption, topical application or delayed release of the nucleic acid along with a pharmaceutically acceptable carrier such as water, alcohols, salts, oils, fatty acids, saccharides, polysaccharides and combinations thereof.

Another embodiment of the invention is directed to a kit for detecting [of] the presence or absence of a metastatic sequence.

Other objects and advantages of the invention are set forth in part in the description which follows, and in part, will be obvious from this description, or may be learned from the practice of the invention.

DESCRIPTION OF THE DRAWINGS

FIG. 1 Schematic showing two paths in the multistep progression to cancer.

FIG. 2 A–B Staining of primary tumor (A) and metastatic deposit (B) from the lung of the same animal

FIG. 3 A–D Staining of normal human prostate (A), moderately differentiated human prostate tumor (B and C), and poorly differentiated prostate tumor (D).

FIG. 4 Schematic of method for isolating a metastatic gene from a gene ablated mouse strain.

FIG. 5 A–B Schematic showing method to establish a tumor and metastatic transplant from fetal tissue (A) and from cell lines and tumors (B).

FIG. 6 Isolation and characterization of *nmb* gene expression by DD-PCR and RNA blot in primary and metastatic cells.

FIG. 7 Differential expression of multiple genes is determined by DD-PCR and RNA blot of primary and metastatic cells.

FIG. 8 Caveolin identified as a differentially expressed gene by DD-PCR.

FIG. 9 Differential expression of genes isolated by DD-PCR confirmed by RNA blots.

FIG. 10 RNA blot analysis of total tumor mRNA using clone 29 GADPH probes.

FIG. 11 RNA blot of three independent MPR metastatic tumors and 5 MPR non-metastatic tumors.

FIG. A–RR 12 Nucleotide sequences of metastatic nucleic acids.

FIG. 13 A–D Characterization of metastatic sequences isolated.

FIG. 14 Immunohistological staining of primary and metastatic human prostate tumors using anti-caveolin antibodies.

DESCRIPTION OF THE INVENTION

As embodied and broadly described herein, the present invention is directed to methods for identifying metastatic sequences, to the metastatic sequences identified, to methods for the detection, diagnosis and treatment of disorders related to metastasis, and to diagnostic kits which comprise these sequences.

The ability of cancers to metastasize makes tumors difficult to eradicate by any means. Malignant cancer involves a multistage progression from, for example, normal tissue through hyperplasia, early adenoma, early carcinoma and finally to a metastatic tumor (FIG. 1). Cells of a typical tumor loosen their adhesion to their original cellular neigh-

bors and cross the basal lamina and endothelial lining to enter the body's circulation. Once in circulation, the metastatic cell exits from the circulation to disseminate throughout *the* body and proliferate in a new environment.

Like the initial oncogenic event, the ability of a cell to metastasize requires additional mutational or epigenetic changes. An understanding of the molecular mechanisms of metastasis allow for the design of treatments to inhibit metastasis. Knowledge of stage specific gene expression for neoplastic disorders allows for early detection and typing of tumors. With early detection and typing, proper treatment may be administered to a patient with the neoplastic disorder earlier, which will lead to a higher probability of a complete cure.

For human prostate tumors, the study of stage specific tumors is difficult, if not impossible, as cell lines are extremely difficult to grow and it is rare that tissue becomes available from the primary tumor as well as metastatic disease from the same patient. This problem is exacerbated because of the infrequent biopsy of metastatic deposits in conjunction with isolation of material from the primary tumor. Furthermore, the growth of cell lines from malignant prostates has proved to be problematic over the last few decades. This is evidenced by the lack of cell lines from prostate cancer obtained under any conditions.

One embodiment of the invention is directed to a method for identifying a metastatic sequence. A mammalian cell is transformed into a pre-neoplastic or neoplastic state or phenotype by transfection with one or more oncogenic sequences. Alternatively, or in addition to transfection, the mammalian cell may be treated with an agent or subjected to a condition that potentiates the metastatic character of the cell or predisposes the cell to metastasis. The transfected or treated cell is implanted into a host animal at a primary site and grown for a period of time sufficient to develop a metastasis at a secondary site. Expressed sequences from cells of the primary site and cells at the secondary site are amplified by differential display polymerase chain reactions. PCR products from these reactions are compared and the metastatic sequence identified by alteration in the levels or patterns of the resulting products.

Mammalian cells from a wide variety of tissue types and species are suitable for transection or treatment including surgically obtained or primary or immortalized cells and cell lines. Cells may be from humans or primates, mice, rats, sheep, cows, rabbits, horses, pigs or guinea pigs or from transgenic or xenogenic host mammals. Cells may be obtained from adult, juvenile or fetal tissue, and used directly from the mammal, from cryogenically preserved samples, or after culturing in vitro or in vivo for a period of time. In vitro culturing typically involves tissue culture conditions (e.g. 37° C.; 5% CO₂) while in vivo culturing may involve successive passage of cells through host animals such as, for example, mice or rabbits. Cells passed in vivo may be obtained from sites proximal or distal to the site of implantation. The tissue type from which the cells are derived or obtained may be any tissue which is susceptible to transfection or other treatment including, for example, urogenital tissues, epithelial cells, hepatic cells, fibroblasts lymphatic tissues, hematopoietic cells, cells of the immune system, cells of the gastrointestinal system and cells of the nervous system.

Cell types useful for the identification of metastatic sequences related to prostate cancer include cells and cell lines of the fetal prostate lineage from normal or transgenic animals, and cells from normal or reconstituted prostate

tissue. One method of generating reconstituted prostate cells is to isolate fetal prostate tissue and microdissect the fetal prostate epithelium away from fetal mesenchyme. Fetal prostate epithelium may be genetically manipulated before reassociation with fetal mesenchyme (FIG. 5A). Genetic manipulation involves treatment or transfection with a metastatic agent or a nucleic acid sequence that affects neoplastic or metastatic potential of the cell. Reassociation of fetal epithelium and mesenchyme is performed by implanting epithelial tissue within a pocket of mesenchymal tissue. After manipulation, cells are reimplanted into a mammalian host in a similar manner as other cells, such as reimplantation into or under the renal capsule.

Mammalian cells may be transfected by a variety of techniques, all of which are well-known to those of ordinary skill. Direct methods involve the introduction of genetic material into the nucleus of a cell by injection. These techniques include high velocity projectile injection, microinjection, and electroporation. Indirect methods, involving the active or passive uptake of the genetic information by the cell, include transduction with recombinant vectors, and chemical or physical treatments such as calcium phosphate uptake, lipofection or dextran sulfate transfection. Chemical techniques rely on chemical carriers to introduce nucleic acids into a cell. These methods, for example, utilize unilamellar phospholipid vesicles (e.g. liposomes) loaded with DNA (or RNA). The approach relies on the fusion of the DNA containing vesicles with the plasma membrane of the recipient cells. After entry, DNA traverse the cytoplasm and enter the nucleus. Another lipofection technique uses a synthetic cationic lipid such as N-[1-(2,3-dioleoyloxy) propyl]-N,N,N-trimethylammonium chloride (DOTMA). DOTMA spontaneously associates with nucleic acids and forms unilamellar vesicles upon sonication. Genetic material is incorporated into these vesicles and subsequently transfected into the cell. Calcium phosphate co-precipitation involves mixing of purified nucleic acid with buffers containing phosphate and calcium chloride which results in the formation of a fine precipitate. Presentation of this precipitate to cells results in incorporation of the nucleic acid into cellular genome. Other chemicals, such as DEAE dextran or polybrene, when present in media with nucleic acids, can also cause the transection of mammalian cells.

Physical methods of transfection rely on electric fields, needles and particles to enable nucleic acids to traverse the cellular membrane. Electric field mediated DNA transfection, commonly called electroporation, is based on the principle that membranes, when subjected to an electric field, undergo a reversible breakdown resulting in pores large enough to permit the passage of nucleic acids. In micro-projectile mediated gene transfer, micro-projectiles of subcellular dimensions are coated with nucleic acid and propelled at high velocity into a cell using a particle gun. The nucleic acid is introduced into the nucleus directly when the particles impinge upon the nucleus. In microinjection, nucleic acid is injected directly into the nucleus of a cell with a needle. Lasers have also been used to introduce minute holes in cellular membrane to allow introduction of nucleic acids. All these methods may be used for transfection and the selection of the method will depend on the cell type, the desired transfection efficiency and the equipment available.

The efficiency of transfection may be monitored and enhanced by the co-transfection of a selectable marker. If a marker is co-transfected with a genetic construct, positively transformed cells may be separated from nontransformed cells by chemical selection. The efficiency of transfection will be increased in most cases because the chemicals will

selectively kill non-transfected cells. The number of transfected cells may also be monitored by analyzing the degree of chemical resistance of the transfected cells. Markers commonly used for selection purposes include, for example, nucleic acids encoding dihydrofolate reductase, metallothionein, CAD, adenosine deaminase, adenylate deaminase, UMP synthetase, IMP 5'-dehydrogenase, xanthine-guanine phosphoribosyltransferase, mutant thymidine kinase, mutant HGPRTase, thymidylate synthetase, P-glycoprotein 170, ribonucleotide reductase, glutamine synthetase, asparagine synthetase, arginosuccinate synthetase, ornithine decarboxylase, HMG-CoA reductase, N-acetylglucosaminyl transferase, thernyl-tRNA synthetase, sodium or potassium dependent ATPase or derivatives or mutants of these nucleic acids. Markers may be used individually or in combination. Chemicals useful for selection include methotrexate, cadmium, PALA, Xyl-A, adenosine, 2'-deoxycoformycin, adenine, azaserine, coformycin, 6-azauridine, pyrazofuran, mycophenolic acid, limiting xanthine, hypoxanthine, aminopterin, thymidine, 5-fluorodeoxyuridine, adriamycin, vincristine, colchicine, actinomycin D, puromycin, cytocholasin B, emetine, maytansine, Bakers' antifolate, aphidicolin, methionine sulfoximine, β -aspartyl hydroxamate, albiziin, canavanine, α -difluoromethylornithine, compactin, tunicamycin, borrelidin, ouabain, and derivatives and analogs and combinations of these chemicals. Some chemicals, such as methotrexate, may be used individually while other chemicals, such as HAT (hypoxanthine, aminopterin and thymidine), need to be used in combination to be effective.

The oncogene transfection efficiency, the fraction of live cells transfected by an oncogene, may be indirectly enhanced by chemical selection for a co-transfected marker. An oncogene is a sequence which can predispose, or induce the cell into a pre-neoplastic or neoplastic condition or otherwise enhance the metastatic potential of the cell. Sequences with these properties are referred to as oncogenes and include abl, ahi, akt, bcl, crk, dsr, erb, ets, evi, fes/fps, fim, fis, fgr, flv, fms, fos, gin, gli, int, jun, kit, mas, lck, met, mil/raf, mis, mlv, mos, myb, myc, neu, onc, pim, raf ras, rel, ros, seq, sis, ski, spi, src, tel, thy, trk, and yes. Some oncogenes, such as ras, are oncogenic when mutated. Other oncogenes, such as myc, are oncogenic when overexpressed or underexpressed. Many oncogenes represent members of multigene families or homologs families. Homologs are proteins that have similar primary, secondary or tertiary structures. Genes may differ in nucleic acid sequence or encoded peptide sequence and still be homologs when the encoded polypeptides have similar spatial folding. Many oncogenes can be classified into dominant oncogenes and recessive oncogenes. One or more dominant oncogenes can confer a neoplastic or preneoplastic phenotype to a cell. One or more recessive oncogenes, when silenced, may also confer a neoplastic or preneoplastic phenotype. Gene silencing is performed by transfecting cells with nucleic acids which cause genetic ablation or by antisense suppression.

While any oncogene may be used, the preferred oncogenes are those that are normally associated with metastasis such as a metastasis specific gene. Such genes include for example, TGF- β 1, Cyclin D1 p21, p34, *mutant* p53, lysyl oxidase, caveolin, actin binding protein, ubiquitin activating enzyme E1, nmb or α -actinin 3. Metastatic-specific genes may be used individually or in combination with other oncogenes.

The metastatic potential of a cell may be altered, for example, by gene ablation [with] of a sequence specific for a recessive oncogene. Recessive oncogenes are those genes

which encode products which can suppress oncogenesis and metastasis. A gene ablation sequence can be designed to specifically suppress a recessive oncogene. Ablation may include pre-transcriptional inhibition such as homologous recombination with endogenous recessive oncogenes and post transcriptional inhibition such as the expression of antisense oncogenes to suppress translation. Gene ablation sequences may be targeted towards well known recessive oncogenes such as, for example, the retinoblastoma gene (Rb) or [Bcg] *Bcl*. Other candidates for ablation include metastatic genes previously isolated by the invention such as, for example, TGF- β 1, cyclin D1, p21, p34, *mutant* p53, lysyl oxidase, caveolin, actin binding protein, ubiquitin activating enzyme E1, nmb or α -actinin-3. The effects of ablating a recessive oncogene may include oncogenesis and metastases.

Alternatively, or in addition to transfection the mammalian cell may be treated with an agent, either before or after transfection, that alters the expression of the cell's nucleic acids. Treatment may comprise contacting the cells with one or more agents which affect the neoplastic predisposition (e.g. neoplastic agents; phorbol esters), metabolism (e.g. metabolis agents), metastasis (e.g. metastatic agents), differentiation (e.g. differentiation agents; retinoic acid), activation or proliferation (e.g. growth factors) of the cell. Agents which can alter gene expression include chemicals such as benzanthrane (BA), dimethyl benzanthrane (DMBA) or 5-azacytidine. Alternatively, treatment may also comprise altered conditions such as hypoxia which involves subjecting a cell to a reduced oxygen content, exposable to radiation or other stresses to the cell.

Treatment may be in vitro or in vivo and may include for example, direct or indirect induction or suppression of well known oncogenic sequences and genes isolated by the invention such as, for example, TGF- β 1, Cyclin D1, *mutant* p53, lysyl oxidase, caveolin, actin binding protein, ubiquitin activating enzyme E1, nmb, α actinin 3, and p34. Gene expression induction includes transfecting expression vectors encompassing coding regions of the gene. Gene repression comprises introducing a gene ablation sequence or a repressor of the gene to the cell.

Cells which have one or more genes ablated may also be used. For example, a metastatic suppressor gene may be ablated to prevent inhibition to metastases. A useful gene for ablation is a gene capable of affecting the phenotype and behavior or a cell or tumor. For example, with prostate tumors, suitable genes include both well known genes and genes isolated by the methods of the invention such as for example, TGF- β 1, Cyclin D1, p21, p34, *mutant* p53, lysyl oxidase, caveolin, actin binding protein, ubiquitin activating enzyme E1, nmb and α actinin 3. Genetic ablation (gene knockout) refers to a process of silencing the expression of a particular gene in a cell. The silencing process may include, for example, gene targeting or antisense blocking. Gene targeting refers to a process of introducing a nucleic acid construct into a cell to specifically recombine with a target gene. The nucleic acid construct inactivates the targeted gene. Inactivation may be by introduction of termination codons into a coding region or introduction of a repression site into a regulatory sequence. Antisense blocking refers to the incorporation into a cell of expression sequences which directs the synthesis of antisense RNA to block expression of a target gene. Antisense RNA hybridizes to the mRNA of the target gene to inhibit expression.

The host animal is preferably the same species as the implanted cell. In cases of xenogeneic transplants, the host may be immunocompromised genetically or by treatment

with drugs such as immunosuppressants. A host may be immunocompromised genetically by breeding such as with nude mice or severe combined immunodeficient (SCID) mice. A host may also be immunocompromised by chemical or irradiation methods. An additional route to immunocompromise a host is to use transgenic technology to introduce an immunosuppressing gene or to introduce a foreign antigen gene. An immunosuppressing gene is a gene that affects the efficiency of the immune system such as a gene which inhibits the formation of cells of the B cell or T cell lineage. A foreign antigen gene, when expressed, may cause the host to tolerate the antigens in a xenogeneic transplant and not mount an immune response.

Cells may be implanted into any primary site in a host animal, such as, for example, subcutaneous implantation, intravenous injection, or implantation into the abdominal cardiac, chest, pulmonary, thoracic or peritoneal cavity. Using techniques known to those of ordinary skill in the art, cells can be placed on or in nearly any organ or tissue. Reasons for choosing a site include ease of implant, proximity of similar tissue type, immunoprivileged position and ease of inspection. Metastases migrate from the primary site to one or more secondary sites such as, for example, the lung, kidney, liver, lymph nodes, brain, testis, bone, spleen, ovaries or mammary. Preferred sites include the renal capsule, the testes, the prostate and the ovaries.

To avoid histocompatibility problems, the implant may be placed into a histocompatible host animal. Such problems are generally avoided if the implant and host animal are syngeneic. Alternatively, a non-histocompatible host may be used if the host can be made immunotolerant. Hosts may also be transgenic or immunocompromised animals or genetically matched to the mammalian cells to be introduced. Immunocompromised animals may be derived from established mouse lines such as nude mice or severe combined immunodeficiency (SCID) mice, or by treatments such as radiation, chemical, pharmaceutical or genetic targeting. Sufficiently immunosuppressed animals can be made tolerant to xenogeneic transplants.

After implantation the host animal is maintained under normal conditions to develop metastases. Alternatively, the host animal may be subjected to an altered treatment or environmental condition to stimulate or repress metastasis or induce other cellular functions. In metastasis, a subpopulation of cells of the implantation site invade and establish one or more secondary colonies in the host animal. The behavior of the implanted cell will depend on the cell type, the transfected sequence and the implantation location. Typical secondary sites for metastatic colonies include lung, kidney, liver, lymph nodes, brain, testis, spleen, bone, ovary, skin and mammary tissue. Metastatic development times vary from days to weeks even months. Cells with a high metastatic potential tend to progress to metastasis quickly while cells with a low metastatic potential may require very long periods of time that span significant portions of the lifespan of the animal.

The host animal may be analyzed for metastatic development weekly, from one week to 20 weeks to six months, nine months or one year after implantation. For animals with longer lifespans such as sheep, the animal may be inspected yearly from one year on up to ten years for metastatic tumors. Metastases can be detected by examinations such as palpation, biopsy, imaging, exploratory surgery, CAT scans, autopsy, X-ray and direct observation. In addition, tissue samples may be taken surgically from the host mammal and subjected to histological or other examinations for the detection of metastases.

Expressed sequences include mRNA, rRNA, hnRNA, DNA, cDNA and any nucleic acid sequence that is expressed in the cell. These sequences may be amplified by in situ techniques or by purification of nucleic acid from collected cells. Expressed sequences may be obtained by extracting nucleic acids from cells before implantation, at the primary site or at the secondary site. Cells collected at these sites may optionally be cultured for a time before nucleic acid extraction. The effects of treatment with gene expression modifying agents or environmental conditions can be ascertained by collecting cells before and after treatment. Treatment may be applied to the cells while the cells are in the host mammal or after the cells are excised and in culture. Nucleic acid are collected from cells using techniques that are well known to those of ordinary skill in the art.

Expressed sequences may be used directly for polymerase chain reaction (PCR) analysis using, for example, the technique of reverse transcriptase polymerase chain reaction (RT-PCR). Alternatively, RNA may be enriched for mRNA using a poly-A RNA enrichment method. Numerous poly-A RNA enrichment methods exist and are commercially available. Techniques used for poly-A RNA enrichment include oligo-dT columns, oligo-dT magnetic beads, and oligo-dT cellulose, RNA may be further processed into cDNA before analysis by reverse transcription using reverse transcriptase. The cells or the extracted nucleic acid may be preserved, such as by freezing, and analyzed at a later time.

Differential display polymerase chain reactions (DD-PCR) are performed on the expressed sequences using two variable primers which may contain the same or entirely different sequences or an anchor primer and a variable primer. If an anchor primer is used, one anchor primer and one variable primer create a single or a single set of reaction products for each reaction. A complete profile may include 25 or more different PCR reactions per sample wherein each PCR reaction is performed with the same anchor primer and a different variable primer. DD-PCR may also be performed using anchor and variable primers which contain the same sequence. Whether a particular reaction is used depends on whether a difference exists between the products of two PCR reactions using the same primers. When a significant difference exists between the expression sequences amplified, one pair of PCR reactions may be sufficient and informative.

Anchor primers are preferably oligonucleotides with a poly-T sequence at the 5'-[terminas] *terminals* and a dinucleotide selected from the group consisting of AA, AG, AC, AT, GA, GG, GC, GT, CA, CG, CC and CT at the 3'-[terminas] *terminals*. For example, the sequence may be 5'-TTTTTTAA-3' or 5'-TTTTTTAG-3'. The length of the poly-T sequence is typically between about 5 to about 30 bases in length and preferably between about 10 to about 20 nucleotides long. The total length of the anchor primer can vary greatly for each experiment but is preferably between about 7 to about 32 and more preferably between about 12 and about 22. Differential diagnostic *display* polymerase chain reaction may also be performed using an anchor primer of any sequence and a length between about 5 to about 30, preferably between about 5 to about 20 and more preferably between about 7 to about 12 bases.

The variable primer may comprise a random sequence, or a specific sequence such as, for example, a sequence of SEQ ID NO. 1 to SEQ ID NO. 24. Variable primers preferably are oligonucleotides with a length between about 5 to about 30, preferably between about 5 to about 20, and more preferably between about 7 to about 12 bases in length.

To enhance detection of the PCR product, the anchor primer or the variable primer, or both, may comprise a

detectable moiety. Examples of detectable moieties include radioactive moieties, phosphorescent moieties, magnetic moieties, luminescent moieties, conjugatable moieties or other detectable moiety. A plurality of detectable moieties may be used to enhance detection or to simplify data analysis. Other detectable moieties include conjugatable moieties and molecules which can bind specifically to other molecules which are themselves detectable. Examples of conjugatable moieties include avidin, streptavidin, biotin, antibody, antigen, cell adhesion molecules and other molecules with similar activities. Detectable moieties are preferably labeled nucleotides. A nucleotide may be any natural or synthetic nucleotide or nucleotide analog capable of incorporation into an elongation reaction in a polymerase chain reaction. Labeled nucleotides include nucleotide triphosphates labeled with one or more radioactive atoms such as ^{32}P , ^{33}P , ^3H , ^{14}C and ^{35}S . Products of DD-PCR reactions are compared to detect the metastatic sequence. Comparisons can be performed between expressed sequences from cells at secondary sites with cells at any stage in the method including untreated mammalian cells, transfected or treated mammalian cells, implanted cells or cells obtained from the primary site in the host animal. DD-PCR products may be analyzed by any method which reliably compares the products of two polymerase chain reactions. Typical analytical methods used for this purpose include polyacrylamide gel electrophoresis, capillary electrophoresis and high pressure liquid chromatography (HPLC). Product produced from DD-PCR may be analyzed in double-stranded or single-stranded forms. When the products of the DD-PCR reaction are labeled the sizes and distribution of the products may be monitored and analyzed by following the labels using a radiation monitor or by autoradiography. For example, DD-PCR performed in the presence of radioactive primers or nucleotide triphosphates, can be analyzed by gel electrophoresis, by capillary electrophoresis, or by HPLC. Products are easily monitored by the presence of radioactivity.

Another method for analyzing and isolating metastatic sequences is to sequence the amplified nucleic acid sequences. Sequencing may be performed using standard methods well known to those of ordinary skill in the art. The resulting sequence may be compared to a sequence database created or well-known, such as Genbank, for identification or for locating homologs. The sequencing information may be used to calculate the physical characteristics of the nucleic acids such as melting temperature and secondary structure. The primary sequence and the physical characteristic may be used to synthesize optimal nucleic acid probes for the detection or staging of metastasis or conditions that are predictive of the presence or absence of the metastatic condition.

Another embodiment of the invention is directed to a method for identifying a metastatic sequence. A mammalian cell is pretreated with a metastatic agent to form a population of cells predisposed to metastasize. The treated cells are introduced into a host mammal at a primary site. The host animal is maintained for a period of time sufficient to develop a metastasis at a secondary site. Expressed sequences of cells at the primary site and cells at the secondary site are treated with a genotoxic agent or subjected to genotoxic conditions. Expressed sequences of the treated cells are amplified by differential display polymerase chain reaction and compared with untreated cells from any previous step to identify the metastasis sequence.

The metastatic agent may be a chemical compound, a nucleic acid or a protein that alters the metastatic potential

of a cell or relates to or is associated with the metastatic process. Chemical compounds include retinoids such as 4-hydroxyphenyl (4HP). Other agents include the proteins TGF- β 1, Cyclin D1, p21, p34, *mutant* p53, lysyl oxidase, caveolin, actin binding protein, ubiquitin activating enzyme E1, nmb or α -actinin 3, or their respective genes. The metastatic agent may be a metastatic stimulant or a metastatic suppressant. Metastatic stimulants may be used to enhance the sensitivity of the metastasis sequence detection method. Conversely metastatic suppressants may be used to decrease the sensitivity of the method enabling the selective identification of potent [metastasis] *metastatic* sequences or sequences specific to a particular tissue type or metastatic disorder. Treatment may comprise direct contact with the metastatic agent or incubation for a period of time. Metastatic agents enhance the metastatic potential of the implanted cells and increase the sensitivity and the speed of the overall method.

The cells at the primary site and the metastatic cells at the secondary site may be treated with a genotoxic agent in vivo or in vitro. In vivo treatment may comprise injecting genotoxic agents directly into the host mammal or specifically applying the agent with, for example, topical formulations. The cells at the primary site and the secondary site may also be isolated from the host animal and treated with the genotoxic agent in culture. Genotoxic agents are chemical compounds, nucleic acids or proteins that alter gene expression by effecting the nucleic acid genome directly by, for example, chemical modification, or indirectly by, for example, altering components associated with gene expression. Such agents include, for example, benzantracene (BA), dimethyl benzantracene (DMBA) and 5-azacytidine, and may include metastatic agents as well. In addition to or in place of genotoxic agents, the cells may be treated to hypoxic conditions or radiation to alter gene expression. Metastatic sequences identified in these methods may be specific for particular genotoxic agents or conditions.

Another embodiment of the invention is directed to the use of a host animal with an altered genotypic or phenotypic predisposition for metastases. A host animal may be screened for endogenous expression of metastases gene. Examples of metastatic sequences which may be screened for include sequences isolated by the method of the invention, such as, for example, the sequences listed in FIG. 12 and FIG. 13. Particularly useful metastatic sequences include TFG- β . A host animal with reduced levels of a metastatic gene product may be used to isolate novel metastatic genes. Host animals may be screened for reduced levels of metastatic gene expression. In addition, transgenic technology may be used to ablate a metastatic gene in the germline of a host animal.

Another embodiment of the invention is directed to analysis of a cell line before their use as a starting material to isolate metastatic genes in a particular pathway. Analysis is useful in identifying cells, and consequently sequences specific to these cells, which are particularly susceptible or resistant to metastatic transformation. For example, a cell highly predisposed to metastasis may be especially sensitive for detecting metastatic genes. Conversely, a cell showing high resistance to metastasis can be used to isolate especially potent metastatic sequences. One method to analyze susceptibility to metastasis is to determine the cellular response to growth factors or growth inhibitors. Briefly, a control population and a test population of cells are exposed to a growth factor or a growth inhibitor and the cellular response (e.g. proliferation, metabolism) recorded. Cells showing abnormal responses to the growth factor or growth inhibitor may

be used as the starting material for metastatic gene isolation. Cellular response include changes in the rate of cellular division (e.g. thymidine uptake), changes in the expression of RNA or proteins, changes in cellular localization or modification patterns of RNA or proteins, and changes in the rate of uptake, release or metabolism of nutrients.

Especially potent or weak metastatic genes may be detected by treating and analyzing the metastatic potential of different cells and selecting a suitable cell type as the starting material. For example, cells may be treated with myc, ras, *mutant* p53 or combinations thereof and analyzed for cyclin D1 expression which is shown to [correlates] *correlate* with metastasis. FIG. 2 shows the in situ analysis of cyclin D1 in primary MPR tumors (FIG. 2A) and in metastatic deposits from the lung of the same animal (FIG. 2B). The gene expression pattern of cyclin D1 in MPR correlates with that of human prostate tumors (FIG. 3) analyzed with stains specific for cyclin D1 expression. Normal human tissue shows no cyclin D1 expression or staining (FIG. 3A). Moderately differentiated prostate cancers with dispersed (FIG. 3B) or focal positively staining (FIG. 3C) show moderate staining. Advanced poorly differentiated prostate cancer show strong nuclear as well as cytoplasmic staining (FIG. 3D) implying strong expression of cyclin D1. After treatment with myc, ras or *mutant* p53, cyclin D1 expression shows correlation with the metastatic potential of the cell. Thus, cyclin D1 expressing cells are a source of cells with high metastatic potential. Conversely, cells with low cyclin D1 expression are a source of potentially [metastatically] *metastasis* resistant cells.

This method may be adjusted for the isolation of metastatic sequences expressed along a particular developmental of differentiation pathway by combining the various treatment and analytical techniques. This approach is schematically represented in FIG. 4. For example, a mammalian cell may be genetically ablated for TGF- β 6, Cyclin D1, *mutant* p53, lysyl oxidase, caveolin, actin binding protein, ubiquitin activating enzyme E1, nmb, α actinin 3, or p34. The genetically altered cell is used in an in vivo mouse prostate reconstitution (MPR) model. Metastatic and nonmetastatic cells isolated from the MPR may be analyzed directly or after induction with an agent such as the TGF- β gene or its product. Analysis involves the use of differential display polymerase chain reaction to identify differentially expressed bands. Sequences identified may be used for subsequent ablation, transformation or differential analysis.

Genetic ablation (gene knockout) may be performed after a cell is selected or by selecting a cell comprising a genotype with the proper genetic ablation. Cells already comprising gene ablation may be acquired from a cell depository, from other laboratories or from a transgenic animal. As transgenic animals comprise genetically ablated genes in every cell, any tissue from a transgenic animal may be used as the starting material.

The effects of oncogenes are at least additive and often synergistic. Thus, dominant oncogenes may be transfected together or multiple recessive oncogenes ablated together for a stronger effect. Furthermore, both methods may be combined and dominant oncogene transfection may be accompanied by recessive oncogene ablation.

The function of the metastatic sequence may be determined by the differential expression pattern. For example, a [dominate] *dominant* metastatic gene will be present in a metastatic cell while a recessive metastatic gene is present in a nonmetastatic cell. Metastatic sequences may be detected as bands which are present in the DD-PCR of metastases

isolated in secondary sites [and] *yet* absent from DD-PCR products of primary cells. These sequences may be dominant metastatic genes whose expression is directly responsible for metastases, or they may be metastasis associated genes whose expression correlates with metastasis. Either are useful for therapy and diagnosis. Conversely, DD-PCR bands which are present in primary site tumors, but absent in secondary metastatic sites, may be dominant metastasis suppression genes. Dominant metastasis suppression genes comprise genes whose expression suppresses metastasis while nonmetastatic genes comprise genes whose expression correlates with non-metastatic tissue. Genes which are highly correlative with either the metastatic phenotype or the non-metastatic phenotype may be isolated. Isolation can be performed by cutting the appropriate nucleic acid [in the] *containing* band [of] *from* a polyacrylamide gel or by collecting the appropriate fraction in an HPLC or capillary electrophoresis. The nucleic acid may be cloned into a plasmid vector, and sequenced, or synthetically prepared.

Another embodiment of the invention is directed to a method for identifying sequences in a metastatic pathway which are responsive or unresponsive to extracellular signals. Such sequences may be used in therapy and diagnosis of metastatic disorders. Implanted cells or cells from a primary site and cells from a secondary site are treated with extracellular signals. RNA sequences from the treated cells are compared with RNA sequences of the untreated cells (FIG. 5B). Treated cells and untreated cells may be derived from a short term or long term in vitro culture of primary tumors and malignant tumors. Alternatively, a part of a primary tumor and a part of a malignant tumor may be collected before the animal is treated with an extracellular cytokine or other factor. Long term cultures, or cell lines of primary and malignant cells may also be used as recipients of extracellular growth signal treatment. Suitable signals for each experiment will depend on the cell type. Generally, growth factors, lymphokines, inhibitory factors, migratory factors or hormones may be used. Factors previously isolated by commercial or methods of the invention and factors associated with or causative or suppressive of metastasis are preferred. Thus, transforming growth factor β 1 (TGF- β 1) may be used to treat cells before DD-PCR analysis. Proteins encoded by the genes isolated by this method are especially useful for the treatment of cells for the isolation of additional sequences. The identification of one sequence responsive to the extracellular signal pathway allows for identification of additional genes upstream and downstream from that sequence.

Another embodiment of the invention is directed to metastatic sequences identified by the methods of the invention. Metastatic sequences are sequences associated with the presence or absence of a metastasis or related to the metastatic process can be used in the therapeutic treatment of metastasis. Metastatic-related sequences include dominant metastatic sequences, recessive metastatic sequences, metastasis associated sequences, dominant oncogenes, recessive oncogenes and cell cycle genes. These genes encode for example, proteins involved in cell cycle, signal processing, DNA replication, growth regulation, inter and intra cellular signaling transcription control and translation control. Isolated sequences are useful in the treatment and for the detection of metastatic and other disorders. Disorders which may be treated comprise diseases involving proteins and sequences which are isolated by interaction with the sequences and proteins isolated by the method of the invention. Both malignant or nonmalignant disorders may be treated. Non malignant disorders include hyperplasia, dys-

plasia and hypertrophy. Examples of nonmalignant disorders include benign enlargement of the prostate, nodular hyperplasia, and benign prostatic hypertrophy.

Treatment may involve gene replacement, gene targeting, antisense inhibition, gene expression or gene suppression. Gene replacement involves replacing a copy of a defective gene with another copy by homologous recombination. Gene targeting involves the disruption of a cellular copy of a gene by homologous recombination. Antisense inhibition exploits the specificity of hybridization reactions between two complementary nucleic acid chains to suppress gene expression. Cloned genes can be engineered to express RNA from only one or the other DNA strands. The resultant RNA hybridizes to the sense RNA and inhibits gene expression. Gene expression and gene suppression involve the introduction of genes whose expression actively inhibits neoplastic transformation and metastasis.

Another embodiment of the invention is directed to nucleic acids which comprise a sequence identified by the methods of the invention. The nucleic acid may be DNA, RNA or PNA and may be used as a diagnostic tool in the treatment of neoplastic disorders and malignant tumors. The nucleic acids may comprise additional sequences such as promoters, for expression of a sense or antisense message, recombination sequences for gene targeting, selectable markers for transfections, or replication origins for passage in a prokaryotic or eukaryotic host such as animal cells, bacteria or yeast.

Another embodiment of the invention is directed to nucleic acids which comprise sequences identified by the method of the invention such as, for example, the caveolin gene, ABP280 (actin binding protein 280), the lysyl oxidase gene, and the nmb gene (clone 29), and other sequences listed in FIG. 12 and FIG. 13. Nucleic acids comprising a sequence corresponding to these genes may be used in treatment or diagnosis and in diagnostic kits for screening biological samples for the presence or absence of metastasis or metastatic potential. Treatment may involve using the sequences in gene therapy, including gene ablation, gene expression and antisense suppression. Diagnosis may involve genotypic analysis of samples to determine the existence and expression levels of the expressed sequences.

Another embodiment of the invention is directed to the use of caveolin gene and protein in the isolation of oncogenes and in the treatment of neoplastic disorders such as, for example, prostate cancer. Caveolin is an integral membrane protein and a principal component of caveolae. Caveolae are small invaginations at or near the plasma membrane of most smooth muscle cells and may function as a component of specific signal transduction pathways. Surprisingly, caveolin expression increases in metastatic human prostate cells as compared to human primary prostate tumors.

As caveolin expression correlates with metastasis, application of biological technologies designed to block the activity of caveolin or the function of caveolae may have therapeutic benefits for the treatment of neoplastic disorders such as human prostate tumors. Specific treatment approaches using caveolin may include the delivery of antisense or dominant negative caveolin sequences using expression or viral vectors; as well as the use of specific anti-caveolin antibodies. Additional approaches could also target the caveolae, but are not specifically based on caveolin function. Additional protein and non-protein components of caveolae could also be targeted for abrogation or the local or systemic administration of nutritional or biological agent may also be used. For example, caveolae are

extremely rich in cholesterol and disruption or depletion of this molecule may alter the function of caveolae.

Another embodiment of the invention is directed to methods for treating a neoplastic disorder comprising administering a pharmaceutically effective amount of composition containing a nucleic acid having a sequence identified according to the methods of this invention, its expression product or fragments of either. The nucleic acid may be in the form of a sense or antisense single-stranded or double-stranded nucleic acid. The composition may be combined with a pharmaceutically acceptable carrier such as water, alcohols, salts, oils, fatty acids, saccharides, polysaccharides administered by injection, pulmonary absorption, topical application or delayed release. More than one carrier may be used together to create a pharmaceutical with desirable properties.

Another embodiment of the invention is directed to a kit or diagnostic [acid] aid for screening biological samples for detection of [metastasis, neoplasia or kits] *metastasis or neoplasia*. Kits comprise sequences isolated according to the methods of the invention and reagents and materials useful in such kits, such as, for example, buffers, salts, preservatives, and carriers, all of which are well known to those of ordinary skill in the art. Kits are useful for the analysis of tissues to screen those for the determination of normal, nonmalignant neoplastic or malignant cells. Kits may comprise additional reagents useful for the extraction of nucleic acids from a tissue sample. Reagents for analyzing the nucleic acid extracted from a tissue sample such as polymerase chain reaction reagents and Southern blots reagents may also be included.

The following experiments are offered to illustrate embodiments of the invention and should not be viewed as limiting the scope of the invention.

EXAMPLES

Example 1

Production of Mouse Prostate Reconstitution Tumors and Metastasis.

Mouse Urogenital Sinus (UGS) tissue was isolated from 17 day old mice embryos. Each isolated UGS was digested with 1% trypsin for three hours at 4° C. The trypsin was inactivated by the addition of fetal calf serum. UGS cells were digested with 0.125% collagenase for 1.5 hours, counted and mixed at the appropriate cell ratios prior to infection with retrovirus in the presence of polybrene. Retroviruses used include Zipras/myc-9. Control experiments were performed using BAGA virus. After a two-hour infection, the infected cells were centrifuged and individual reconstitutions containing 1.5×10^6 cells produced by resuspending the cells in rat tail collagen at a density of 6.0×10^7 cells per ml. Aliquots of the infected UGS cells were placed in (DME) with 10% fetal calf serum overnight at 37° C., 5% CO₂.

The next morning each cell/collagen reconstitution was implanted under the renal capsule of an adult male +/- animal. Reconstitutions were harvested from the mice five weeks later when they showed signs of obvious distress from the tumor burden. Metastasized tumors were isolated from the same mice at sites outside the renal capsule. Isolated tumors and metastasises were either stored in liquid nitrogen or in preservatives such as 10% buffered formalin.

Cell lines were derived from fresh tumors by mincing a small portion of the primary and metastatic tumor and placing each in explant culture in Dulbecco's Modified Eagle Medium (DMEM) supplemented with 10% fetal calf

serum. Cells which grow from each explant were propagated in DMEM and 10% fetal calf serum.

For histological analysis, a portion of a fresh tumor was fixed in 10% buffered formalin and embedded in paraffin for sectioning and staining with hematoxylin and eosin (H&E) or immunohistochemical staining. Immunohistochemical localization of cytokeratins was detected using polyclonal cytokeratin antiserum A575 (Dake Co.; Carpinteria, Calif.) and Vectastain ABC kit (Vector Laboratories; Burlingame, CA).

Example 2

Isolation of C-DNA for DD-PCR.

Total cellular RNA was isolated by ultracentrifugation through cesium chloride. Briefly, up to one gram of cells from culture, tumors or organs was placed into 4 ml of ice-cold GIT buffer (4M guanidine isothiocyanate, 0.025M sodium acetate, 0.1M M β-mercaptoethanol) and homogenized in a tissue homogenizer (Polytron or equivalent). The homogenate was carefully layered over 4 ml of 5.7M CsCl, 0.024M sodium acetate (1.8 g CSC1 per ml) in a centrifuge tube. The layers were centrifuged at 35,000 RPM for 18 hours in a SW50.1 rotor. DNA was collected from the interface between the cushion and the supernatant, diluted two folds with water, added to 2.5 volumes of ethanol and spooled out on a glass rod. RNA that formed a pellet on the bottom of the CsCl layer was resuspended, and once extracted with an equal volume of phenol:chloroform (1:1), twice with chloroform and precipitated with ethanol and resuspended in diethylpyrocarbonate treated water. The concentration of DNA and RNA were be determined by absorption at 260 nanometers.

Example 3

Differential Display Polymerase Chain Reaction.

mRNA isolated from primary tumors or metastasis was reverse transcribed with one of the primers and subjected to DD-PCR using the same primer as both the forward and reverse primer. A set of 24 primers comprising short oligonucleotides were used for both the reverse transcription of mRNA into c-DNA and for differential display polymerase chain reaction. The sequence of the primers used are shown in Table 1.

TABLE 1

Primer No.	Sequence	Sequence number
1	5'-TGACAATCG-3'	(SEQ. ID. NO. 1)
2	5'-AGCTAAGGTC-3'	(SEQ. ID. NO. 2)
3	5'-TCTGCGATCC-3"	(SEQ. ID. NO. 3)
4	5'-ATACCGTTGC-3'	(SEQ. ID. NO. 4)
5	5'-TACGAAGGTG-3'	(SEQ. ID. NO. 5)
6	5'-TGGATTGGTC-3'	(SEQ. ID. NO. 6)
7	5'-CTTTCTACCC-3'	(SEQ. ID. NO. 7)
8	5'-GGAACCAATC-3'	(SEQ. ID. NO. 8)
9	5'-TGGTAAAGGG-3'	(SEQ. ID. NO. 9)
10	5'-TCGGTCATAG-3'	(SEQ. ID. NO. 10)
11	5'-CTGCTTGATG-3'	(SEQ. ID. NO. 11)
12	5'-GATCAAGTCC-3'	(SEQ. ID. NO. 12)
13	5'-GATCCAGTAC-3'	(SEQ. ID. NO. 13)
14	5'-GATCACGTAC-3'	(SEQ. ID. NO. 14)
15	5'-GATCTGACAC-3'	(SEQ. ID. NO. 15)
16	5'-TTAGCACCTC-3'	(SEQ. ID. NO. 16)
17	5'-ACCTGCATGC-3'	(SEQ. ID. NO. 17)
18	5'-GCTATACTGC-3'	(SEQ. ID. NO. 18)
19	5'-AGTTGCCAGG-3'	(SEQ. ID. NO. 19)
20	5'-AAGCCGTGTC-3'	(SEQ. ID. NO. 20)
21	5'-TCAACGCTCA-3'	(SEQ. ID. NO. 21)
22	5'-TGTTCGAATC-3'	(SEQ. ID. NO. 22)
23	5'-CGAGTCAGAC-3'	(SEQ. ID. NO. 23)
24	5'-TATGAGTCCG-3'	(SEQ. ID. NO. 24)

PCR was performed using standard conditions with 40 cycles of denaturation at 94° C. for 40 seconds, annealing at

40° C. for 2 minutes, and elongation at 72° C. for 35 seconds. After PCR, the products were analyzed with non-denaturing polyacrylamide gel electrophoresis (PAGE) at 12 watts for 15 hours. Bands which differed between test and control samples were eluted from the gel, subjected to reamplification by PCR and cloned. Polyacrylamide gel electrophoresis of DD-PCRs, and the accompanying RNA blot analysis showing the isolation of sequences with substantial similarity to nmb and TGF-β is shown in FIG. 6 and FIG. 7 respectively. Additional sequences isolated by this method show substantial similarity to lysyl oxidase, actin binding protein, ubiquitin activating enzyme E1, α-actinin, and P34 ribosomal binding protein sequence (FIG. 8). Differential expression of caveolin was demonstrated by DD-PCR followed by PAGE (FIG. 9).

Example 4

p53 Allelotype Determination.

The p53 allelotype of a cell sample was determined by PCR. Briefly, nucleic acid is extracted from a tissue sample or a cell culture sample. An aliquot of nucleic acids in placed in 45 μl aliquot of a master mix which contained a final concentration of 0.2 mM of each dATP, dTTP, dGTP, dCTP, 1.5 mM MgCl₂, 0.5 unit Taq polymerase, 0.05 μM of each of two primers set specific for the normal wildtype allele of p53 (5'-GTGTTTCATTAGTTCCCCACCTTGAC-3', SEQ. ID NO. 25; 5'-AGAGCAAGAATAAGTCAGAAGCCG-3', SEQ. ID NO. 26). A control set of primers specific for the fibroblast growth factor-7 gene was used to monitor the polymerase chain reaction experiment (5'-ACAGACCGTGCTTCCACCTCGTC-3', SEQ. ID NO. 27; 5'-CCTCATCTCCTGGGTCCCTTTCA-3', SEQ. ID NO.28). One μl of the reaction from the first round of PCR was used as the starting material for a second round of PCR using a second set of wildtype p53 specific primer (5'-GTCCGCGCCATGGCCATATA-3', SEQ. ID NO. 29; 5'-ATGGGAGGCTGCCAGTCCTAACCC-3', SEQ. ID NO. 30). This second round of PCR was also monitored using a control set of primers specific for the fibroblast growth factor-7 (5'-ACAGACCGTGCTTCCACCTCGTC-3'. SEQ. ID NO 27; 5'-CCTCATCTCCTGGGTCCCTTTCA-3', SEQ. ID NO 28).

After PCR the products were analyzed with non-danturing polyacrylamide gel electrophoresis (PAGE) at 12 watts for 15 hours. Bands which differed between test and control were eluted from the gel, subjected to reamplification by PCR and cloned.

Example 5

Induction of cell lines with TGFβ6 Influence Cellular Gene Expression.

1481-PA cells were grown overnight in DME supplemented with 10% fetal calf serum overnight at 37° C., and 5% CO₂. Induction was performed by treatment with TGF-β1 at a concentration of 2 nanograms per ml. The treated cells were returned to the incubator and cultured for 12 hours. After induction, cells were washed in phosphate buffered saline and harvested and concentrated by centrifugation.

RNA was extracted from treated and untreated cells and subjected to DD-PCR. Differentially expressed bands detected by DD-PCR were cloned and differential expressions were confirmed using RNA blots (FIG. 10). Subsequent cloning and sequencing identified the bands as ABP280 or filamin.

One gene isolated showed differential expression in cells induced by TGF-β (FIG. 11, clone 29), while a control probe on the same cell line showed no difference in expression levels (FIG. 11, GAPDH).

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Example 6

Metastatic Sequences Isolated.

Using the methods of Examples 1, 2, 3, 4, and 5, a plurality of metastatic sequences were isolated and sequenced. The expression of the metastatic sequences in primary cells and in metastatic cells were determined using RNA blots. The nucleic acid sequences of other isolated sequences are listed in FIG. 12. Sequence analysis and expression analysis was performed on the isolated cloned and the results of these studies are summarized in FIG. 13.

Example 7

Caveolin Immunoassay in Human Prostate Cancers.

Primary site human prostate tumors and metastases were isolated and analyzed for caveolin expression by immunoassay. The results of the assay is shown in Table 3. Metastases shows higher levels of caveolin proteins in metastases than in primary tumors. Immunohistology of tissue sections reveals both elevated levels and distinct distribution of caveolin protein in metastatic human prostate when compared to a primary human prostate tumor (FIG. 14).

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TABLE 3

Patients	Primary-site	Metastases in lymph node
1	+	++
2	++	+++
3	++	+++
4	++	++
5	+	+
6	++	++
7	++	+++
8	+	+
9	-	-
10	+	+
11	+	+
12	++	++
13	+	+
14	++	+++

Other embodiments and uses of the invention will be apparent to those skilled in the art from consideration of the specification and practice of the invention disclosed herein. The specification and examples should be considered exemplary only with the true scope and spirit of the invention indicated by the following claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(iii) NUMBER OF SEQUENCES: 175

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TGACAATCG

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

-continued

(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:	
AGCTAAGGTC	10
(2) INFORMATION FOR SEQ ID NO: 3:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 10 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:	
TCTGCGATCC	10
(2) INFORMATION FOR SEQ ID NO: 4:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 10 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:	
ATACCGTTGC	10
(2) INFORMATION FOR SEQ ID NO: 5:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 10 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:	
TACGAAGGTG	10

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(2) INFORMATION FOR SEQ ID NO: 6:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 10 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:	
TGGATTGGTC	10
(2) INFORMATION FOR SEQ ID NO: 7:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 10 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:	
CTTTCTACCC	10
(2) INFORMATION FOR SEQ ID NO: 8:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 10 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:	
GGAACCAATC	10
(2) INFORMATION FOR SEQ ID NO: 9:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 10 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	

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(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:	
TGGTAAAGGG	10
(2) INFORMATION FOR SEQ ID NO: 10:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 10 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:	
TCGGTCATAG	10
(2) INFORMATION FOR SEQ ID NO: 11:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 10 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:	
CTGCTTGATG	10
(2) INFORMATION FOR SEQ ID NO: 12:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 10 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:	

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GATCAAGTCC	10
(2) INFORMATION FOR SEQ ID NO: 13:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 10 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:	
GATCCAGTAC	10
(2) INFORMATION FOR SEQ ID NO: 14:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 10 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:	
GATCACGTAC	10
(2) INFORMATION FOR SEQ ID NO: 15:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 10 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:	
GATCTGACAC	10
(2) INFORMATION FOR SEQ ID NO: 16:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 10 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	

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(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(v) FRAGMENT TYPE: <Unknown>
(vi) ORIGINAL SOURCE:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
TTAGCACCTC 10

(2) INFORMATION FOR SEQ ID NO: 17:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(v) FRAGMENT TYPE: <Unknown>
(vi) ORIGINAL SOURCE:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
ACCTGCATGC 10

(2) INFORMATION FOR SEQ ID NO: 18:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(v) FRAGMENT TYPE: <Unknown>
(vi) ORIGINAL SOURCE:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:
GCTATACTGC 10

(2) INFORMATION FOR SEQ ID NO: 19:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(v) FRAGMENT TYPE: <Unknown>
(vi) ORIGINAL SOURCE:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:	
AGTTGCCAGG	10
(2) INFORMATION FOR SEQ ID NO: 20:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 10 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:	
AAGCCGTGTC	10
(2) INFORMATION FOR SEQ ID NO: 21:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 10 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:	
TCAACGCTCA	10
(2) INFORMATION FOR SEQ ID NO: 22:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 10 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:	
TGTTCGAATC	10
(2) INFORMATION FOR SEQ ID NO: 23:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 10 base pairs	

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(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:	
CGAGTCAGAC	10
(2) INFORMATION FOR SEQ ID NO: 24:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:	
TATGAGTCCG	10
(2) INFORMATION FOR SEQ ID NO: 25:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:	
GTGTTTCATT AGTCCCCAC CTTGAC	26
(2) INFORMATION FOR SEQ ID NO: 26:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	

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(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:	
AGAGCAAGAA TAAGTCAGAA GCCG	24
(2) INFORMATION FOR SEQ ID NO: 27:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 23 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:	
ACAGACCGTG CTTCCACCTC GTC	23
(2) INFORMATION FOR SEQ ID NO: 28:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 23 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:	
CCTCATCTCC TGGGTCCCTT TCA	23
(2) INFORMATION FOR SEQ ID NO: 29:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 20 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:	
GTCCGCGCCA TGGCCATATA	20
(2) INFORMATION FOR SEQ ID NO: 30:	

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

ATGGGAGGCT GCCAGTCCTA ACCC	24
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(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

AATTTTTTTTTT TTCGACGGCC CAACGGAATT TTTTTTTTCG ACGGCCCAAC GGAATTTTTTTT	60
TTTTTCGACGG CCCAACGGGA ATTCGGCTTA GCTAAGGTCA CCCAGACTTC ATGGACTTGT	120
CTATTTTCTT GCCCAAAGGG ATAGTTCCTC AGGTATTTGG GGACAGCATT CACCTCTTGC	180
AGGAGCTATG CCTGTGTGTT TGTGCTAAGT TGATACTTTC TGCGATGATC TCAC	234

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 266 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

TACCATCGGA GAAAGAAGAC CAAGCAAGGC TCAGGCAGCC ACCGCCTGCT TCGCACTGAG	60
CCTCCTGACT CAGACTCAGA GTCCAGCACA GACGAAGAGG AATTGGAGA ATTGGAAATC	120
GCTCTCGTTT TGTCAAGGGA GACTATCCCG ATGCTGCAAG ATCTGCTGTC CCTCTGGCCT	180
TTGTCATCCT CGCGCCTGCG TTGTGGCCTC TGTGGGCTTG GTGTGGAGCA AATGGCTCTC	240

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AAGGAGGACT GAGTCTCAAG GAAATT		266
(2) INFORMATION FOR SEQ ID NO: 33:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 300 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:		
AGCTAAGGTC AGGAGGTGTC TGAAGAATTG GCTGATGCAT GGCAGGGATG TTGTTGACCT	60	
GCTTTTAGAA CAATACTTCC ATTTAATTAT AGCATATCTT ATGTGTGTAT TAAAGCAGAG	120	
CCGATCTGGT GGGGCTCATT AAGTAAATGT ACTTACTGCA AAAGGTTCAA CTGGTGACCC	180	
CAGTTTTCCC CAGAAGCAAT ATGATAGGAC AGAGGCGACT CCTGCAAGTT GTCTCAGACT	240	
TCACACATAC ATTGTGACAT TCTCTGAGCA TGTGCACTGT ACATGATATG ACACTATCAA	300	
(2) INFORMATION FOR SEQ ID NO: 34:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 312 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:		
AGCTAAGGTC CACTACCTTG TGAAGATGTA TAAACACCTG AAATGTAGAA GCGATCCGTA	60	
TGTCAAGATC GAGGGGAAGG ACGCTGACGA CTGGCTGTGT GTGGACTTTG GGAGTATGGT	120	
GATCCATTTG ATGCTTCCAG AAACCAGAGA AACCTATGAA TTAGAGAAAC TATGGACTCT	180	
ACGTTCTTTT GATGACCTTA GCTAAGCCGA ATCAGCACAC TGGCGGCGTT ACTAGTGGAT	240	
CGAGCTCGTA CAGCTGATGC ATAGCTTGAG TATCTATAGG TTAATAATAG CTGGCTATCA	300	
TGTCAAGCGT TC	312	
(2) INFORMATION FOR SEQ ID NO: 35:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 281 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		

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(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:		
AGCTAAGGTC AAAATAAAAG CTCAAGATGA CATCAGTCCC ATTTGTCCTA AGTCCTGGTG	60	
TTGTATGGAT GGTAAGCAGC AGCCAATTAT GGTGACAGGT GATAGATCCA ATTTGTTAAC	120	
ATTTCTCCAT CTCTAAGCCA TCCTTAAAGA AAATCATGAA TGGAGTCACA CCATCTTCAC	180	
GGTAGTCCAG GAGAGCAACC ATACCATCTG GATTCATGTT TCACCAATAA AAACGGTAG	240	
TTATTGAATT AGCAAGGATG TGCTACTCTC TGCAGCTCAG C	281	
(2) INFORMATION FOR SEQ ID NO: 36:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 240 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:		
AGCTAAGGTC TCATGCAATG GAACTTAATT CTTAGAACTG TAAGAATTAC ATCAAACATA	60	
AAAGCCTCCC TATTAATGTA GTCCACAAAA CTGGCAGGTA TATATGCCTT CTGAATTTGT	120	
CTCCAGTGAC TTTGGTAAAT CTAATAAAT TTTTAAAAAT TCTTAATGAA TTTATCGTCA	180	
ACAACAACCA CCTCTTGGA AATTAACCCCT TGCAGTGTCT GTGTTAGACT CAGAAGTCAA	240	
(2) INFORMATION FOR SEQ ID NO: 37:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 203 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:		
GAATTCGGCT TAGCTAAGGT CAGCGTGAAG TTTAAGCAGA CATGAGTCTG AAACAGTCTC	60	
ATGACACATC TGATAGGATT TTTTAAGACT GCCTGGCTTA GTCTTACTGC TGTTAGTGTA	120	
TATTAGGTGT TGTACACATT ATAAAGAAAA TTATGTCTCA TTATCTTGTT TAAGTCAAGG	180	
AAAATAGAGA ACTTTGGTCA AAT	203	
(2) INFORMATION FOR SEQ ID NO: 38:		

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(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 194 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:		
GAATTCGGCT TAGCTAAGGT CAGCGTGAAG TTTAAGCAGA CATGAGTCTG AAACAGTCTC	60	
ATGACACATC TGATAGGATT TTTTAAGACT GCCTGGCTTA GTCTTACTGC TGTTAGTGTA	120	
TATTAGGTGT TGTACACATT ATAAAGAAAA TTATGTCTCA TTATCTTGTT TAAGTCAAGG	180	
AAAATAGAGA ACTT	194	
(2) INFORMATION FOR SEQ ID NO: 39:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 230 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:		
GAATTCGGCT TAGCTAAGGT CAAAATACAC GGATTGCAAT CACTTTTCTA AACAAAAGAA	60	
ACAAAGTAAC TGCTGAGGTT AGCAAAGATG AGTTCTCGTC ATACTGCCTT GTACTGTTTT	120	
GTGAACTGTG TTATTAAAAA TCTGAGCTTA ACAAATCTT TACAAGTCAC CTCATGAAAA	180	
CAGCATTTGG CCAATAAGAG TTTAATTCCA CACCAGTGAG ACCTTAGCCT	230	
(2) INFORMATION FOR SEQ ID NO: 40:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 242 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:		
GAATTCGGCT TTCTGCGATC CACTCTTTGA AGCTATTGGC AAGATATTCA GCAACATCCG	60	
CATCAGCACG CAGAAAGAGA TATGAGGGAC ATTTCAAGGA TGAAAGGTTT TTTTCCCCC	120	

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TTACTATTTTC CTTGGTGCCA ATTCCAAGTT GCTCTCGCAG CAGCAAATTT ATGAATGGTT 180
TGTCTTGATC AAGAACAAAG AATTCATTCC CACCATTCTC ATATATACTA CTTTCTCTTC 240
TT 242

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: <Unknown>
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GAATTCGGCT TTCTGCGATC CACTCTTTGA AGCTATTGGC AAGATATTCA GCAACATCCG 60
CATCAGCAGC CAGAAAGAGA TATGAGGGAC ATTTCAAGGA TGAAAGGTTT TTTTCCCCC 120
TTACTATTTTC CTTGGTGCCA ATTCCAAGTT GCTCTCGCAG CAGCAAATTT ATGAATGGTT 180
TGTCTTGATC AAGAACAAAG AATTCATTCC ACCATTCTCA TATATCTACG TCTCTTCTAG 240

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 154 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: <Unknown>
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

GAATTCGGCT TTCTGCGATC CTAGAGCAGG TAAGTGAAGA AGGCCAGTAA GTTTTAAGGA 60
TGGCCTTGTT GCCTTCTATC AAGTTCTCTG GGACTTTGTA ATTTTGATTA CTACTATTGA 120
TACATGGTTA TGGTCAGAAG GCCTCTTCTC CCTT 154

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: <Unknown>

-continued

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

AGCTAAGGTC CGGACTCTAT GGCATGACCC CAAAAACATT GGCTGGAAAG ATTACACTGC 60
CTACAGGTGG CACCTGATTC ACAGGCCTAA GACAGGCTAC ATGAGAGTCT TAGTG CATGA 120
AGGAAAGCAA GTCATGGCTG ACTCAGGACC AATTTATGAC CAAACCTACG CTGGTGGACG 180
GCTGGGCTGT TTGTCTTCTC CAAGAGATGG TCTATTCTCG GACCTCAAGT ATGAGTGCAG 240
AGATGCTAGA GAGCAGGCTC AGTCTCAGCA 270

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 285 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

TGACCATCGA GTGCATCAGC CTCATCGGGC TGGCCGTCGG GAAGGAGAAA TTCATGCAGG 60
ATGCTTCAGA TGTGATGCAG CTATTGTTGA AGACACAGAC AGACTTCAAT GATATGGAAG 120
ATGACGACCC CCAGATTTCT TACATGATCT CAGCATGGGC CAGGATGTGC AAAATCTTGG 180
GAAAGAATTC CAGCAGTACC TTCCCGTGGT TATGGGGCCG CTGATGAAGA CTGCTTCAAT 240
TAAGTCCTGA GTGCCTCTAG ACACCAGGAC ATGAGATATG AGGTA 285

(2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 260 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

TGACCATCGT GTAGTTGGTG TGCTTGTTGT CGAAGATGAG GGCCTCCTGG ATGAGCTGGT 60
GCTGCTGCTC CAGCAGGTCC AGGCTGGGCT TGTAGTCCAC GATGCTGCGC TCGTACTGCT 120
TCAGGTGGCT CAGCTGGTCT TCCAGAGTCC CGTTCATCTC AATGGAGATG CGCCCGATCT 180
CCTCCATCTT AGTCTGGATC CACGGCCCCA CCATATTGGC TTGGCTGGCG AACTGTCCGC 240
GAAGGCTGCA TTGGATTGCT 260

(2) INFORMATION FOR SEQ ID NO: 46:

-continued

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 283 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

TGACCATCGA ACACCCCAAC ACTCTCCACT ACCTGCCATT TCTTCCAGCC TTATCCACAC	60
CACCCCGTTT CTCCTGAAGA CTGATTGCT TAGCAACTGC ACTGAGCCAA CCCTGAAGAC	120
ACATGATTAT TGGTTGGGCT CCATTAAACA ACAAGCCTAG TGCTTGGGAA GGGGGGTGGG	180
GAGGGGAAGA GACGTGAGAA GCATGTTGGC GTAGACCTTG AGGCATGGAT GAAGCATCTG	240
CCGGCCTGAC CTGGTACAGG TGGCATCTGC ACTGCAGCAA GGC	283

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 277 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

TGACCATCGA AGTGCAAAGG AAATGACTTG ATTTTCATGAA GTATCTCCAG AAGTAACGCT	60
TTGTTTTCTG CATCCTGAAC TTTATTCCCA GTGAAGAGCT GAAAATCTGG ACGCTCAAAA	120
AATGGAAGCA CTTTGGAGAG AGCCCTTAAC TCTATCAGGT ACAGGAAGTA CAAGTTCCTC	180
AGCCTTCGTG GGCCTTCTCC TTCAGTCAGA ATCCATCAAA GGTGCTGGAA CTCTGTGACA	240
TTGTGACCCA TTCTTTCAGC CAGTATCTGT AAGATAC	277

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 215 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

-continued

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:		
GGGAACGAAT GATCTGGAAC TGTGGCTTGT AGACAACCCA AATATCTTAG GTAGGTAAGA	60	
AATTCCAGCA TCACACTATA TAGGAAATAC TGTGCGAAAC TGACAGTTAA CTGTGCACAA	120	
AGTTCAATGG CTTCAAAATA ATGTATAAAG GATAAGAAGA AACCAGTTTA CCATTTTGGT	180	
ATTATTTTGG TTGCTTTGTA TAACTTCAAT AATTT	215	
(2) INFORMATION FOR SEQ ID NO: 49:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 215 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:		
GGGAACGAAT GATCTGGAAC TGTGGCTTGT AGACAACCCA AATATCTTAG GTAGGTAAGA	60	
AATTCCAGCA TCACACTATA TAGGAAATAC TGTGCGAAAC TGACAGTTAA CTGTGCACAA	120	
AGTTCAATGG CTTCAAAATA ATGTATAAAG GATAAGAAGA AACCAGTTTA CCATTTTGGT	180	
ATTATTTTGG TTGCTTTGTA TAACTTCAAT AATTT	215	
(2) INFORMATION FOR SEQ ID NO: 50:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 10 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:		
GACGTAAGCC	10	
(2) INFORMATION FOR SEQ ID NO: 51:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 189 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		

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(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:	
CCACAAAGCA AGCTTCTGTC TGGAGTACAG CTCCTGTGAC TATGGGTACC ACAGGGCCTT	60
TGCGTGCACT GCACACACAC AGGGATTGAG TCCTGGATGT TATGACACCT ATGCGGCAGA	120
CATAGACTGC CAGTGGATTG ATATTACAGA TGTACAACCT GGAAACTACA TTCTAAAGGT	180
CAGTGTA	189
(2) INFORMATION FOR SEQ ID NO: 52:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 227 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:	
CTATCAATGA AGGGGAGAT CACTGGGTAA GTTCGAATGC CCTCAGGCAA GGTGGCCCAG	60
CCTTCCATTA CTGAATTCAA AGATGGCACT GTTACTGTAC GTTACTCACC CAGTGAAGCT	120
GGCCTGCATG AAATGGACAT TCGCTATGAC AATATGCATA TCCCAGGAAG CCCTCTGCAG	180
TTCTATGTTG ATTATGTCAA CTGTGGCCAC ATCACTGCTT ATGGTCC	227
(2) INFORMATION FOR SEQ ID NO: 53:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 373 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:	
TTAGCACCTC GACCACGAAA TGAGGAAGAT GCAACAGACG TGGTGGGCCT GGCTCAGGCT	60
GTAAACGCTC GGTCCCCACC TTCAGTAAAA CAGAACAGCT TGGATGAAGA CCTTATTCGG	120
AAGCTAGCTT ATGTTGCTGC TGGGGACCTG GCACCCATAA ATGCTTTCAT TGGGGGCCTT	180
GCTGCCCAGG AAGTCATGAA GGCCTGCTCT GGAAAGTTTA TGCCCATCAT GCAGTGGTTG	240
TACTTTGATG CTCTTGAATG TCTCCCAGAA CGGACAAAGA GGCTCTGACA GAGGAGAGTG	300
CCTCCCACGT CAGAACCGTT ACGATGGGCA GGTAGCTGTA TTGGTCAGAC TTCAGGAGAA	360
GCTGAGAAGC AAA	373
(2) INFORMATION FOR SEQ ID NO: 54:	

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(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 257 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:		
TTAGCACCTC CAATGGCTGG GTACCAGCCA GCCGCAATGT CCGCTCCACA AATTTGGAGT	60	
CTGTGAGGTA CTGATTAACA TTTTCTGCTG GCTGCTTGAA AAGGCCTTCA AATTCATCCC	120	
GGGCCCCACTG AAGAGTGTGT TCGATGGCAT TGGGAAAGTT TTTCAGGGTA CAAATGGGGA	180	
TGGATTTCTC TGGTGGATCC TGGCTAGACG TGATGGATTC TGTCAGGAAG GGGATTACCA	240	
CCTGCACGTT GCCCTTT	257	
(2) INFORMATION FOR SEQ ID NO: 55:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 298 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:		
TTAGCACCTC AACTCACAT GCCCTTCTAC ATAGAGACTG GTTAAACAGC CCTCCCTCCC	60	
TTGTCCCGAC TTGACTTCCA GGCCCTCTG CTTTCCTCTC ACAACCACAC CAGGTCTGAT	120	
GGAGTCCAGT GCCTGCAGTG ACCCAACATA GACTGCACTT TCACCTACCT ACTGGATGGT	180	
CCTGCAGCCC AGACGGCTGC TCTTCTTTCT CATGGAGTTT CTCTCCTGCC TGAGATATGC	240	
TATCTGGTCT GCCCTGTGT AGCTCCCATG GGATCCCTTA AAATCGATCC TTTTTTAA	298	
(2) INFORMATION FOR SEQ ID NO: 56:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 337 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:		

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TTAGCACCTC	GTGAGGAGAC	TGTTGTCCAC	AGGCCAGCTA	GTGGTACCCT	ACTGAGAAGT	60
TGGGTTTTTG	TTTTGTTTCC	CTTGAAGGGT	CGCTGTTAGA	GGATGGAAGT	AACTTCTAAT	120
TCTTGATCTG	TTTGTGGTTC	TTGTTTTTCT	TACTTTTTTGC	CAGTTGTATA	CACTTGGAGA	180
GGGAATTTGT	ATGCCTGTAA	TCTTGTTCCT	GAGGTCAGAA	ATTCAAAACA	TTGGGAGCTT	240
TTGTTGTAAA	GGTTAAACTG	TGAATCCATA	TAGCAAATGC	AGATCCTTTT	ACAGTGTAAT	300
CCACATTTCC	TGCCTCAGCC	TAAAGCACTG	GTCATTTT			337

(2) INFORMATION FOR SEQ ID NO: 57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: <Unknown>
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

ACCTGCATGC	CTAAAGGAGT	AGGCTTAGGG	GTGGGGAGAG	AGAAGGCATA	GGCTTTTCTA	60
GTTATACAAA	GCTGTGTAAG	GCAAGGTTCC	TTTCTACTAA	ATGGTCAGCT	GTCACTACAT	120
TTATACTTTT	GTATGTCATA	AACCCTTTCT	TTCATTCTCT	CCTGGGTAAC	CAGGACAATC	180
GGAGGGCAGT	GTGTTACTGG	GATTAGAGGA	CTAGCAATAC	TGGGTAACCC	GCCTAAGCTG	240
GAAGGTGACG	TAATACGTTT	CTTTAAAGAT	TCAGTCAGTC	AAGCAGTTTA	GCAATATCAA	300
AATGTCTGGC	TGTTTGGTCC	AGTGTAACAT	GTT			333

(2) INFORMATION FOR SEQ ID NO: 58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 296 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: <Unknown>
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

GCTATCTGCG	AACTACAGA	AAGGAAGACA	GCTTGCCCCA	GCGCGGTGAA	GTTCAGAATT	60
CACTAGGTAG	TTGTTGTTGG	TTGACTTGGA	GGTAGCTGGG	TAATCAACAG	CTTTCACTTT	120
AGATTCAATG	TGAACCGCAG	AGTTACTCAT	GACCAAGAGT	CTGGCAAAC	CATTAATGCT	180
GTTTAATACT	TGTTTGATAT	TTTTTCACCT	TTTGAGCCCT	TTTCCCAAAG	AATTCAATAT	240
CAGTTTAGTA	GCAACAGTAC	AGTTGCCATT	TAAATTGGTT	TAGTTGCAGT	ATAGCA	296

(2) INFORMATION FOR SEQ ID NO: 59:

-continued

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 296 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GCTATCTGCG AACTACAGA AAGGAAGACA GCTTGGCCCA GCGCGGTGAA GTTCAGAATT	60
CACTAGGTAG TTGTTGTTGG TTGACTTGGA GGTAGCTGGG TAATCAACAG CTTTCACTTT	120
AGATTCAATG TGAACCGCAG AGTTACTCAT GACCAAGAGT CTGGCAAACCT CATTAATGCT	180
GTTTAATACT TGTTTGATAT TTTTTCACCT TTTGAGCCCT TTTCCCAAAG AATTCAATAT	240
CAGTTTAGTA GCAACAGTAC AGTTGCCATT TAAATTGGTT TAGTTGCAGT ATAGCA	296

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 273 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

GCTATACTGC AACTAAACCA ATTTAAATGG CAACTGTACT GTTGCTACTA AACTGATATT	60
GAATTCCTTTG GGAAAAGGGC TCAAAAGGTG AAAAAATATC AAACAAGTAT TAAACAGCAT	120
TAATGAGTTT GCCAGACTCT TGGTCATGAG TAACTCTGCG GTTCACATTG AATCTAAAGT	180
GAAAGCTGTT GATTACCCAG CTACCTCCAA GTCAACCAAC AACAACTACC TAGTGAATTC	240
TGAACTTCAC CGCGCTGGGC CAAGCTGTCT TCC	273

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

-continued

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:		
GCTATACTGC CCACCACATT GCCACACTCG GAATGACATT TCTATATTTT CACCTCCCCA	60	
GATTTCCATT TCTTCATCGT AACTTCCAAT GTGCTCAAAA TATTTTTTTAG ATATAGAAAA	120	
AAGGCCTCCT GCAAAGGTGG GGGTCTTAAT TGGGTAGGTT TCATCTTTCC TTCTTTGCTT	180	
CTCATGATCA GGAAGTGACT CCCAGCCAAA GGAAAGGCTC CAGTCAAAAT TTCCACGGTT	240	
ATGGTTGCTT CCGTACGGAG AAGGCTTGTT GAATTCAAAT GTGTTTAGAT CTATGGATGC	300	
GATGTCTGGA CTCACCACGG CA	322	
(2) INFORMATION FOR SEQ ID NO: 62:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 262 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:		
GCTATACTGC TGAAGGAGAT CATTTTGGTG GATGATGCTA GTGTAGACGA CTACCTGCAT	60	
GAAAAGCTGG AGGAATACAT AAAACAGTTT TCTATTGTGA AAATAGTCAG GCAGCAAGAA	120	
AGGAAAGGCC TGATCACCGC GCGGTTGCTA GGGGCAGCTG TAGCAACTGC CGAGACGCTC	180	
ACGTTCTTAG ATGCTCACTG TGAGTGCTTC TATGGCTGGC TGGAACCTCT GCTGGCCAGG	240	
ATAGCTGAGA ACTACACTGC CG	262	
(2) INFORMATION FOR SEQ ID NO: 63:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 295 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:		
AGTTGCCAGG GGGCAGCTCA CGGCGCAGCT CATCCTCTGT GATGTAATTC TTATCTCCAG	60	
CCAGGATCTT GAAGGAAGCC ATGACCTGAT CTGCAGTATC AGTATCTGCC GTCTCTCGGG	120	
ACATAAAGTC GATGAAGGCC TGGAACGTCA CTACCCCCAA GCGGTTGGGG TCTACAATGC	180	
TCATGATTCG GGCAAACCTCT GCCTCTCCCA TGTTGTAACC CATGGAGATA AGGCAGGCGC	240	
GGAAATCGTC TGTGTCCATC ATGCCCGTCT TCTTCCGGTC AAAGTGGTTG AAAGA	295	
(2) INFORMATION FOR SEQ ID NO: 64:		

-continued

(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 287 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:		
AAGCCGTGTC GCTGAACTGG GAGGACACAC TGCTCACCTT AGAAGGCTCT GGCTGACCCT	60	
CCGCCCCGGTT AAACAGGGAC TTTGTGGCCA TGTGCTGGCG ACACAGGTCC TGGTACTCAA	120	
AAGTAGTGTC ACCATGGGCC CCCTCCGGCC CCAGCGCTGC CAGGCGTCCT TATCCCGCTG	180	
TCTCGAATGA TGGCGCATAC CAAGGCCACT GAAAGCCACT AGCAGCCCAG CGACGCCTGC	240	
CAGGGCCACT AGAGTAAGCA GCACTGAGCG CATGGGAGAT ATGCCAT	287	
(2) INFORMATION FOR SEQ ID NO: 65:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 332 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:		
AAGCCGTGTC TGGACGTCCG TGTGTCCGGC TCTTGCTCAC GCAGTCATGG CCTCCGGAAC	60	
GCGCAAATCG GAAAGTCGGC TCCTGACTTC ACGGCCACAG CGGTGGTGGA TGGTGCCTTC	120	
AAGGAAATCA AGCTTTCGGA CTACAGAGGG AAGTACGTTG TCCTCTTTTT CTACCCACTG	180	
GACTTCACTT TTGTTTGCCC CACGGAGATC ATCGCTTTTA GCGACCATGC TGAGGACTTC	240	
CGAAAGCTAG GCTGCGAGGT GCTGGGAGTG TCTGTGGACT CTCAGTTCAC CCACCTGGCG	300	
TGGATCAATA CCCACGGAA AGAGGGAGGC TT	332	
(2) INFORMATION FOR SEQ ID NO: 66:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 331 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		

-continued

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

AAGCCGTGTC	GGAGGGCACC	AAGGCTGTCA	CCAAGTACAC	CAGCTCCAAG	TGAGTGCTCA	60
AGACTCAGCT	CTTAACCCAA	AGGCTCTTTT	CAGAGCCACT	CAAGACTTCA	AAATTGGAGC	120
TTTAATGCTG	ACTTAGTGAC	TACCGGGAAA	ATAACTGACT	TCATCTGCAG	GATTGTGTAC	180
AAACACTTAT	GGTTTAGTAA	ATCGAAAAGA	TAGACATTGC	CCATCAGTTC	TGTCTGGTCC	240
ACTTAAATAT	GCTTTTTTCT	TAGAAGTTCT	AAGAACCCTG	TCAATAACCT	ATCTAGGTCC	300
AGTCCTTGAG	TTCAAAGGCC	AAATACCAAT	G			331

(2) INFORMATION FOR SEQ ID NO: 67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 359 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

CAACGCTCAG	GATGTAAGCT	GTTTCCAGCA	CCTGGTTCAA	GCGAATGTAA	GAAATAAGAA	60
GGTGTTGAAA	GATGCCGTGA	ATAACATTAC	AGCAAAGGGG	ATCACAGATT	ACAAGAAAGG	120
CTTTAGCTTT	GCCTTCGAAC	AGCTACTTAA	TTATAATGTT	TCCAGAGCTA	ATTGCAATAA	180
GATTATCATG	TTATTCACGG	ATGGAGGAGA	AGAGAGAGCC	CAGGAGATAT	TTGCCAAATA	240
CAATAAAGAC	AAAAAAGTCC	GTGTGTTTAC	ATTTTCCGTC	GGTCAACATA	ATTATGACAG	300
AGGACCTATT	CAGTGGATGG	CTTGTGAAAT	AAAGGTTACT	ATTATGAGAT	TCCTCCATT	359

(2) INFORMATION FOR SEQ ID NO: 68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 317 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

TCAACGCTCA	TCACACCAAG	AATCAACTGG	TTCTTCAAGT	TTGTCTTATT	TTCAGATTGG	60
CCAGTGACGT	TGAAGACTGG	TAGAGTTCCA	GTAATGACAA	GTCCCAGTTC	CAGGGCATCC	120
AAATACACAT	TTGTCCATTG	AACTTGCTTC	GCTTTGTCAC	CAGCTAAAAC	CATTGGTCTT	180
CCCAGAACAT	CTAGATATTC	CTGAGTATTG	ATTCTTATTG	CACCAATGGA	GGGAATCTCA	240
TAATAGTAAC	CTTTATTTTC	ACAAGCCATC	CACTGAATAG	GTCTCTGTCA	TAATTATGTT	300

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GACCGACGGA AATGTAA		317
(2) INFORMATION FOR SEQ ID NO: 69:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 317 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:		
TAACGCTCAG GAGAAGAATA GGAATGCAGA GAACTCTGCC ACAGCCCCCA CGCTCCCGGG	60	
CAGCACCTCA GCCACCACCG CAACCACCAC CCCTGCTGTA GATGAAAGCA AGCCTTGGAA	120	
CCAGTATCGC TTGCCTAAGA CTCTTATACC TGA CTCTAC CGGGTGATCT TGAGACCCTA	180	
CCTCACCCCC AACAATCAGG GCCTGTACAT CTTCCAAGGC AACAGTACTG TTCGCTTTAC	240	
CTGCAACCAG ACCACGGATG TCATTATCAT CCACAGCAAA AAGCTCAACT ACACCCCTCAA	300	
AGGAAACCAC AGGGTGG	317	

(2) INFORMATION FOR SEQ ID NO: 70:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 287 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:		
CGAGTCAGAC GGCTTCAGCA TCGAGACCTG TAAGATCATG GTGGACATGC TGGATGAAGA	60	
TGGGAGTGGC AAGCTTGGCC TGAAGGAGTT CTACATCCTC TGGACGAAGA TTCAGAAATA	120	
CCAAAAAATC TACCGGGAAA TCGATGTGGA CAGGTCTGGA ACTATGAATT CCTACGAGAT	180	
GCGGAAAGCA CTGGAAGAAG CAGGTTTCAA GCTGCCCTGT CAACTCCATC AAGTCATCGT	240	
TGCCCCGTTT GCAGACGACG AGCTAATCAT CGACTTTGAC AATTTTG	287	

(2) INFORMATION FOR SEQ ID NO: 71:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 311 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		

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(iv)	ANTI-SENSE:	NO	
(v)	FRAGMENT TYPE:	<Unknown>	
(vi)	ORIGINAL SOURCE:		
(xi)	SEQUENCE DESCRIPTION:	SEQ ID NO: 71:	
	CGAGTCAGAC AACCTGTTCA AGTGGGGTGG GGACCATCCA CGGAGCAGCC GGCACCGTAT	60	
	ATGAAGACCT GAGGTACAAA CTCTCCCTAG AGTTCCCCAG CGGCTACCCT TACAACGCAC	120	
	CCACAGTGAA GTTCCTCACA CCCTGCTACC ACCCCAACGT GGACACCCAG GGCAACATCT	180	
	GCCTGGACAT CCTCAAGGAT AAGTGGTCTG CACTATATGA TGTCAGGACT ATCTTGCTCT	240	
	CTATCCAGAG CCTGCTAGGA GAACCCAACA TCGATAGCCT TTGAACACAC ACGCTGCGGA	300	
	ACTCTGGAAA A	311	
(2)	INFORMATION FOR SEQ ID NO: 72:		
(i)	SEQUENCE CHARACTERISTICS:		
	(A) LENGTH:	352 base pairs	
	(B) TYPE:	nucleic acid	
	(C) STRANDEDNESS:	single	
	(D) TOPOLOGY:	linear	
(ii)	MOLECULE TYPE:	cDNA	
(iii)	HYPOTHETICAL:	NO	
(iv)	ANTI-SENSE:	NO	
(v)	FRAGMENT TYPE:	<Unknown>	
(vi)	ORIGINAL SOURCE:		
(xi)	SEQUENCE DESCRIPTION:	SEQ ID NO: 72:	
	TATGAGTCCG GAGCGACGGC TACGAGTGTG AACTGTTCCA GCCCCGAGCG ACACACCAGA	60	
	AGTTATGACT ACATGGAAGG AGGGGATATA AGGGTGAGAA GACTGTTCTG TCGCACCCAG	120	
	TGGTACCTGA GGATTGACAA ACGAGGCAAA GTGAAAGGGA CCCAGGAGAT GAAGAACAGC	180	
	TACAACATCA TGGAAATCAG GACCGTGGCA GTTGAATTG TGGCAATCAA AGGGGTGGAA	240	
	AGTGAATACT ATCTTGCCAT GAACAAGGAA GGGAACTCT ATGCAAAGAA AGAATGCAAT	300	
	GAGGATTGCA ACTTCAAAGA ACTGATTCTG GAAAACCATT ATAACACCTA TG	352	
(2)	INFORMATION FOR SEQ ID NO: 73:		
(i)	SEQUENCE CHARACTERISTICS:		
	(A) LENGTH:	317 base pairs	
	(B) TYPE:	nucleic acid	
	(C) STRANDEDNESS:	single	
	(D) TOPOLOGY:	linear	
(ii)	MOLECULE TYPE:	cDNA	
(iii)	HYPOTHETICAL:	NO	
(iv)	ANTI-SENSE:	NO	
(v)	FRAGMENT TYPE:	<Unknown>	
(vi)	ORIGINAL SOURCE:		
(xi)	SEQUENCE DESCRIPTION:	SEQ ID NO: 73:	
	TATGAGTCCG AGGAGGAGCA CAATGCTGGG AGTGTGGAAA GCCAGGTTGT CCCCAGCACA	60	
	CACCGAGTGA CCGATTCCAA GTTCCATCCA CTCCATGCCA AGATGGATGT CATCAAAAAA	120	
	GGCCACGCCA GGGACAGCCA GCGCTACAAA GTTGACTATG AGTCTCAAAG CACAGACACC	180	

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CAGAACTTCT CCTCCGAGTC TAAGCGGGAG ACAGAATACG GTCCCTGCCG CAGAGAAATG 240
GAGGACACAC TGAATCATCT GAAGTTCCTC AATGTGCTGA GTCCAGAGTC TCACATCCAA 300
ACTGTGACAA GAAGGGG 317

(2) INFORMATION FOR SEQ ID NO: 74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 247 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: <Unknown>
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

TCGCCCCGGA CTTTCATGCGA TTGAGAAGAT TGTCTACCAA ATATAGAACA GAAAAGATTT 60
ATCCCACAGC CACTGGAGAA AAAGAAGAAA ATGTTAAAAA GAACAGATAT AAGGACATAC 120
TGCCATTTGA TCACAGCCGA GTTAAGTTGA CTTTGAAGAC TCCATCCCAA GATTCAGATT 180
ATATCAATGC AAATTTTATT AAGGGTGTGT ATGGGCCAAA AGCATATGTG GCAACCCAAG 240
GGCCTTT 247

(2) INFORMATION FOR SEQ ID NO: 75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 256 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: <Unknown>
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

TGTGGAAAGC CAGGTTGTCC CCAGCACACA CCGAGTGACC GATTCCAAGT TCCATCCACT 60
CCATGCCAAG ATGGATGTCA TCAAAAAAGG CCACGCCAGG GACAGCCAGC GCTACAAAGT 120
TGA CTATGAG TCTCAAAGCA CAGACACCCA GAACTTCTCC TCCGAGTCTA AGCGGGAGAC 180
AGAATACGGT CCCTGCCGCA GAGAAATGGA GGACACACTG AATCATCTGA AGTTCCTCAA 240
TGTGCTGAGT CCAGAG 256

(2) INFORMATION FOR SEQ ID NO: 76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

-continued

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

TGACCATCGA AGTGCAAAGG AAATGACTTG ATTTTCATGAA GTATCTCCAG AAGTAACGCT	60
TTGTTTTCTG CATCCTGAAC TTTATTCCCA GTGAAGAGCT GAAAATCTGG ACGCTCAAAA	120
AATGGAAGCA CTTTGGAGAG AGCCCTTAAC TCTATCAGGT ACAGGAAGTA CAAGTTCCTC	180
AGCCTTCGTG GGCCTTCTCC TTCAGTCAGA ATCCCATCAA AGCGCTGCTG GAACTCTGTG	240
ACATTGTGAC CCCATTTCTT TTCCAGCCAA GTATCTTGTA AAAGATACCT TGCACTCAAA	300
TGCACATTAA TGCTTGCGTG CAGGCCAGAT ATAAGTCTGT AGAATCGCTC TTTCTACACA	360
GAGGCCTTCT AGCCAGTTGT AAA	383

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

CTGCTTGATG CTAAGCCCGG CAGCCTGTGT TTCATCTACA GGATGCACAA CATAAAAGAA	60
AAGATCTGAT TCCCGCAGGT TCTCTTCTGA CCTACACACA CACACACTAA AATAACATTT	120
AAAAATATGT GCCAAATTAT ATTTGTTCCG GTGCCACCTT CCACCAGCTT ACCACTACGG	180
TAGAACTGTC AAATTCATCT CCCTGAATTT GTCTTAAAGG GGTGTCCATG CACAGGCCCA	240
AGAGTCACCT CCAATGAAAT AAATGTAATA CTGAAGTATG CCATGATGTT TGTGTTTTTC	300
TTTCATCGTA AGCCTGTAAG CAGGAAAAAT AGTAATAGAT AGAATAGAGA CTTACCAGTG	360
GTCGATGGCC TGGTCAGTCT GTGCGGTGAC TAGGACCAGG	400

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 343 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:		
ACCTGCATGC CGAGTGTGAC GCCTTTGAGG AGAAGATCCA GGCTGCCGGA GGGATCGAAC	60	
TCTTTGTCGG AGGCATTGGC CCCGATGGAC ACATTGCCTT CAATGAGCCA GGCTCCAGCC	120	
TGGTGTCCAG GACCCGTGTG AAGACTCTGG TTATGGACAC CATCCTGGCC AACGCTAGGT	180	
TCTTTGATGG TGATCTTGCC AAGGTGCCCCA CCATGGCCCT GACAGTGGGT GTCGGCACTG	240	
TCATGGATGC TAAAGAGGTG ATGATCCTCA TCACAGGCGC TCACAAGGCC TTTGCTCTGT	300	
ACAAAGCCAT CGATGGAGGC GTGAACCACA TGTGGACGGT GTG	343	
(2) INFORMATION FOR SEQ ID NO: 79:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 337 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:		
GCTATACTGC AATGTTAGGG GAATGAACGC GTTTTCCTAC TGCACTGGGG ACTTTTAGAT	60	
AGGTTAATGA AAGGCCTTTT ATTCTGTTAC TGGACACGAA AACTTTGTCT AATTTCCTAT	120	
ACTCTATTGT ACGTTTACAG TCGCAGCACT AAAATGGAAG ACATCAAACA TTTTTAACAG	180	
AAAAAAAAAA AGATGTAAAA ACTAACTAAG GACTATTTAT TGATAATGTT TTGCTACTCC	240	
TGTCAGACAA TGGCTATAAA CTGAATTAGG CAGTCTTAAA AAAAAAAAAA GAAAAAAAAAG	300	
AAAAAAGAAA AAAAGAAAAG AAAAGAAAAA AAACCTGG	337	
(2) INFORMATION FOR SEQ ID NO: 80:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 371 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:		
AGCTAAGGTC GGGTACTCTG ATACTTCAGA GTTTAAAATC ATCAGCCCTT GTAGATCTAT	60	
TCCTAAATCT TATGAAAATG CTCAGATGTT TACACAGCTG TGAAACAGGG TCAGTTCAGA	120	
TCGCTGATGG CTTGAGAATG TGTTTCTTGT TGACATCAGG AACTGGAAAT GTTTACTTCC	180	
CGTCATTTAT GAGTCATCAA GTATCTCGGC TCTTTTAAGA GCGCAAGATA AAACAAGCTT	240	
AAACCAGGTG ATAAGAGCAG AGTCCACTTG AGTCTGAGCT CACCCGAGAA CTTGCTATCG	300	
AGGACATTTG GAATGGGAGT GTGCAGGCTT CCTTCAGTTA CTGAATGAGT CCATCTGCTA	360	

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GTCACCTTGA C 371

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

AGCTAAGGTC CAGGGGGCAA AGCGGTGACG TGTGCACATC GATATGAGAA ACGGCAGCAC	60
GTCAACACGA AGCAGGAGTC GCGGGATATC TTTGGAAGAT GTTATGTCCT AAGTCAGAAT	120
CTCAGAATTG AAGATGATAT GGACGGAGGA GACTGGAGTT TCTGCGATGG CCGGTTGAGA	180
GGCCATGAAA AGTTTGGGCTC CTGTCAGCAA GGAGTAGCGG CTACTTTCAC TAAGGACTTT	240
CATTACATTG TTTTGGAGC CCCAGGGACT TACAACTGGA AAGGGATCGT CGTGTAGAAC	300
AAAAGAATAA CACTTTTTT	319

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 368 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

AAGCCGTGTC TGTGCTCAAG GAAGAAACCC ACTGGACCAA CTTCTGTCAG AAAGGAAAAC	60
CTTGTTCAAA GTTTCAGGAC CCTGTTCTTT GCTTATTTGC ACATGGTCAC CTTGGTCTGA	120
GCTAGCCACC ATTGTCACCC ACAGCTGCAA AGAAAGCAGA CCTTAGGAAA CACTGTCACG	180
GCTGAGTGTG ACTGCCTTGT TCATCCCCTG GACTGGTACT GTGTTGCCTG CAGTACCATT	240
GGGATCCCAT AGCAAGAGAG GGAGAGGGAG ATGTTAGTTA GCCTTTGCTA CGAACCAAGC	300
TGTCCCAAGT CTCAACAGCT AAACAGGTAT TCATTTACCA TGATTCTATG GTTAGCTAAG	360
CTCTTGAG	368

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

-continued

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

CTTTCTACCC TGGAGGATGT GCTTGAGGCA CACTGCTCCT GTGCTCTCCA CTTGAGGCAT	60
AAGCCCAGTC AGTTGTGCAT AGATGATTAA CCTCTGACCC CTAAAGATGG TAAGTTGCTC	120
TGGAGAAAGC ATTTTAAACAG ACAAACCAGG AGGCAAATCC CAACTTAGAG AGATGTTATC	180
CACTGCACAC TGTAGAGCAA ACTTGAGAGA CCCAAGAGCC TTGGTCTGCA TCCTGTCCTT	240
GCCTGTGATA AACACTCGAG TACCCCCTGA TACCGGGCGA TATTTTGTGAT TAACTGGTCG	300
AGGCTCCTTG TCCAATTCCA AAAGAGAACA TCTGTGTTTC	340

(2) INFORMATION FOR SEQ ID NO: 84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 252 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

TGGTAAAGGG CATCTGTAAA TACACTCTAT GAGGAAATTA AAAC TTGAAC ATGGCAGTCT	60
GACATTGCAA AACAAAACAA AACAAAAC TG ACCCTCCAAT AGCAGCGAAA ACAACGTGAA	120
AGATACAAAG CAATGAGAAT CTGGTTCTGA ACGCCTGGGA TCCTGGGAGT CATCGGTAGC	180
AGCGCCATGA GAGGAGCCGT GGCCTGTCCC ATGTGGTCCC ACCTTCACCT CTTCCCTCAC	240
ATCCCTCTTA AG	252

(2) INFORMATION FOR SEQ ID NO: 85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

TGGTAAAGGG GGCAAGGGCA AAGGCACGGG AGACAGAGGC CACTGCATCT GTACCCACAT	60
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CAGACATGTT TGTCCATTTT CTCTCATTTG GCCTTAGACC ATTGGCAAGA GTAAATGCTC	120
TTAGTCCCGT TATCTAGAAA TTTCTTCCTT TGGGGAGAAC CACTTATAGA CAATATCAGC	180
TCTCTACAAA TAACACGAAA GGTCTGTAACA CAGCAAGTGA CCAGAAAGTG CCCGTCCTTG	240
CGGCTCTGAT CCACGTGGCT CTCCGTAGAC AAATTGTTTT TTCTTGTAGG GATATCTGTT	300
TTGCTTCTGA ACTTTCTTAC AAGTGTTTGG GACTCTTCGG GTGGCGTT	348

(2) INFORMATION FOR SEQ ID NO: 86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: <Unknown>
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

TGGTAAAGGG TCAAGTGTTT GATCAGAGTG GAGCTCCATT ACCGAATGTA ATCGTGGAAG	60
TCCAAGACAG AAAGCATATC TGCCCGTTTA GAACCAACAA GCTTGGAGAA TACTATCTGC	120
TTCTGCTGCC CGGGTCCTAC GTGATCAATG TTACAGTCCC TGGACACGAC TCCTACCTCA	180
CGAAGCTTAC TATTCCAGGG AAATCCCAGC CCTTCAGTGC TCTTAAAAAG GATTTTCACC	240
TCCCGCTGCG ATGGCAGCCG GATTCCATCT CCGTATCCAA TCCTTCGTGC CGATGATTCC	300
GCTGTACAAA TTCATGCCAA GCCACTCGGC TGCCACAAAG CCTAGTCTGG G	351

(2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 242 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: <Unknown>
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

GAATTCGGCT TTCTGCGATC CACTCTTTGA AGCTATTGGC AAGATATTCA GCAACATCCG	60
CATCAGCACG CAGAAAGAGA TATGAGGGAC ATTTCAAGGA TGAAAGGTTT TTTTCCCCC	120
TTACTATTTT CTTGGTGCCA ATTCCAAGTT GCTCTCGCAG CAGCAAATTT ATGAATGGTT	180
TGTCTTGATC AAGAACAAAG AATTCATTCC CACCATTCTC ATATATACTA CTTTCTCTTC	240
TT	242

(2) INFORMATION FOR SEQ ID NO: 88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 240 base pairs

-continued

(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:	
GAATTCGGCT TTCTGCGATC CACTCTTTGA AGCTATTGGC AAGATATTCA GCAACATCCG	60
CATCAGCACG CAGAAAGAGA TATGAGGGAC ATTTCAAGGA TGAAAGGTTT TTTTCCCCC	120
TTACTATTTT CTTGGTGCCA ATTCCAAGTT GCTCTCGCAG CAGCAAATTT ATGAATGGTT	180
TGTCTTGATC AAGAACAAAG AATTCATTCC ACCATTCTCA TATATCTACG TCTCTTCTAG	240
(2) INFORMATION FOR SEQ ID NO: 89:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 687 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:	
ACGAGGGGAA ACCTCCTCAG AGCCTGCAGC CAGCCACGCG CCAGCATGTC TGGGGGCAAA	60
TACGTAGACT CCGAGGGACA TCTCTACACT GTTCCCATCC GGGAACAGGG CAACATCTAC	120
AAGCCCAACA ACAAGGCCAT GGCAGACGAG GTGACTGAGA AGCAAGTGTA TGACGCGCAC	180
ACCAAGGAGA TTGACCTGGT CAACCGCGAC CCCAAGCATC TCAACGACGA CGTGGTCAAG	240
ATTGACTTTG AAGATGTGAT TGCAGAACCA GAAGGGACAC ACAGTTTCGA CGGCATCTGG	300
AAGGCCAGCT TCACCACCTT CACTGTGACA AAATATTGGT TTTACCGCTT GTTGTCTACG	360
ATCTTCGGCA TCCCAATGGC ACTCATCTGG GGCATTTACT TTGCCATTCT CTCCTTCCTG	420
CACATCTGGG CGGTTGTACC GTGCATCAAG AGCTTCCTGA TTGAGATTCA GTGCATCAGC	480
CGCGTCTACT CCATCTACGT CCATACCTTC TGCGATCCAC TCTTTGAAGC TATTGGCAAG	540
ATATTCAGCA ACATCCGCAT CAGCACGCAG AAAGAGATAT GAGGGACATT TCAAGGATGA	600
AAGGTTTTTT TCCCCCTTA CTATTTCCCTT GGTGCCAATT CCAAGTTGCT CTCGCAGCAG	660
CAAATTTATG AATGGTTTGT CTTGATC	687
(2) INFORMATION FOR SEQ ID NO: 90:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 560 amino acids	
(B) TYPE: amino acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: peptide	

-continued

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Met Glu Cys Leu Tyr Tyr Phe Leu Gly Phe Leu Leu Leu Ala Ala Arg
1 5 10 15

Leu Pro Leu Asp Ala Ala Lys Arg Phe His Asp Val Leu Gly Asn Glu
20 25 30

Arg Pro Ser Ala Tyr Met Arg Glu His Asn Gln Leu Asn Gly Trp Ser
35 40 45

Ser Asp Glu Asn Asp Trp Asn Glu Lys Leu Tyr Pro Val Trp Lys Arg
50 55 60

Gly Asp Met Arg Trp Lys Asn Ser Trp Lys Gly Gly Arg Val Gln Ala
65 70 75 80

Val Leu Thr Ser Asp Ser Pro Ala Leu Val Gly Ser Asn Ile Thr Phe
85 90 95

Ala Val Asn Leu Ile Phe Pro Arg Cys Gln Lys Glu Asp Ala Asn Gly
100 105 110

Asn Ile Val Tyr Glu Lys Asn Cys Arg Asn Glu Ala Gly Leu Ser Ala
115 120 125

Asp Pro Tyr Val Tyr Asn Trp Thr Ala Trp Ser Glu Asp Ser Asp Gly
130 135 140

Glu Asn Gly Thr Gly Gln Ser His His Asn Val Phe Pro Asp Gly Lys
145 150 155 160

Pro Phe Pro His His Pro Gly Trp Arg Arg Trp Asn Phe Ile Tyr Val
165 170 175

Phe His Thr Leu Gly Gln Tyr Phe Gln Lys Leu Gly Arg Cys Ser Val
180 185 190

Arg Val Ser Val Asn Thr Ala Asn Val Thr Leu Gly Pro Gln Leu Met
195 200 205

Glu Val Thr Val Tyr Arg Arg His Gly Arg Ala Tyr Val Pro Ile Ala
210 215 220

Gln Val Lys Asp Val Tyr Val Val Thr Asp Gln Ile Pro Val Phe Val
225 230 235 240

Thr Met Phe Gln Lys Asn Asp Arg Asn Ser Ser Asp Glu Thr Phe Leu
245 250 255

Lys Asp Leu Pro Ile Met Phe Asp Val Leu Ile His Asp Pro Ser His
260 265 270

Phe Leu Asn Tyr Ser Thr Ile Asn Tyr Lys Trp Ser Phe Gly Asp Asn
275 280 285

Thr Gly Leu Phe Val Ser Thr Asn His Thr Val Asn His Thr Tyr Val
290 295 300

Leu Asn Gly Thr Phe Ser Leu Asn Leu Thr Val Lys Ala Ala Ala Pro
305 310 315 320

Gly Pro Cys Pro Pro Pro Pro Pro Pro Pro Arg Pro Ser Lys Pro Thr
325 330 335

Pro Ser Leu Gly Pro Ala Gly Asp Asn Pro Leu Glu Leu Ser Arg Ile
340 345 350

Pro Asp Glu Asn Cys Gln Ile Asn Arg Tyr Gly His Phe Gln Ala Thr
355 360 365

-continued

Ile	Thr	Ile	Val	Glu	Gly	Ile	Leu	Glu	Val	Asn	Ile	Ile	Gln	Met	Thr
370						375					380				
Asp	Val	Leu	Met	Pro	Val	Pro	Trp	Pro	Glu	Ser	Ser	Leu	Ile	Asp	Phe
385					390					395					400
Val	Val	Thr	Cys	Gln	Gly	Ser	Ile	Pro	Thr	Glu	Val	Cys	Thr	Ile	Ile
				405					410					415	
Ser	Asp	Pro	Thr	Cys	Glu	Ile	Thr	Gln	Asn	Thr	Val	Cys	Ser	Pro	Val
			420					425					430		
Asp	Val	Asp	Glu	Met	Cys	Leu	Leu	Thr	Val	Arg	Arg	Thr	Phe	Asn	Gly
		435					440					445			
Ser	Gly	Thr	Tyr	Cys	Val	Asn	Leu	Thr	Leu	Gly	Asp	Asp	Thr	Ser	Leu
	450					455					460				
Ala	Leu	Thr	Ser	Thr	Leu	Ile	Ser	Val	Pro	Asp	Arg	Asp	Pro	Ala	Ser
465					470					475					480
Pro	Leu	Arg	Met	Ala	Asn	Ser	Ala	Leu	Ile	Ser	Val	Gly	Cys	Leu	Ala
				485					490					495	
Ile	Phe	Val	Thr	Val	Ile	Ser	Leu	Leu	Val	Tyr	Lys	Lys	His	Lys	Glu
			500					505					510		
Tyr	Asn	Pro	Ile	Glu	Asn	Ser	Pro	Gly	Asn	Val	Val	Arg	Ser	Lys	Gly
		515					520					525			
Leu	Ser	Val	Phe	Leu	Asn	Arg	Ala	Lys	Ala	Val	Phe	Phe	Pro	Gly	Asn
	530					535					540				
Gln	Glu	Lys	Asp	Pro	Leu	Leu	Lys	Asn	Gln	Glu	Phe	Lys	Gly	Val	Ser
545					550					555					560

(2) INFORMATION FOR SEQ ID NO: 91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2669 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

CAGATGCCAG	AAGAACACTG	TTGCTCTTGG	TGGACGGGCC	CAGAGGAATT	CAGAGTTAAA	60
CCTTGAGTGC	CTGCGTCCGT	GAGAATTCAG	CATGGAATGT	CTCTACTATT	TCCTGGGATT	120
TCTGCTCCTG	GCTGCAAGAT	TGCCACTTGA	TGCCGCCAAA	CGATTTTCATG	ATGTGCTGGG	180
CAATGAAAGA	CCTTCTGCTT	ACATGAGGGA	GCACAATCAA	TTAAATGGCT	GGTCTTCTGA	240
TGAAAATGAC	TGGAATGAAA	AACTCTACCC	AGTGTGGAAG	CGGGGAGACA	TGAGGTGGAA	300
AAACTCCTGG	AAGGGAGGCC	GTGTGCAGGC	GGTCCTGACC	AGTGACTCAC	CAGCCCTCGT	360
GGGCTCAAAT	ATAACATTTG	CGGTGAACCT	GATATTCCCT	AGATGCCAAA	AGGAAGATGC	420
CAATGGCAAC	ATAGTCTATG	AGAAGAACTG	CAGAAATGAG	GCTGGTTTAT	CTGCTGATCC	480
ATATGTTTAC	AACTGGACAG	CATGGTCAGA	GGACAGTGAC	GGGGAAAATG	GCACCGGCCA	540
AAGCCATCAT	AACGTCTTCC	CTGATGGGAA	ACCTTTTCCT	CACCACCCCG	GATGGAGAAG	600
ATGGAATTTT	ATCTACGTCT	TCCACACACT	TGGTCAGTAT	TTCCAGAAAT	TGGGACGATG	660

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TTCAGTGAGA	GTTTCTGTGA	ACACAGCCAA	TGTGACACTT	GGGCCTCAAC	TCATGGAAGT	720
GACTGTCTAC	AGAAGACATG	GACGGGCATA	TGTTCCCATC	GCACAAGTGA	AAGATGTGTA	780
CGTGGTAACA	GATCAGATTC	CTGTGTTTGT	GACTATGTTC	CAGAAGAACG	ATCGAAATTC	840
ATCCGACGAA	ACCTTCCTCA	AAGATCTCCC	CATTATGTTT	GATGTCCTGA	TTCATGATCC	900
TAGCCACTTC	CTCAATTATT	CTACCATTAA	CTACAAGTGG	AGCTTCGGGG	ATAATACTGG	960
CCTGTTTGTT	TCCACCAATC	ATACTGTGAA	TCACACGTAT	GTGCTCAATG	GAACCTTCAG	1020
CCTTAACCTC	ACTGTGAAAG	CTGCAGCACC	AGGACCTTGT	CCGCCACCGC	CACCACCACC	1080
CAGACCTTCA	AAACCCACCC	CTTCTTTAGG	ACCTGCTGGT	GACAACCCCC	TGGAGCTGAG	1140
TAGGATTCCT	GATGAAAAC	GCCAGATTAA	CAGATATGGC	CACTTTC	CAAGCCACATCAC	1200
AATTGTAGAG	GGAATCTTAG	AGGTTAACAT	CATCCAGATG	ACAGACGTCC	TGATGCCGGT	1260
GCCATGGCCT	GAAAGCTCCC	TAATAGACTT	TGTCGTGACC	TGCCAAGGGA	GCATTCCCAC	1320
GGAGGTCTGT	ACCATCATTT	CTGACCCAC	CTGCGAGATC	ACCCAGAACA	CAGTCTGCAG	1380
CCCTGTGGAT	GTGGATGAGA	TGTGTCTGCT	GACTGTGAGA	CGAACCTTCA	ATGGGTCTGG	1440
GACGTACTGT	GTGAACCTCA	CCCTGGGGGA	TGACACAAGC	CTGGCTCTCA	CGAGCACCT	1500
GATTTCTGTT	CCTGACAGAG	ACCCAGCCTC	GCCTTTAAGG	ATGGCAAACA	GTGCCCTGAT	1560
CTCCGTTGGC	TGCTTGGCCA	TATTTGTCAC	TGTGATCTCC	CTCTTGGTGT	ACAAAAACA	1620
CAAGGAATAC	AACCCAATAG	AAAATAGTCC	TGGGAATGTG	GTCAGAAGCA	AAGGCCTGAG	1680
TGTCTTTCTC	AACCGTGCAA	AAGCCGTGTT	CTTCCCGGGA	AACCAGGAAA	AGGATCCGCT	1740
ACTCAAAAC	CAAGAATTTA	AAGGAGTTTC	TTAAATTTG	ACCTTGTTTC	TGAAGCTCAC	1800
TTTTCAGTGC	CATTGATGTG	AGATGTGCTG	GAGTGGCTAT	TAACCTTTTT	TTCTTAAAGA	1860
TTATTGTTAA	ATAGATATTG	TGGTTTG	AAGTTGAATT	TTTTATAGGT	TAAATGTCAT	1920
TTTAGAGATG	GGGAGAGGGA	TTATACTGCA	GGCAGCTTCA	GCCATGTTGT	GAAACTGATA	1980
AAAGCAACTT	AGCAAGGCTT	CTTTTCATTA	TTTTTTATGT	TTCACTTATA	AAGTCTTAGG	2040
TAAGTAGTAG	GATAGAAACA	CTGTGTCCCG	AGAGTAAGGA	GAGAAGCTAC	TATTGATTAG	2100
AGCCTAACCC	AGGTAACTG	CAAGAAGAGG	CGGGATACTT	TCAGCTTTCC	ATGTAAGTGT	2160
ATGCATAAAG	CCAATGTAGT	CCAGTTTCTA	AGATCATGTT	CCAAGCTAAC	TGAATCCCAC	2220
TTCAATACAC	ACTCATGAAC	TCCTGATGGA	ACAATAACAG	GCCCAAGCCT	GTGGTATGAT	2280
GTGCACACTT	GCTAGACTCA	GAAAAAATAC	TACTCTCATA	AATGGGTGGG	AGTATTTTGG	2340
TGACAACCTA	CTTTGCTTGG	CTGAGTGAAG	GAATGATATT	CATATATTCA	TTTATTCCAT	2400
GGACATTTAG	TTAGTGCTTT	TTATATACCA	GGCATGATGC	TGAGTGACAC	TCTTGTGTAT	2460
ATTTCCAAAT	TTTTGTATAG	TCGCTGCACA	TATTTGAAAT	CATATATTAA	GACTTTCCAA	2520
AGATGAGGTC	CCTGGTTTTT	CATGGCAACT	TGATCAGTAA	GGATTTACCC	TCTGTTTGTA	2580
ACTAAAACCA	TCTACTATAT	GTTAGACATG	ACATTCTTTT	TCTCTCCTTC	CTGAAAAATA	2640
AAGTGTGGGA	AGAGACAAAA	AAAAAAAAAA				2669

(2) INFORMATION FOR SEQ ID NO: 92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

-continued

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

AAGGTGAAAG ATGTGTATGT GATAACAGAT CAGATCCCTG TATTCGTGAC CATGTCCCAG

60

AAGAATGACA GGAAC TTGTC TGATGAGATC TTCCTCAGAG ACCTCCCCAT CGTCTTCGAT

120

GTCCTCATTC ATGATCCCAG CCACTTCCTC AACGACTCTG CCATTTCCCTA CAAGTGGAAC

180

TTTGGGGACA ACACTGGCCT GTTTGTCTCC AACAATCACA CTTTGAATCA CACTTATGTG

240

CTCAATGGAA CCTTCAACCT TAACCTCACC GTGCAAACCTG CAGTGCCCGG GCCATGCCCT

300

CCCCCTTCGC CTTCGACTCC GCCTCCACCT TCGTA

335

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

AAGGTGAAAG ATGTGTATGT GATAACAGAT CAGATCCCTG TATTCGTGAC CATGTCCCAG

60

AAGAATGACA GGAAC TTGTC TGATGAGATC TTCCTCAGAG ACCTCCCCAT CGTCTTCGAT

120

GTCCTCATTC ATGATCCCAG CCACTTCCTC AACGACTCTG CCATTTCCCTA CAAGTGGAAC

180

TTTGGGGACA ACACTGGCCT GTTTGTCTCC AACAATCACA CTTTGAATCA CACTTATGTG

240

CTCAATGGAA CCTTCAACCT TA

262

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 335 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

AAGGTGAAAG ATGTGTATGT GATAACAGAT CAGATCCCTG TATTCGTGAC CATGTCCCAG

60

AAGAATGACA GGAAC TTGTC TGATGAGATC TTCCTCAGAG ACCTCCCCAT CGTCTTCGAT

120

-continued

GTCCTCATTC ATGATCCCAG CCACTTCCTC AACGACTCTG CCATTTCCCTA CAAGTGGAAC	180
TTTGGGGACA ACACTGGCCT GTTTGTCTCC AACAAATCACA CTTTGAATCA CACTTATGTG	240
CTCAATGGAA CCTTCAACCT TAACCTCACC GTGCAAACCTG CAGTGCCCGG GCCATGCCCT	300
CCCCCTTCGC CTTCGACTCC GCCTCCACCT TCGTA	335

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 190 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: <Unknown>
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

TACGAAGGTG GAGGCGGAGT CGAAGGCGAA GGGGGAGGGC ATGGCCCGGG CACTGCAGTT	60
TGCACGGTGA GGTTAAGGTT GAAGGTTCCA TTGAGCACAT AAGTGTGATT CAAAGTGTGA	120
TTGTTGGAGA CAAACAGGCC AGTGTGTGCC CCAAAGTTCC ACTTGTAGGA AATGGCAGAG	180
TCGTTGAGGA	190

(2) INFORMATION FOR SEQ ID NO: 96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: <Unknown>
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

AAGGTGAAAG ATGTGTATGT GATAACAGAT CAGATCCCTG TATTCGTGAC CATGTCCCAG	60
AAGAATGACA GGAACCTGTC TGATGAGATC TTCCTCAGAG ACCTCCCCAT CGTCTTCGAT	120
GTCCTCATTC ATGATCCCAG CCACTTCCTC AACGACTCTG CCATTTCCCTA CAAGTGGAAC	180
TTTGGGGACA ACACTGGCCT GTTTGTCTCC AACAAATCACA CTTTGAATCA CACTTATGTG	240
CTCAATGGAA CCTTCAACCT TAACCTCACC GTGCAAACCTG CAGTGCCCGG GCCATGCCCT	300
CCCCCTTCGC CTTCGACTCC GCCTCCACCT TCGTA	335

(2) INFORMATION FOR SEQ ID NO: 97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

-continued

- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

Arg Arg Trp Arg Arg Ser Arg Arg Arg Arg Gly Arg Ala Trp Gly His
1 5 10 15
Cys Ser His Gly Val Lys Val Gly Ser His Ser Val Ser Val Val Gly
20 25 30
Asp Lys Ala Ser Val Val Lys Val Val Gly Asn Gly Arg Val Val Val
35 40 45
Ala Gly Met Asn Asp Asp Asp Gly Val Ser Asp Arg Val Val Gly His
50 55 60
Gly His Tyr Arg Asp Cys Tyr His His His
65 70

(2) INFORMATION FOR SEQ ID NO: 98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

Lys Val Lys Asp Val Tyr Val Thr Asp Val Val Thr Met Ser Lys Asn
1 5 10 15
Asp Arg Asn Ser Asp Arg Asp Val Asp Val His Asp Ser His Asn Asp
20 25 30
Ser Ala Ser Tyr Lys Trp Asn Gly Asp Asn Thr Gly Val Ser Asn Asn
35 40 45
His Thr Asn His Thr Tyr Val Asn Gly Thr Asn Asn Thr Val Thr Ala
50 55 60
Val Gly Cys Ser Ser Thr Ser
65 70

(2) INFORMATION FOR SEQ ID NO: 99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal

-continued

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

Tyr Gly Gly Gly Gly Val Gly Gly Gly Gly His Gly Gly Thr Ala Val
1 5 10 15
Cys Thr Val Arg Arg Lys Val Ser Thr Val Lys Val Thr Asn Arg Val
20 25 30
Ser Lys His Met Ala Ser Arg Lys Trp Gly Ser Met Arg Thr Ser Lys
35 40 45
Thr Met Gly Arg Ser Arg Lys Ser Ser Asp Lys Ser Trp Asp Met Val
50 55 60
Thr Asn Thr Gly Ser Val Thr Tyr Thr Ser Thr
65 70 75

(2) INFORMATION FOR SEQ ID NO: 100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 376 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

Met Cys Tyr Tyr Gly Ala Ala Arg Asp Ala Ala Lys Arg His Asp Val
1 5 10 15
Gly Asn Arg Ser Ala Tyr Met Arg His Asn Asn Gly Trp Ser Ser Asp
20 25 30
Asn Asp Trp Asn Lys Tyr Val Trp Lys Arg Gly Asp Met Arg Trp Lys
35 40 45
Asn Ser Trp Lys Gly Gly Arg Val Ala Val Thr Ser Asp Ser Ala Val
50 55 60
Gly Ser Asn Thr Ala Val Asn Arg Cys Lys Asp Ala Asn Gly Asn Val
65 70 75 80
Tyr Lys Asn Cys Arg Asn Ala Gly Ser Ala Asp Tyr Val Tyr Asn Trp
85 90 95
Thr Ala Trp Ser Asp Ser Asp Gly Asn Gly Thr Gly Ser His His Asn
100 105 110
Val Asp Gly Lys His His Gly Trp Arg Arg Trp Asn Tyr Val His Thr
115 120 125
Gly Tyr Lys Gly Arg Cys Ser Val Arg Val Ser Val Asn Thr Ala Asn
130 135 140
Val Thr Gly Met Val Thr Val Tyr Arg Arg His Gly Arg Ala Tyr Val
145 150 155 160
Ala Val Lys Asp Val Tyr Val Val Thr Asp Val Val Thr Met Lys Asn
165 170 175
Asp Arg Asn Ser Ser Asp Thr Lys Asp Met Asp Val His Asp Ser His
180 185 190
Asn Tyr Ser Thr Asn Tyr Lys Trp Ser Gly Asp Asn Thr Gly Val Ser
195 200 205

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Thr	Asn	His	Thr	Val	Asn	His	Thr	Tyr	Val	Asn	Gly	Thr	Ser	Asn	Thr
210					215					220					
Val	Lys	Ala	Ala	Ala	Gly	Cys	Arg	Ser	Lys	Thr	Ser	Gly	Ala	Gly	Asp
225					230					235					240
Asn	Ser	Arg	Asp	Asn	Cys	Asn	Arg	Tyr	Gly	His	Ala	Thr	Thr	Val	Gly
				245					250					255	
Val	Asn	Met	Thr	Asp	Val	Met	Val	Trp	Ser	Ser	Asp	Val	Val	Thr	Cys
			260					265					270		
Gly	Ser	Thr	Val	Cys	Thr	Ser	Asp	Thr	Cys	Thr	Asn	Thr	Val	Cys	Ser
		275					280					285			
Val	Asp	Val	Asp	Met	Cys	Thr	Val	Arg	Arg	Thr	Asn	Gly	Ser	Gly	Thr
290						295					300				
Tyr	Cys	Val	Asn	Thr	Gly	Asp	Asp	Thr	Ser	Ala	Thr	Ser	Thr	Ser	Val
305					310					315					320
Asp	Arg	Asp	Ala	Ser	Arg	Met	Ala	Asn	Ser	Ala	Ser	Val	Gly	Cys	Ala
				325					330					335	
Val	Thr	Val	Ser	Val	Tyr	Lys	Lys	His	Lys	Tyr	Asn	Asn	Ser	Gly	Asn
			340					345					350		
Val	Val	Arg	Ser	Lys	Gly	Ser	Val	Asn	Arg	Ala	Lys	Ala	Val	Gly	Asn
		355					360					365			
Lys	Asp	Lys	Asn	Lys	Gly	Val	Ser								
370					375										

(2) INFORMATION FOR SEQ ID NO: 101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2669 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

CAGATGCCAG	AAGAACACTG	TTGCTCTTGG	TGGACGGGCC	CAGAGGAATT	CAGAGTTAAA	60
CCTTGAGTGC	CTGCGTCCGT	GAGAATTCAG	CATGGAATGT	CTCTACTATT	TCCTGGGATT	120
TCTGCTCCTG	GCTGCAAGAT	TGCCACTTGA	TGCCGCCAAA	CGATTTTCATG	ATGTGCTGGG	180
CAATGAAAGA	CCTTCTGCTT	ACATGAGGGA	GCACAATCAA	TTAAATGGCT	GGTCTTCTGA	240
TGAAAATGAC	TGGAATGAAA	AACTCTACCC	AGTGTGGAAG	CGGGGAGACA	TGAGGTGGAA	300
AAACTCCTGG	AAGGGAGGCC	GTGTGCAGGC	GGTCCTGACC	AGTGA CTCAC	CAGCCCTCGT	360
GGGCTCAAAT	ATAACATTTG	CGGTGAACCT	GATATTCCCT	AGATGCCAAA	AGGAAGATGC	420
CAATGGCAAC	ATAGTCTATG	AGAAGAACTG	CAGAAATGAG	GCTGGTTTAT	CTGCTGATCC	480
ATATGTTTAC	AACTGGACAG	CATGGTCAGA	GGACAGTGAC	GGGGAAAATG	GCACCGGCCA	540
AAGCCATCAT	AACGTCTTCC	CTGATGGGAA	ACCTTTTCCT	CACCACCCCG	GATGGAGAAG	600
ATGGAATTTT	ATCTACGTCT	TCCACACACT	TGGTCAGTAT	TTCCAGAAAT	TGGGACGATG	660
TTCAGTGAGA	GTTTCTGTGA	ACACAGCCAA	TGTGACACTT	GGGCCTCAAC	TCATGGAAGT	720

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GACTGTCTAC	AGAAGACATG	GACGGGCATA	TGTTCCCATC	GCACAAGTGA	AAGATGTGTA	780
CGTGGTAACA	GATCAGATTC	CTGTGTTTGT	GACTATGTTC	CAGAAGAACG	ATCGAAATTC	840
ATCCGACGAA	ACCTTCCTCA	AAGATCTCCC	CATTATGTTT	GATGTCCTGA	TTCATGATCC	900
TAGCCACTTC	CTCAATTATT	CTACCATTAA	CTACAAGTGG	AGCTTCGGGG	ATAATACTGG	960
CCTGTTTGTT	TCCACCAATC	ATACTGTGAA	TCACACGTAT	GTGCTCAATG	GAACCTTCAG	1020
CCTTAACCTC	ACTGTGAAAG	CTGCAGCACC	AGGACCTTGT	CCGCCACCGC	CACCACCACC	1080
CAGACCTTCA	AAACCCACCC	CTTCTTTAGG	ACCTGCTGGT	GACAACCCCC	TGGAGCTGAG	1140
TAGGATTCCT	GATGAAAAC	GCCAGATTAA	CAGATATGGC	CACTTTCAAG	CCACCATCAC	1200
AATTGTAGAG	GGAATCTTAG	AGGTTAACAT	CATCCAGATG	ACAGACGTCC	TGATGCCGGT	1260
GCCATGGCCT	GAAAGCTCCC	TAATAGACTT	TGTCGTGACC	TGCCAAGGGA	GCATTCCCAC	1320
GGAGGTCTGT	ACCATCATTT	CTGACCCAC	CTGCGAGATC	ACCCAGAACA	CAGTCTGCAG	1380
CCCTGTGGAT	GTGGATGAGA	TGTGTCTGCT	GACTGTGAGA	CGAACCTTCA	ATGGGTCTGG	1440
GACGTACTGT	GTGAACCTCA	CCCTGGGGGA	TGACACAAGC	CTGGCTCTCA	CGAGCACCCCT	1500
GATTTCTGTT	CCTGACAGAG	ACCCAGCCTC	GCCTTTAAGG	ATGGCAAACA	GTGCCCTGAT	1560
CTCCGTTGGC	TGCTTGGCCA	TATTTGTCAC	TGTGATCTCC	CTCTTGGTGT	ACAAAAACA	1620
CAAGGAATAC	AACCCAATAG	AAAATAGTCC	TGGGAATGTG	GTCAGAAGCA	AAGGCCTGAG	1680
TGTCTTTCTC	AACCGTGCAA	AAGCCGTGTT	CTTCCCGGGA	AACCAGGAAA	AGGATCCGCT	1740
ACTCAAAAC	CAAGAATTTA	AAGGAGTTTC	TTAAATTTTCG	ACCTTGTTTC	TGAAGCTCAC	1800
TTTTCAGTGC	CATTGATGTG	AGATGTGCTG	GAGTGGCTAT	TAACCTTTTT	TTCTAAAGA	1860
TTATTGTTAA	ATAGATATTG	TGGTTTGGGG	AAGTTGAATT	TTTTATAGGT	TAAATGTCAT	1920
TTTAGAGATG	GGGAGAGGGA	TTATACTGCA	GGCAGCTTCA	GCCATGTTGT	GAAACTGATA	1980
AAAGCAACTT	AGCAAGGCTT	CTTTTCATTA	TTTTTTATGT	TTCACTTATA	AAGTCTTAGG	2040
TAAGTAGTAG	GATAGAAACA	CTGTGTCCCG	AGAGTAAGGA	GAGAAGCTAC	TATTGATTAG	2100
AGCCTAACCC	AGGTAACTG	CAAGAAGAGG	CGGGATACTT	TCAGCTTTCC	ATGTAACTGT	2160
ATGCATAAAG	CCAATGTAGT	CCAGTTTCTA	AGATCATGTT	CCAAGCTAAC	TGAATCCCAC	2220
TTCAATACAC	ACTCATGAAC	TCCTGATGGA	ACAATAACAG	GCCCAAGCCT	GTGGTATGAT	2280
GTGCACACTT	GCTAGACTCA	GAAAAAATAC	TACTCTCATA	AATGGGTGGG	AGTATTTTGG	2340
TGACAACCTA	CTTTGCTTGG	CTGAGTGAAG	GAATGATATT	CATATATTCA	TTTATTCCAT	2400
GGACATTTAG	TTAGTGCTTT	TTATATACCA	GGCATGATGC	TGAGTGACAC	TCCTGTGTAT	2460
ATTTCCAAAT	TTTTGTATAG	TCGCTGCACA	TATTTGAAAT	CATATATTAA	GACTTTCCAA	2520
AGATGAGGTC	CCTGGTTTTT	CATGGCAACT	TGATCAGTAA	GGATTCACC	TCTGTTTGTA	2580
ACTAAAACCA	TCTACTATAT	GTTAGACATG	ACATTCTTTT	TCTCTCCTTC	CTGAAAAATA	2640
AAGTGTGGGA	AGAGACAAAA	AAAAAAAAA				2669

- (2) INFORMATION FOR SEQ ID NO: 102:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 376 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

Met  Cys  Tyr  Tyr  Gly  Ala  Ala  Arg  Asp  Ala  Ala  Lys  Arg  His  Asp  Val
 1          5          10          15

Gly  Asn  Arg  Ser  Ala  Tyr  Met  Arg  His  Asn  Asn  Gly  Trp  Ser  Ser  Asp
          20          25          30

Asn  Asp  Trp  Asn  Lys  Tyr  Val  Trp  Lys  Arg  Gly  Asp  Met  Arg  Trp  Lys
          35          40          45

Asn  Ser  Trp  Lys  Gly  Gly  Arg  Val  Ala  Val  Thr  Ser  Asp  Ser  Ala  Val
 50          55          60

Gly  Ser  Asn  Thr  Ala  Val  Asn  Arg  Cys  Lys  Asp  Ala  Asn  Gly  Asn  Val
 65          70          75          80

Tyr  Lys  Asn  Cys  Arg  Asn  Ala  Gly  Ser  Ala  Asp  Tyr  Val  Tyr  Asn  Trp
          85          90          95

Thr  Ala  Trp  Ser  Asp  Ser  Asp  Gly  Asn  Gly  Thr  Gly  Ser  His  His  Asn
          100          105          110

Val  Asp  Gly  Lys  His  His  Gly  Trp  Arg  Arg  Trp  Asn  Tyr  Val  His  Thr
          115          120          125

Gly  Tyr  Lys  Gly  Arg  Cys  Ser  Val  Arg  Val  Ser  Val  Asn  Thr  Ala  Asn
 130          135          140

Val  Thr  Gly  Met  Val  Thr  Val  Tyr  Arg  Arg  His  Gly  Arg  Ala  Tyr  Val
 145          150          155          160

Ala  Val  Lys  Asp  Val  Tyr  Val  Val  Thr  Asp  Val  Val  Thr  Met  Lys  Asn
          165          170          175

Asp  Arg  Asn  Ser  Ser  Asp  Thr  Lys  Asp  Met  Asp  Val  His  Asp  Ser  His
          180          185          190

Asn  Tyr  Ser  Thr  Asn  Tyr  Lys  Trp  Ser  Gly  Asp  Asn  Thr  Gly  Val  Ser
          195          200          205

Thr  Asn  His  Thr  Val  Asn  His  Thr  Tyr  Val  Asn  Gly  Thr  Ser  Asn  Thr
 210          215          220

Val  Lys  Ala  Ala  Ala  Gly  Cys  Arg  Ser  Lys  Thr  Ser  Gly  Ala  Gly  Asp
 225          230          235          240

Asn  Ser  Arg  Asp  Asn  Cys  Asn  Arg  Tyr  Gly  His  Ala  Thr  Thr  Val  Gly
          245          250          255

Val  Asn  Met  Thr  Asp  Val  Met  Val  Trp  Ser  Ser  Asp  Val  Val  Thr  Cys
          260          265          270

Gly  Ser  Thr  Val  Cys  Thr  Ser  Asp  Thr  Cys  Thr  Asn  Thr  Val  Cys  Ser
          275          280          285

Val  Asp  Val  Asp  Met  Cys  Thr  Val  Arg  Arg  Thr  Asn  Gly  Ser  Gly  Thr
 290          295          300

Tyr  Cys  Val  Asn  Thr  Gly  Asp  Asp  Thr  Ser  Ala  Thr  Ser  Thr  Ser  Val
 305          310          315          320

Asp  Arg  Asp  Ala  Ser  Arg  Met  Ala  Asn  Ser  Ala  Ser  Val  Gly  Cys  Ala
          325          330          335

Val  Thr  Val  Ser  Val  Tyr  Lys  Lys  His  Lys  Tyr  Asn  Asn  Ser  Gly  Asn
          340          345          350

Val  Val  Arg  Ser  Lys  Gly  Ser  Val  Asn  Arg  Ala  Lys  Ala  Val  Gly  Asn
          355          360          365

Lys  Asp  Lys  Asn  Lys  Gly  Val  Ser
 370          375

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-continued

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 247 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

CTGACCAGGA ACCCACTCTT CTGTGCATGT ATGTGAGCTG TGCAGAAGTA TGTGGCTGGG	60
AACTGTTGTT CTCTAAGGAT TATTGTAAAA TGTATATCGT GGCTTAGGGA GTGTGGTTAA	120
ATAGCATTTT AGAGAAGAAA AAAAAAAAAA AAAAAACTCG AGAGTACTTC TAGAGCGGCC	180
GCGGCGCCAT CGATTTTCCA CCCGGGTGGG GTACCAGGTA AGTGTACCCA ATTCGCCTAT	240
AGTGAGT	247

(2) INFORMATION FOR SEQ ID NO: 104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

AGGACAAGCC AAGGACACTC TAAGTCTTTG GCCTTCCCTC TGACCAGGAA CCCACTCTTC	60
TGTGCATGTA TGTGAGCTGT GCAGAAGTAT GTGGCTGGGA ACTGTTGTTC TCTAAGGATT	120
ATTGTAAAT GTATATCGTG GCTTAGGGAG TGTGGTTAAA TAGCATTTTA GAGAAGACAT	180
GGGAAGACTT AGTGTTCCTT CCCATCTGTA TTGTGGTTTT TACACTGTTC GTGGGGTGGA	240
CACGCTGTGT CTGAAGGGGA GGTGGGGGTC ACTGCTACTT AAGGTCCTAG GTTAACTGGG	300
GGAGATACCA CAGATGCTCA GCTTTCCACA TAACATGGGC ATGAACCAGC TAATCACACT	360
GAA	363

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 524 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

-continued

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

GGATCCTTCT	CCTGGTCTCC	TCGGAAGAAC	GGGGCTTTCG	CGTGA	CTGAG	GAGA	CACTC	60
AGGCCCTTGC	CCTTGACCGT	GTTCTGGGG	CAGTTTCCTA	TTGGCTTGTA	CGCCTTGTGT			120
TTTTTGTACA	GCAAGATGGT	AACCATGGTG	ACAAGCACAG	CCAGGCAGCC	GATGGAGATC			180
AGGACACCAT	TCACTGCTCT	CAGAGGGAGT	CTGGGTCTTT	GCCAGGGATA	GAGATCAGGG			240
TGCTGGTGAG	GGCCAGGCTT	CGATCATCTC	CCAGAGTGAA	ATTCACACAG	TAGGTGCCAG			300
ACCCATTGAA	GGCTCTTCTC	ACAGACAGCA	GCACAGCCCA	TCCACAGCCA	CAGGGCTGCA			360
GACCCGGTTC	TGGGCGATCT	GGCAGGTGGG	GTCGGAGATG	ATCGTACAGG	CTTC	CATGGG		420
GGTGGCCCT	TTGCAGGTCA	CAGTGAAGTC	CATCAGGGAG	TTGGCAGGCT	GCGGTGTGGG			480
CATGGGGACA	TCTGCTATCT	GCATGATGCT	GA	CTTCCAGG	ATCC			524

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 309 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

TAGCAGATGT	CCCCATGCCC	ACACCGCAGC	CTGCCAACTC	CCTGATGGAC	TTCACTGTGA	60
CCTGCAAAGG	GGCCACCCCC	ATGGAAGCCT	GTACGATCAT	CTCCGACCCC	ACCTGCCAGA	120
TCGCCCAGAA	CCGGGTCTGC	AGCCCTGTGG	CTGTGGATGG	GCTGTGCTGC	TGTCTGTGAG	180
AAGAGCCTTC	AATGGGTCTG	GCACCTACTG	TGTGAATTTT	ACTCTGGGAG	ATGATCGAAG	240
CCTGGCCCTC	ACCAGCACCC	TGATCTCTAT	CCCTGGCAAA	GACCCAGACT	CCCTCTGAGA	300
GCAGTGAAT						309

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 292 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

-continued

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:		
GGATCCTTCT	CCTGGTCTCC	TCGGAAGAAC
GGGGCTTTCG	CGTGACTGAG	GAGAACACTC
60		
AGGCCCTTGC	CCTTGACCGT	GTTCTGGGG
CAGTTTCCTA	TTGGCTTGTA	CGCCTTGTGT
120		
TTTTTGTACA	GCAAGATGGT	AACCATGGTG
ACAAGCACAG	CCAGGCAGCC	GATGGAGATC
180		
AGGACACCAT	TCACTGCTCT	CAGAGGGAGT
CTGGGTCTTT	GCCAGGGATA	GAGATCAGGG
240		
TGCTGGTGAG	GGCCAGGCTT	CGATCATCTC
CCAGAGTGAA	ATTACACACAG	TA
292		
(2) INFORMATION FOR SEQ ID NO: 108:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 263 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:		
TTTTTTTTTT	TTTTTTT TAG	ACTGCCTTTT
TAATGAGTAG	AATATGTACA	CACACGCACC
60		
ATACACAAAG	CCCGGGCCCA	TTATAATTTT
GTCAGGAGCT	CAGGCATGCT	CAGTGAGTTG
120		
GAAGGCAGAT	GAAGCATGCC	TTCAGGTGGT
GATTAGCTGG	GTTCATGCCC	ATGTTATCGT
180		
GGAAAGCTGA	GGCATCTGTG	GTATCTCCCC
CAGTTAACCT	AGGACCTTAA	GTAGCAGTGA
240		
CCCACCTCCC	TTCAGACACA	GCG
263		
(2) INFORMATION FOR SEQ ID NO: 109:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 270 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:		
GGATCCTGGA	AGTCAGCATC	ATGCAGATAG
CAGATGTCCC	CATGCCCACA	CCGCAGCCTG
60		
CCAACTCCCT	GATGGACTTC	ACTGTGACCT
GCAAAGGGGC	CACCCCATG	GAAGCCTGTA
120		
CGATCATCTC	CGACCCACC	TGCCAGATCG
CCCAGAACCG	GGTCTGCAGC	CCTGTGGCTG
180		
TGGATGGGCT	GTGCTGCTGT	CTGTGAGAAG
AGCCTTCAAT	GGGTCTGGCA	CCTACTGTGT
240		
GAATTTCACT	CTGGGAGATG	ATCGAAGCCT
270		
(2) INFORMATION FOR SEQ ID NO: 110:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 239 base pairs		

-continued

(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:	
TTTTTTTTTTT TTTTTTTTTC TTCTCTAAAA TGCTATTTAA CCACACTCCC TAAGCCACGA	60
TATACATTTT ACAATAATCC TTAGAGAACAC ACAGTTCCCA GCCACATACT TCTGCACAGC	120
TCACATACAT GCACAGAAGA GTGGGTTTCCT GGTCTAGAGGG AAGGCCAAAG ACTTAGAGTG	180
TCCTTGGCTT GTCTGGAGCA ATGGATCCTT CTCCTGGTCT CCTCGGAAGA ACGGGCTTT	239
(2) INFORMATION FOR SEQ ID NO: 111:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 335 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:	
AAACTGCAGT GCCCGGGCCA TGCCCTCCCC CTTCGCCTTC GACTCCGCCT CCACCTTCAA	60
CTCCGCCCTC ACCTCCGCCC TCACCTCTGC CCACATTATC AACACCTAGC CCCTCTTTAA	120
TGCCTACTGG TTACAAATCC ATGGAGCTGA GTGACATTTC CAATGAAAAC TGCCGAATAA	180
ACAGATATGG CTACTTCAGA GCCACCATCA CAATTGTAGA GGGGATCCTG GACGCAGCAT	240
CATGCAGATA GCAGATGTCC CATGCCCACA CCGCAGCCGT CCAACTCCTG ATGGACTTCA	300
CTGTGACCTC AAGGGCACCC ATGGAAGCTG TCAGA	335
(2) INFORMATION FOR SEQ ID NO: 112:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 217 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:	
CCTCAACGAC TCTGCCATTT CCTACAAGTG GAACTTTGGG GACAACACTG GCCTGTTTGT	60

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CTCCAACAAT CACACTTTGA ATCACACTTA TGTGCTCAAT GGAACCTTCA ACCTTAACCT 120
CACCGTGCAA ACTGCAGTGC CCGGGCCATG CCCTCCCCCT TCGCCTTCGA CTCCGCCTCC 180
ACCTTCAACT CCGCCCTCAC CTCCGCCCTC ACCTCTG 217

(2) INFORMATION FOR SEQ ID NO: 113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

CCTCAACGAC TCTGCCATTT CCTACAAGTG GAACTTTGGG GACAACACTG GCCTGTTTGT 60
CTCCAACAAT CACACTTTGA ATCACACTTA TGTGCTCAAT GGAACCTTCA ACCTTAACCT 120
CACCGTGCAA ACTGCAGTGC CCGGGCCATG CCCTCCCCCT TCGCCTTCGA CTCCGCCTCC 180
ACCTTCAACT CCGCCCTCAC CTCCGCCCTC ACCTCTGCCC ACATTATCAA CACCTAGCCC 240
CTCTTTAATG CCTACTGGTT ACAAATCCAT GGAGCTGAGT GACATTTCCA ATGAAAAC TG 300
CCGAATAAAC AGATATGGCT ACTTCAGAGC CACCATCACA ATTGTAGAGG GGATCCTGGA 360
AGTCAGCATC ATGCAGATAG CAGATGTCCC CATGCCCACA CCGCAGCCTG CCAACTCCCT 420
GATGGACTTC ACTGTGACCT GCAAAGGGGC CACCCCCATG GAAGCCTGTA CGATCATCTC 480
CGACCCACCG TGCCAGATCG CCCAGAACCG GGTCTGCAGC CCTGTGGCTG TGGATGGGCT 540
GTGCTGCTGT CTGTGAGAAG AGCCTTCAAT GGGTCTGGCA CCTACTGTGT GAATTTCACT 600
CTGGGAGATG ATGCAAGCCT 620

(2) INFORMATION FOR SEQ ID NO: 114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

GGATCCCCTC TACAATTGTG ATGGTGGCTC TGAAGTAGCC ATATCTGTTT ATTCGGCAGT 60
TTTCATTGGA AATGTCACTC AGCTCCATGG ATTTGTAACC AGTAGGCATT AAAGAGGGGC 120
TAGGTGTTGA TAATGTGGGC AGAGGTGAGG GCGGAGGTGA GGGCGGAGTT GAAGGTGGAG 180
GCGGAGTCGA AGGCGAAGGG GGAGGGCATG GCCCGGGCAC TGCAGTTTGC ACGGTGAGGT 240

-continued

TAAGGTTGAA GGTTCATTG AGCACATAAG TGTGATTCAA AGTGTGATTG TTGGAGACAA	300
ACAGGCCAGT GTTGTCCCAA AGTTCCACTT GTAGGAATGG CAGAGTCGTT GAGG	354

(2) INFORMATION FOR SEQ ID NO: 115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 473 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

CCTCAACGAC TCTGCCATTT CCTACAAGTG GAACTTTGGG GACAACACTG GCCTGTTTGT	60
CTCCAACAAT CACACTTTGA ATCACACTTA TGTGCTCAAT GGAACCTTCA ACCTTAACCT	120
CACCGTGCAA ACTGCAGTGC CCGGGCCATG CCCTCCCCCT TCGCCTTCGA CTCCGCCTCC	180
ACCTTCAACT CCGCCCTCAC CTCCGCCCTC ACCTCTGCCC ACATTATCAA CACCTAGCCC	240
CTCTTTAATG CCTACTGGTT ACAAATCCAT GGAGCTGAGT GACATTTCCA ATGAAAAGT	300
CCGAATAAAC AGATATGGCT ACTTCAGAGC CACCATCACA ATTGTAGAGG GGATCCTGGA	360
AGTCAGCATC ATGCAGATAG CAGATGTCCC CATGCCCACA CCGCAGCCTG CCAACTCCCT	420
GATGGACTTC ACTGTGACCT GCAAAGGGGC CACCCCCATG GAAGCCTGTA CGA	473

(2) INFORMATION FOR SEQ ID NO: 116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 223 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

GAAGGTGGAG GCGGAGTCGA AGGCGAAGGG GGAGGGCATG GCCCGGGCAC TGCAGTTTGC	60
ACGGTGAGGT TAAGGTTGAA GGTTCATTG AGCACATAAG TGTGATTCAA AGTGTGATTG	120
TTGGAGACAA ACAGGCCAGT GTTGTCCCAA AAGTTCCACT TGTAGGAAAT GGCAGAGTCG	180
TTGAGGAAGT GGCTGGGATC ATGAATGAGG ACATCGAAGA CGA	223

(2) INFORMATION FOR SEQ ID NO: 117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 247 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:		
GAATTCGCAC GAGGGGAGTC AGAGTCAAGC CCTGACTGGT TGCAGGCGCT CGGAGTCAGC	60	
ATGGAAAGTC TCTGCGGGGT CCTGGGATTT CTGCTGCTGG CTGCAGGACT GCCTCTCCAG	120	
GCTGCCAAGC GATTTCTGTA TGTGCTGGGC CATGAACAGT ATCCCGATCA CATGAGAGAG	180	
CACAACCAAT TACGTGGCTG GTCTTCGGAT GAAAATGAAT GGGTTCCAAT ATCACTTTTG	240	
TGGTGAA	247	
(2) INFORMATION FOR SEQ ID NO: 118:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 240 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:		
GAATTCGGCA CGAGGAAGGA GGCCGTGTGC AGGCAGTCCT GACCAAGTGAC TCACCGGCTC	60	
TGGTGGGTTC CAATATCACT TTTGTGGTGA ACCTGGTGTT CCCCAGATGC CAGAAGGAAG	120	
ATGCTAATGG CAATATCGTC TATGAGAAGA ACTGCAGGAA TGATTTGGGA CTGACATCTG	180	
ACCTGCATGT CTACAAC TGG ACTGCAGGGG CAGATGATGG TGA CTGGGAA GATGGCACCT	240	
(2) INFORMATION FOR SEQ ID NO: 119:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 260 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:		
GAAGGTGGAG GCGGAGTCGA AGGCGAAGGG GGAGGGCATG GCCCGGGCAC TGCAGTTTGC	60	
ACGGTGAGGT TAAGGTTGAA GGTTCATTG AGCACATAAG TGTGATTCAA AGTGTGATTG	120	
TTGGAGACAA ACAGGCCAGT GTTGTCCCCA AAGTTCCACT TG TAGGAAAT GGCAGAGTCG	180	
TTGAGGAAGT GGCTGGGATC ATGAATGAGG ACATCGAAGA CGATGGGGAG GTCTCTGAGG	240	

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AAGATCTCAT CAGACAAGTT 260

(2) INFORMATION FOR SEQ ID NO: 120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

GAATTCGGCA CGAGGTCAAG CCCTGACTGG TTGCAGGCGC TCGGAGTCAG CATGGAAAGT	60
CTCTGCGGGG TCCTGGGATT TCTGCTGCTG GCTGCAGGAC TGCCTCTCCA GGCTGCCAAG	120
CGATTTTCGTG ATGTGCTGGG CCATGAACAG TATCCCGATC ACATGAGAGA GCACAACCAA	180
TTACGTGGCT GGTCTTCGGA TGAAAAATGAA TGGATGAACA CCTTGTATCC A	231

(2) INFORMATION FOR SEQ ID NO: 121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

AAGGGGGAGG GCATGGCCCG GGCAGTGCAG TTTGCACGGT GAGGTTAAGG TTGAAGGTTT	60
CATTGAGCAC ATAAGTGTGA TTCAAAGTGT GATTGTTGGA GACAAACAGG CCAGTGTGTG	120
CCCCAAAGTT CCACTTGTAG GAAATGGCAG AGTCGTTGAG GAAGTGGCTG GGATCATGAA	180
TGAGGACATC GAAGACGATG GGGAGGTCTC TGAGGAAGAT CTCATCAGAC AAGTTCCTGT	240
CATTCTTCTG GGACATGGTC ACGAATACAG GGATCTGATC TGTTAT	286

(2) INFORMATION FOR SEQ ID NO: 122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 224 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

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(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

GAATTCGGCA CGAGCCGACA CTGTGACTCC TGGTGGATGG GACTGGGGAG TCAGAGTCAA	60
GCCCTGACTG GTTGCAAGCG CTCGGAGTCA GCATGGAAAG TCTCTGCGGG GTCCTGGGAT	120
TTCTGCTGCT GGCTGCAGGA CTGCCTCTCC AGGCTGCCAA GCGATTTCGT GATGTGCTGG	180
GCCATGAACA GTATCCCGAT CACATGAGAG AGCACAACCA ATTA	224

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

AAGGTGAAAG ATGTGTATGT GATAACAGAT CAGATCCCTG TATTCGTGAC CATGTCCCAG	60
AAGAATGACA GGAAC TTGTC TGATGAGATC TTCCTCAGAG ACCTCCCCAT CGTCTTCGAT	120
GTCCTCATTC ATGATCCCAG CCACTTCCTC AACGACTCTG CCATTTCCTA CAAGTGGAAC	180
TTTGGGGACA ACACTGGCCT GTTTGTCTCC AACAA TCACA CTTTGAATCA CACTTATGTG	240
CTCAATGGAA CCTTCAACCT TAACCTCACC GTGCAAACTG CAGTGCCCGG GCCATGCCCT	300
CCCCCTTCGC CTTCGACTCC GCCTCCACCT TCGTA	335

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

TACCATCGGA GAAAGAAGAC CAAGCAAGGC TCAGGCAGCC ACCGCCTGCT TCGCACTGAG	60
CCTCCTGACT CAGACTCAGA GTCCAGCACA GACGAAGAGG AATTTGGAGA ATTGGAAATC	120
GCTCTCGTTT TGTCAAGGGA GACTATCCCG ATGCTGCAAG ATCTGCTGTC CCTCTGGCCT	180
TTGTCATCCT CGCGCCTGCG TTGTGGCCTC TGTGGGCTTG GTGTGGAGCA AATGGCTCTC	240
AAGGAGGACT GAGTCTCAAG GAAATT	266

(2) INFORMATION FOR SEQ ID NO: 125:

-continued

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 300 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

AGCTAAGGTC AGGAGGTGTC TGAAGAATTG GCTGATGCAT GGCAGGGATG TTGTTGACCT	60
GCTTTTAGAA CAATACTTCC ATTTAATTAT AGCATATCTT ATGTGTGTAT TAAAGCAGAG	120
CCGATCTGGT GGGGCTCATT AAGTAAATGT ACTTACTGCA AAAGGTTCAA CTGGTGACCC	180
CAGTTTTCCC CAGAAGCAAT ATGATAGGAC AGAGGCGACT CCTGCAAGTT GTCTCAGACT	240
TCACACATAC ATTGTGACAT TCTCTGAGCA TGTGCACTGT ACATGATATG ACACTATCAA	300

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 312 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

AGCTAAGGTC CACTACCTTG TGAAGATGTA TAAACACCTG AAATGTAGAA GCGATCCGTA	60
TGTCAAGATC GAGGGGAAGG ACGCTGACGA CTGGCTGTGT GTGGACTTTG GGAGTATGGT	120
GATCCATTTG ATGCTTCCAG AAACCAGAGA AACCTATGAA TTAGAGAAAC TATGGACTCT	180
ACGTTCTTTT GATGACCTTA GCTAAGCCGA ATCAGCACAC TGGCGGCGTT ACTAGTGGAT	240
CGAGCTCGTA CAGCTGATGC ATAGCTTGAG TATCTATAGG TTAATAATAG CTGGCTATCA	300
TGTCAAGCGT TC	312

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 281 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

-continued

(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:	
GCTGAGCTGC AGAGAGTAGC ACATCCTTGC TAATTCAATA ACTACCAGTT TTTATTGGTG	60
AAACATGAAT CCAGATGGTA TGGTTGCTCT CCTGGACTAC CGTGAAGATG GTGTGACTCC	120
ATTCATGATT TTCTTTAAGG ATGGCTTAGA GATGGAGAAA TGTTAACAAA TTGGATCTAT	180
CACCTGTCAC CATAATTGGC TGCTGCTTAC CATCCATACA ACACCAGGAC TTAGGACAAA	240
TGGGACTGAT GTCATCTTGA GCTTTTATTT TGACCTTAGC T	281
(2) INFORMATION FOR SEQ ID NO: 128:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 295 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:	
AGCTAAGGTC AGAGCCAATA GTATCATGAG AACTGAAGAA GTAATAAAGC AACTTCTCCA	60
GAAATTTAAG ATTGAGAATA GCCCTCGGGA TTTCGCTCTT TACATTATTT TTGGGACAGG	120
AGAGCAGAGA AAGCTAAAGA AGACCGATGT CCACTGCTGC AGAGGTTACT ACAAGGACCA	180
TCCAAAAGCA ATGCTCGGAT CTCTCATGGA TAAAGATGCA GAAGAATCAC GAGAGATGTG	240
GCTCGTACAT TATTTCACTT TCTTCTGATC ATACTCAAGA TAGATGAGAG AGAAT	295
(2) INFORMATION FOR SEQ ID NO: 129:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 240 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:	
TTGACTTCTG AGTCTAACAC AGACACTGCA AGGGTTAATT TTCCAAGAGG TGGTTGTTGT	60
TGACGATAAA TTCATTAAAGA ATTTTAAAAA ATTTAGTTAG ATTTACCAA GTCACTGGAG	120
ACAAATTCAG AAGGCATATA TACCTGCCAG TTTTGTGGAC TACATTAATA GGGAGGCTTT	180
TATGTTTGAT GTAATTCTTA CAGTTCTAAG AATTAAGTTC CATTGCATGA GACCTTAGCT	240
(2) INFORMATION FOR SEQ ID NO: 130:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 196 base pairs	

-continued

(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:	
AAGGTGAATC CCCGACGGCT CTGGGCCCCGA GGAGAAGCGT CGCCGTGGCA AATTGGCACT	60
GCAGGAGAAG CCCTCCACAG GTACTTGGA AAAGTGGTCT CTGAGGCCAA GGCCAGCTCC	120
GAGACATTCA GGACTTCTGG ATCAGCCTCC AGGGACACTG TGCAGTGAGA AGATGGCCAT	180
GAGTCCTGCC AGTGAG	196
(2) INFORMATION FOR SEQ ID NO: 131:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 187 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:	
AATTTTTTTT TTCGACGGCC CAACGGGGGC TTGGTGGATG GAAATATGGT TTTGTGAGTT	60
ATTGCACTAC CTGGAATATC TATGCCTCTT ATTTGCGTGT ACTGTTGCTG CTGATCGTTT	120
GGTGCTGTGT GAGTGAACCT ATGGCTTAGA AAAACGACTT TGTCTTAAAC TGAGTGGGTG	180
TTCAGGG	187
(2) INFORMATION FOR SEQ ID NO: 132:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 197 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:	
CACCTGATTT AAAGGAAAAG CATTCTGACG TAAGAAGCTG AAAGGCGGCC CTTGCGTGCT	60
TTGAACTTTC TTATACAGCA CAGTCATCTG AAGCTTCCTG TGTGACCAAG ACAAGAACGC	120
GTGCACAAGA CTGAGAAACA GCAAGAAACA ACCCGGCATT CTACTTTCTC AACACTATCA	180

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TACTTTAAAC CTTTCAC 197

(2) INFORMATION FOR SEQ ID NO: 133:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

CTAGCTTACG CTAGTCCCC ATGCATAAAG ACTGATCGCT TTTCCTTAGA AAGGTGAGAG	60
GGTTAGGACA AGGCCGTGTG GTAACAACAC CCGCAGCTCG AAAAACCAAT GGCTTGTTAA	120
CGTGTCAGTG AGGCACTGTA CGGACGTCCA TAGTCCACAT CTTCAAATTC CCGCAGAAGG	180
CTTCCTATTC TTAAACTCTA	200

(2) INFORMATION FOR SEQ ID NO: 134:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

CTACATTTCT GTATCCATTC CTCTGTTGAA GGCTCTGGTT CTTTCCAGCT TCTGGCTATT	60
ATAAATAAGG CTGCTATAAA CACAGTGGAG GCATGTGTCC TTGTTATATT TTGGAGCATC	120
TTTTGGGTAT ATGCCCAGAA GTGCTATAGC TGGTTCCTCA GGTAGTACTA TGTCGAATTT	180
TCTGAGGAAC TGCCAGACTG ATTTCCAGAG TGGTTGTACC AGCTTGCAAT CCCACCAGCA	240
ATAGAGGAGT GTTCCTCTTT CTCTATATTC TTGCCAACAT CTGCTGTCAC CTGAGTGTTT	300

(2) INFORMATION FOR SEQ ID NO: 135:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 243 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

-continued

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

TGGTAAAGGG GGAATGATGT CGAGGCCATC CTGGGCTGTA GAGCCAGGCC CTGGCTTGGG	60
GAGTGGGCAT TGTTAACTTG TTGCTGACTT TGTGTTGACC CCTGCATCAG CAACTATTTC	120
CTTAAATCCA GGATACAACT TGTTAAGTGT GACAGCTTTC CTTTACACAC CATTTTGTG	180
GGTGTATATA TATATTGAC TTGGGGAGAA TTATTTTTTA CAAAATACA AAATAGCTTT	240
TAA	243

(2) INFORMATION FOR SEQ ID NO: 136:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

AGCTAAGGTC CGGACTCTAT GGCATGACCC CAAAAACATT GGCTGGAAG ATTACACTGC	60
CTACAGGTGG CACCTGATTC ACAGGCCTAA GACAGGCTAC ATGAGAGTCT TAGTGATGA	120
AGGAAAGCAA GTCATGGCTG ACTCAGGACC AATTTATGAC CAAACCTACG CTGGTGGACG	180
GCTGGGCTGT TTGTCTTCTC CAAGAGATGG TCTATTCTCG GACCTCAAGT ATGAGTGCAG	240
AGATGCTAGA GAGCAGGCTC AGTCTCAGCA	270

(2) INFORMATION FOR SEQ ID NO: 137:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 260 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

TGACCTACGT GTAGTTGGTG TGCTTGTTGT CGAAGATGAG GGCCTCCTGG ATGAGCTGGT	60
GCTGCTGCTC CAGCAGGTCC AGGCTGGGCT TGTAGTCCAC GAGTCTGCGC TCGTACTGCT	120
TCAGGTGGCT CAGCTGGTCT TCCAGAGTCC CGTTCATCTC AATGGAGATG CGCCCGATCT	180
CCTCCATCTT AGTCTGGATC CACGGCCCCA CCATATTGGC TTGGCTGGCG AACTGTCCGC	240
GAAGGCTGCA TTGATTGCT	260

(2) INFORMATION FOR SEQ ID NO: 138:

-continued

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 187 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

AATTTTTTTT	TTCGACGGCC	CAACGGGGGC	TTGGTGGATG	GAAATATGGT	TTTGTGAGTT	60
ATTGCACTAC	CTGGAATATC	TATGCCTCTT	ATTTGCGTGT	ACTGTTGCTG	CTGATCGTTT	120
GGTGCTGTGT	GAGTGAACCT	ATGGCTTAGA	AAAACGACTT	TGTCTTAAAC	TGAGTGGGTG	180
TTCAGGG						187

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 197 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

CACCTGATTT	AAAGGAAAAG	CATTCTGACG	TAAGAAGCTG	AAAGGCGGCC	CTTGCGTGCT	60
TTGAACTTTC	TTATACAGCA	CAGTCATCTG	AAGCTTCCTG	TGTGACCAAG	ACAAGAACGC	120
GTGCACAAGA	CTGAGAAACA	GCAAGAAACA	ACCCGGCATT	CTACTTTCTC	AACACTATCA	180
TACTTTAAAC	CTTTCAC					197

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

CTAGCTTACG	CTAGTCCCCC	ATGCATAAAG	ACTGATCGCT	TTTCCTTAGA	AAGGTGAGAG	60
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GGTTAGGACA AGGCCGTGTG GTAACAACAC CCGCAGCTCG AAAAACCAAT GGCTTGTTAA	120
CGTGTCAGTG AGGCACTGTA CGGACGTCCA TAGTCCACAT CTTCAAATTC CCGCAGAAGG	180
CTTCCTATTC TTAAACTCTA	200

(2) INFORMATION FOR SEQ ID NO: 141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: <Unknown>
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

CTACATTTCT GTATCCATTC CTCTGTTGAA GGCTCTGGTT CTTTCCAGCT TCTGGCTATT	60
ATAAATAAGG CTGCTATAAA CACAGTGGAG GCATGTGTCC TTGTTATATT TTGGAGCATC	120
TTTTGGGTAT ATGCCCAGAA GTGCTATAGC TGGTTCCTCA GGTAGTACTA TGTCGAATTT	180
TCTGAGGAAC TGCCAGACTG ATTTCCAGAG TGGTTGTACC AGCTTGCAAT CCCACCAGCA	240
ATAGAGGAGT GTTCCTCTTT CTCTATATTC TTGCCAACAT CTGCTGTCAC CTGAGTGTTT	300

(2) INFORMATION FOR SEQ ID NO: 142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 243 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: <Unknown>
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

TGGTAAAGGG GGAATGATGT CGAGGCCATC CTGGGCTGTA GAGCCAGGCC CTGGCTTGGG	60
GAGTGGGCAT TGTTAACTTG TTGCTGACTT TGTGTTGACC CCTGCATCAG CAACTATTTT	120
CTTAAATCCA GGATACAACT TGTTAAGTGT GACAGCTTTC CTTTACACAC CATTTTTGTG	180
GGTGTATATA TATATTTGAC TTGGGGAGAA TTATTTTTTA CAAAATACA AAATAGCTTT	240
TAA	243

(2) INFORMATION FOR SEQ ID NO: 143:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

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(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:		
AGCTAAGGTC CGGACTCTAT GGCATGACCC CAAAAACATT GGCTGGAAAG ATTACACTGC	60	
CTACAGGTGG CACCTGATTC ACAGGCCTAA GACAGGCTAC ATGAGAGTCT TAGTGCAATGA	120	
AGGAAAGCAA GTCATGGCTG ACTCAGGACC AATTTATGAC CAAACCTACG CTGGTGGACG	180	
GCTGGGCTGT TTGTCTTCTC CAAGAGATGG TCTATTCTCG GACCTCAAGT ATGAGTGCAG	240	
AGATGCTAGA GAGCAGGCTC AGTCTCAGCA	270	
(2) INFORMATION FOR SEQ ID NO: 144:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 260 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:		
TGACCTACGT GTAGTTGGTG TGCTTGTTGT CGAAGATGAG GGCCTCCTGG ATGAGCTGGT	60	
GCTGCTGCTC CAGCAGGTCC AGGCTGGGCT TGTAGTCCAC GAGTCTGCGC TCGTACTGCT	120	
TCAGGTGGCT CAGCTGGTCT TCCAGAGTCC CGTTCATCTC AATGGAGATG CGCCCGATCT	180	
CCTCCATCTT AGTCTGGATC CACGGCCCCA CCATATTGGC TTGGCTGGCG AACTGTCGGC	240	
GAAGGCTGCA TTGGATTGCT	260	
(2) INFORMATION FOR SEQ ID NO: 145:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 255 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:		
TGACCATCGA TAAGTTTAAT AACTACAGAC TTTTCCCAAG ACTACAAAAG CTTCTTGAAA	60	
GTGACTACTT TAGATATTAC AAGGTGAACT TGAAGAAGCC TTGTCCTTTC TGGAATGACA	120	
TCAACCAGTG TGGAAGAAGA GACTGTGCCG TCAAACCCTG CCATTCTGAT GAAGTTCCTG	180	
ATGGAATTAA GTCTGCCGAG CTACAAGTAT TCTGAGGAAG CCCAACCGCA TTGAAGAATG	240	

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TGAGCAAGCT GAGCG 255

(2) INFORMATION FOR SEQ ID NO: 146:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 236 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

AACTCTGTGA ACCGTGCCTT TCTCTGTGGA GGTGGAGGTG TCGGTTGAAG ACAAGCGAGG	60
TCCTCCAAGG GGCTGTGTCT TATGTTGCCA TCTCCCCTTG TAGCTTGGCT GCCCACCTC	120
CAGACTGTGC GCCATGGCTC CAAGGCTGTG ACCCGCCACT GGAGTCATGC ACTTCCAGCG	180
GCAGAAGCTG ATGCTATAAC TGAGTATATT CCTCCAAACC TGCCATCAAC CCGAGA	236

(2) INFORMATION FOR SEQ ID NO: 147:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

ACTTCTCCAG AGAATTTAAG ATTGAGAATA GCCCTCGGGA TTTGCTCTT TACATTATTT	60
TTGGGACAGG AGAGCAGAGA AAGCTAAAGA AGACCGATGT CCCACTGCTG CAGAGGTTAC	120
TACAAGGACC ATCCAAAAGC AATGCTCGGA TCTTCCTCAT GGATAAAGAT GCAGAAGAAA	180
TCAGCAGAGA TGTGGCTCCG TACATTAATT TCACTTTTCT TTCTTGATC CATCCTTCAA	240
GATTAGATGA AGAAGAGAAA TGGAGATTGA GAGAATATGC AATCATACCG A	291

(2) INFORMATION FOR SEQ ID NO: 148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 255 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

-continued

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

AGGGTTACTT CAGGCTAAGG CAATAGAAAT CCATTTTAAG ATGGTGTGCT AAAGGCTTGA 60
TGGATGTTCA TCGTCTGTCT AAAGGAGAAT GAAGTCATCA ACAGGATGTC AGGGGAAAAGT 120
GAGATCATCG CAGAAAGTAT CAACTTAGCA CAAACACACA GGCATAGCTC CTGCAAGAGG 180
TGAATGCTGT CCCCAAATAC CTGAGGAACT ATCCCTTTGG GCAAGAAAAT AGACAAGTCC 240
ATGAAGTCTG GGTGA 255

(2) INFORMATION FOR SEQ ID NO: 149:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 284 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

GACCAGGTAC ACTTGAGCAA AGCACCCAGT ATTTAATTCC TTACAGAAAG GAGAGGAAAG 60
GTCTGCAGTT GGA CTGATGG TATGCTAACA CCGCAAATGA CTGTCATTG ATCTCAGAAG 120
TTCAGGATTG ATTGCTATGT TTTAGCTCTA ATTGTGAGAA ACAGTAGTCA TTTTAGTCTT 180
AAATTTTGCC CTCAGGAAAT TCAGGGAGAC TGAGCCTTCC TTCCCCCACC TTCGTAAAGC 240
CGAATTCCAG CACACGGCGG CCGTTACTAG TGGATCCGAG CTCG 284

(2) INFORMATION FOR SEQ ID NO: 150:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

TACAAGGTGG GATGGCAGGA ACTGAAGGCT TCTGTAAATC CAGTTTGGC TCTCTCTCTG 60
GTCTTTCTTT CTCTTCTGTT CTGTTTGAA GGGTTTCTGG TCTTTCAGGA GGTATTTTTT 120
TAATTTTCATG TTTTCTCTCT GTGGTACCTG CCCCTTGTTT GACGACAGGA GCTGATGGAG 180
GTGGCGGTTT CTTGGGTCTA TTCCCTTCCT TGTCAAAGTC CGATGGAAGT AACTTCACGA 240
AGTTGTCAGG AAACACGCCT CGTCTGCCAT TGAGTTCTCC TTCCCACCAG CCTACGCGAT 300
GCAGTCTTAT TGATGAGAGT CACTATATCT CCTTA 335

-continued

(2) INFORMATION FOR SEQ ID NO: 151:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 254 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: <Unknown>
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

TCACCCATGA CTTCTATGGA CTTGTCTATT TTCTTGCCCA AAGGGATAGT TCCTCAGGTA	60
TTTGGGGACA GCATTCACCT CTTGCAGGAG CTATGCCTGT GTGTTTGTGC TAAGTTGATA	120
CTTTCTGCGA TGATCTCACT TTCCCCTGAC ATCCTGTTGA TGACTTCATT CTCCTTTAGA	180
CAGACGATGA ACATCCATCA GGCCTTTATG CACACCATCT TAAAATGGAT TTCTATTGCC	240
TTAGCCTGAA GTCC	254

(2) INFORMATION FOR SEQ ID NO: 152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: <Unknown>
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

CCCATAGAGA TAGGTTTGCT CCAGAACCTG CAGCATTTGC ACATCACAGG GAACAAGGTG	60
GACATTCTGC CAAAACAGTT GTTTAAGTGC GTGAAGTTGA GGACTTTGAA CCTGGGGCAG	120
AACTGTATCG CCTCCCTGCC TGAGAAAAATC AGTCAGCTCA CCCAGCTCAC TCAGCTGGAG	180
CTGAAGGGCA ACTGCCTAGA CCGCCTGCCA GCCCAGCTGG CAGTGTCGAT GCTCAAGAAG	240
A	241

(2) INFORMATION FOR SEQ ID NO: 153:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 256 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: <Unknown>

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(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:		
CAATAATCCA GGTAAAATAG AGTAAAATAG TCTGCTAGCA GCAAGTTCCT ACCATACTTT	60	
CAACAACACT CACGAGATAC GGAATGATTA CAGCATTAAG AATATTTTCAG AAATGACAGG	120	
TAGGTGTGGT GGACAGGTGG CTCACATTCA AGACTCAAGT CTACTTAAAA AAGAAAATCT	180	
CACTAGCACT AGATTCTAGC TCCTTTGTTT CCCCCTTTCT TTTGGTTTCA AAGGCGTTTC	240	
TACAACCCAT AAGAGG	256	
(2) INFORMATION FOR SEQ ID NO: 154:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 404 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:		
GCCAAGCTAT TATGACACTA TAGATACTCA ACGTATCGAT CAACGTTGGT ACCGAGCTCG	60	
GATCCACTAG TAACGGCCGC CAGTGTGCTG GAATTCGGCT TGGATTGGTC AGAGCAGTGT	120	
GCAATATGAT CCAACTAAGT CTCCTCCCTT GGCCCCTCCC CAAAATGTTT GCAGTGTTAT	180	
TTTTGTGGGT TTTTTTTTAA CACCCTGACA CCTGTTGTGG ACATTGTCAA CCTTTGTAAG	240	
AAAACCCAAA TAAAAATTGA AAAATAAAAT AAAAAGAAAC CCATGAACAT TCGCACCCT	300	
TGTGGCTTCT GACTATCTTC CACAGAGGGA AGTTTAAAC CCAAACCTCC AAAGGTTTGA	360	
ACTACCTCAA GACACTTTCG CAGTGGAGTC GTAGACCAAT CCCA	404	
(2) INFORMATION FOR SEQ ID NO: 155:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 167 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:		
TAAATAAATT AAAAACTAT TAAACCTAAA AACGTCCACC AAACCCTAAA ACCATTAAAC	60	
AACCAACAAA CCCACTAACA ATTAAACCTA AACCTCCATA AATAGGTGAA GGCTTTAATG	120	
CTAACCCAAG ACAACCAACC AAAAATAATG AACTTAAAC AAAAATA	167	
(2) INFORMATION FOR SEQ ID NO: 156:		

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(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 212 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:		
GGTAAAGGGG ACCTGGAGAA CGCCTTCCTG AACCTGGTCC AGTGCATCCA GAACAAGCCC	60	
CTGTACTTCG CTGACCGGCT GTACGACTCC ATGAAGGGCA AGGGGACTCG AGACAAGGTC	120	
TGATTAGAAT CATGGTCTCT CGCAGTGAAG TGGACATGCT GAAAATCAGA TCTGAATTCA	180	
AGAGGAATAT GGCAAGTCCT GTACTACTAC AT	212	
(2) INFORMATION FOR SEQ ID NO: 157:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 214 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:		
AGAGCAGCAG GCCAGCTGTA CTTGGTTTGG CAAGAAAAAG AAGCAGTACA AAGATAAATA	60	
TTTGGCAAAG CACAACGCAG TGTTTGATCA ATTAGATCTT GTCACATATG AAGAAGTAGT	120	
CAAAC TGCCA GCATTCAAAA GGAAAACATT AGTCTTATTA GGTGCACATG GTGTTGGAAG	180	
AAGACACATA AAAAAATACC TCATCACAAA GCAC	214	
(2) INFORMATION FOR SEQ ID NO: 158:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 342 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:		
TCGGTCATAG TAGTAAGGGA AATCTCCCAG GTAAGATGAA TACTGCGGTA GGACGAACAA	60	
TCCTCCAGGA TGTTTGTTCC ATATTAAACT GTTACGTGAT ATGTGCTTGA ATATTCTGTC	120	

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CTGAATAATC TCTAGTGTAG TTAATACAAT CTTCTCAACT GAAGAAAAAT AAGCCTCCCA	180
CAAGAACTGT GTCTGCTGTC TAAGTGCTAG GATTTTATCC TGATGAATAG ACCTGATTGT	240
AGAAGGAATC TGTAATAGCA ATCTCTCATC GCCTATGACC GAAAGCCGAA TTCTGCAGAT	300
ATCCATCACA CTGGCCGGCC GCTCGAGCAT CGATCTAGAG GG	342

(2) INFORMATION FOR SEQ ID NO: 159:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

CTGCTTGATG ACAAAGGGTG TAGTCTTCAT CTTTTCCTGG ATTATTTTGG AAGTGACAGG	60
TGGAAATTCC ATCGTCACGT TTATGTGGTC TGTAAGCCA ACGATCTCAA ATTCTGGCGG	120
CTCAAGAGGA GCGTTTGCA GACGATGTA GTCTGAGCAG CGGCACACGG TCAAGTCCCC	180
TCTGTGCACT ATGACGATGG CGACGACGTA GCTCTCCATG CCCTCCAACC ACTTATCTGT	240
CACGTCACAT GATGACTTCG TGGTATCTGA ACAGTTCTTA ACCTTCGTCA GATTTTCGTC	300
TTT	303

(2) INFORMATION FOR SEQ ID NO: 160:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

AAATCGTTGC TTCAGAAAGA CTCAATAACA CTTACTTGTG CCTGGCTGTG CTGACAGTAC	60
ATTCTGTGTC ATTTTCCTTC ATGGGCGGAA CAGTCCACAG AGCTCACCAA CAAGTACTCC	120
AAACTGAGC AAGAGTTTAA GCTTCGAGAT GCAACCAGAT GAGCTTCTAG AAAAGCCCAT	180
GTCTCCCATG CAGTACGCAC GGTCTGGACT AGGGACAGCA GAGATGAATG GCAAATCAT	240
AGCTGCAGGT GGTATAACA GAGAGGAATG TCTTCGAACA GTTGAATGCT ATGATCCACA	300
TACAGATCAC TGGTCCTTCC TTGCTCCCAT GAGAACATCA AGCAG	345

(2) INFORMATION FOR SEQ ID NO: 161:

- (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 315 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:	
CTTTCCGAAG AGCACACCCCT CCTCTCAATG AGCTTGTGAG GTCTCTTTCT TCTCTTCCTT	60
CCAACGTGGT GCTAGCTCCA GGCGAGCGAC GTGAGAGTGC CACCTGAGAC AGACACCTTG	120
GTCTCAGTTA GAAGGAAGAT GCAGGTCTAA GAGGAATCCC CGCAGGTCTG TCTGAGCTGT	180
GATCAAGAAT ATTCCGCAAT GTGCCTTTTC TGAGATCGTG TTAGCTCCAA AGCTTTTTTC	240
TATCGCAGAG TGTTCAGTTT GTGTTTGTTT GTTTTTGTTT TGTTTTGTTT TTCCCTTGGC	300
GGATTTCCCG TGTGT	315
(2) INFORMATION FOR SEQ ID NO: 162:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 243 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:	
CCTATTGAAC GGTCTTGCAA TGACGAGCAT TCAGATGCTT AAGGAAAGCA TTGCTGCTAC	60
AAATATTTCT ATTTTGTAGAA AGGGTTTTTA TGGACCAATG CCCCAGTTGT CAGTCAAAGC	120
CGTTGGTGTT TTCATTGTTT AAAATGTCAC CTATAAAACG GGCATTATTT ATGTTTTTTT	180
TCCCTTTGTT CATATTCTTT TGCATTCTTG ATTATTGTAT GTATCGTGTA AAGGAAGTCT	240
GTA	243
(2) INFORMATION FOR SEQ ID NO: 163:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 243 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:		
CCTATTGAAC GGTCTTGCAA TGACGAGCAT TCAGATGCTT AAGGAAAGCA TTGCTGCTAC	60	
AAATATTTCT ATTTTATAGAA AGGGTTTTTA TGGACCAATG CCCCAGTTGT CAGTCAAAGC	120	
CGTTGGTGTT TTCATTGTTT AAAATGTCAC CTATAAAACG GGCATTATTT ATGTTTTTTT	180	
TCCCTTTGTT CATATCTTTT TGCATTCCTG ATTATTGTAT GTATCGTGTA AAGGAAGTCT	240	
GTA	243	
(2) INFORMATION FOR SEQ ID NO: 164:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 266 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:		
CCTGGGTCCG TCCTCCAACC CCTCACGCCC AAACCCTCCG ACTTTCCTT CTTGAAGTGA	60	
TCGGAAAGGG CAGTTTGTGA AAGGTTCTTC TGGCTAGGCA CAAGGCAGAA GAAGTATTCT	120	
ATGCAGTCAA AGTTTACAG AAGAAGCCAT CCTGAAGAAG AAAGGAAGGA AGCATATTAT	180	
GTCAGAGCGG AATGTTCTGT TGAAGAATGT GAAGCACCTT TTCCTGGTGG GCCTTCACTT	240	
CTCATTCAG ACCGCTGACA AGCTCT	266	
(2) INFORMATION FOR SEQ ID NO: 165:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 204 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: NO		
(v) FRAGMENT TYPE: <Unknown>		
(vi) ORIGINAL SOURCE:		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:		
GATGCTGAAC AAAAAAGAA AGAAGAAAAG GAAGAGGAGG AGCAAGAGAA GCTGAAGGGA	60	
GGGAGCCTTG GCGAAAATCA GATCAAAGAT GAGAAGATTA AAAAGGACAA AGAGCCCCAA	120	
GAAGAGTCAA GAGCTTCTTG GATAGAAAGA AAGGATTTAC AGAGTGAGGC GCAGAATGGA	180	
GATTCATGAC CCACAACTT AAAC	204	
(2) INFORMATION FOR SEQ ID NO: 166:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 200 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		

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(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:	
AAAGCCAATT GGTAGAGAAA TTGAAGACAC AAATGCTGGA TCAGGAAGAG CTTCTGGCAT	60
CAACCAGAAG GGATCAAGAT AATATGCAAG CTGAACTGAA TCGCCTCCAA GCAGAAAATG	120
ATGCTTCTAA AGAAGAGTAA AGAGTTTTAC AGGCCTTAGA GGA CTGCTGT TAATTATGAT	180
CAGAGTTCAG GAGTTAAGAC	200
(2) INFORMATION FOR SEQ ID NO: 167:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 337 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:	
CTGCTTGATG TCCTGTGTAG CGAATGTCAC AGCGTACAAC ATTGTTAGTG TAGTCTGATT	60
CAGGCACCAG GTAGCTGGGG TTTACACTGA CCTTTAGAAT GTAGTTTCCA GGTTGTACAT	120
CTGTAATATC AATCCACTGG CAGTCTATGT CTGCCGCATA GGTGTCATAA CATCCAGGAC	180
TCAATCCCTG TGTGTGTGCA GTGCACGCAA AGGCCCTGTG GTACCCATAG TCACAGGACG	240
TGTCCTCCAG ACAGAAGCTT GCTTTGTGGC CTTCAGCCAC TCTCCTCTGT GTGTTGGCAT	300
CAACGAGAAG CCGAATTCTC GAGATATCCA TCACACT	337
(2) INFORMATION FOR SEQ ID NO: 168:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 337 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:	
CTGCTTGATG TCCTGTGTAG CGAATGTCAC AGCGTACAAC ATTGTTAGTG TAGTCTGATT	60
CAGGCACCAG GTAGCTGGGG TTTACACTGA CCTTTAGAAT GTAGTTTCCA GGTTGTACAT	120

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CTGTAATATC AATCCACTGG CAGTCTATGT CTGCCGCATA GGTGTCATAA CATCCAGGAC	180
TCAATCCCCTG TGTGTGTGCA GTGCACGCAA AGGCCCTGTG GTACCCATAG TCACAGGACG	240
TGTCCTCCAG ACAGAAGCTT GCTTTGTGGC CTTCAGCCAC TCTCCTCTGT GTGTTGGCAT	300
CAACGAGAAG CCGAATTCTC GAGATATCCA TCACACT	337

(2) INFORMATION FOR SEQ ID NO: 169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 374 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

GATCTGACAC TACAGCATGA GCGTTAGATT TCATAAAATT ATTTTCTTC TAAATGCTGG	60
AAACTCTAAG GGTTTATTCA GAAAAAAAC TGGCCAATTT TCAAATGGCT TAGAAGCAGG	120
GTTAATTAAG TATTGAATGA GCCACTGTGA TATCCTGATG ACACCCAGTC ACAATGACAG	180
TTTTGAAGCA TACAACCAA ACAATTGAGA TCTCAAACT ATTTTACATC ACTTATGGTA	240
ATGTTATGTA AAAATGAAAA TGCTTCTGT GGAAGTTACA TTCTTTACCA GGTCTTTAAC	300
ATAAATTAAC ACGACGTCGA GTAAGCCTTT GTTCGGAAGA CAACTAGTT TGTGAGTTCA	360
GTCAGATCCC AGCT	374

(2) INFORMATION FOR SEQ ID NO: 170:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

AGTTGCCAGG ACCACCACCA TAGTTGCCAG GTTCATCATA AACAAATCCA ACATCAATCT	60
TAAATTCCCC CATCAGACAA TCTGCCCTCA AAGAATGGGA ATTATAAACC CGGATACTGA	120
TGATCTCATC CATGAGCTCA GAGGGTGTGA TGTGCACATT GTAGAAAAAT AACTCGTCAA	180
AAAACGGATT GTTCCCTCTC TTGATTCTCG TGCGATGCGT CTGACCACAG ATGTGAACTT	240
TCACCACGGG CCTTATGTTG TTGCCGCATA ACTGACGGCC CTCGATCACT CTGACACGGA	300
TCTGGAAATC TGTGGCTTGT TGGACAGCAT CCTT	334

(2) INFORMATION FOR SEQ ID NO: 171:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

AAGCCGTGTC CCAAAGAATG GATAGAGACG CGATCAGATG CGACAGTGCT GTGGAGAAAG	60
CCCAGGAACC TGCACAATTG CCCTGGTCCA ATGGCTCGTG GATCAGGTTG GGCCACTTCT	120
CTGAAGCTTC AAAGGCAGTG GGTAGCACTT CCCCTTGGCC CAGCACCGTA TAAATCTCAT	180
TCATATTCAT GACAGTGGAG GATGGGCGGA TTGTGCCCAG GCGGTACGGA ATGCCCTCAT	240
CCAGGGTCAT GCCCCAGAAG GCACTGTGGT TCCCAGCCTG CCACCCGTAG TTGCCTCGGT	300
TGATGGCTTT AATCATGTCT GGTCACTAGA CACGGCTTAA GCGAATCTCG AGATATCCAT	360
CACACTGGCG GCGTCGAGAT	380

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 353 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: <Unknown>

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

AAGCCGTGTC TGATGATGGA GGTAGTGGTG GGGGAGGAGG GACTGAGGGT CCTGAGGTGG	60
TGGCCCCCTGG AACTGATCCC ACATAGTTAC CCACTGCTAG TTCTGACCCC GTGGACAACG	120
TGCCAGAGGC CATGACTGGC AGTATGGCAA TGTCCCCATC CCCTTTCTTC TTAATTTTAA	180
TGGTCCCTTG TTTCTCCAGT TCGTGAATCT TTTTTTCCAG GGTAGACTGT CTTTGAATGG	240
CTTCTTCCTT TTCTTTGACC ATTTTCTTA ACGTGTGAAC TTGGGTATTT GCATCTTTGT	300
AGATTTCCGG ACAACATCAG TTCCTTATTC CTCTGCATAA GTTGCTTTCA GTT	353

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

-continued

(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:	
CGAGTCAGAC ACATGAAAGC AAAACGCGGG CAGATAAAAC GATCGCCTTA CCTTCTAGCA	60
AAAATCTGAA GCTTGTGTCA GAAACAAAGA CTCAGAAAGG TTTGTTTTCA GATGAAGAAG	120
ACTCTGAGGA TTTGTTTTCT TCTCAAAGTT CAAGTAAGCC AAAAAGTGCA TCACTTTCAT	180
CCAGCCAGCC CCCAACATCA GTCTCCCTTT TTGGTGATGA AGATGAAGAG GACAGTCTTT	240
TTGGGAGTGC AGCAGCTAAG AAGCAGACTT CATCTCTACA ACCTCAGAGT CAAGAGAAAG	300
CAAAGCCTTC CGAGCAGCCC TCAAAGAAGA CATCTGCCTT GTTGTCAGA	350
(2) INFORMATION FOR SEQ ID NO: 174:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 377 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:	
CGAGTCAGAC TTAATTTAAA AACGAAACAA AACAAAAATA ACATAGTTTA GAAATCAAGG	60
AGAAAGGACA GATAGTCTAA GAAAAAAGAC AACACAAAAG AGGGGCAGGG CGGCCAGCTT	120
GCATCAGGGA TCTTGCTGG AGACCTGCTT TGAATAGGTT TCTTGCAGGT ATTTCTTAAA	180
TGCTGTGGGG TTTTCCAGA GTTCCGCAGC GTGTGTGTTT AAAGGGCTAT CGATGTTGGG	240
TTCTCCTAGC AGGCTCTGGA TAGAGAGCAA GATAGTCCTG ACATCATATA GTGCAGACCA	300
CTTATCCTTG AGGATGTCCG GCAGATGTTG CCTGGGTGTC ACGTTGGGGT GGTAGCAGGG	360
TGTGAGGAAC TTCACTG	377
(2) INFORMATION FOR SEQ ID NO: 175:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 326 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: <Unknown>	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:	
CGAGTCAGAC ACTCCTGGCT CCTGGATTCT TTAGATGCCT CCATCAGACT GGGTACTTTA	60
GATGCCTCCA TCAGACTACT TCGTCATTGT ATTTCTCAGT TCGCTCAGGG CAAGCGGCAG	120

-continued

TCTCTGGGCT	GCTGTGGCAG	GTGCCACCAC	TGCATTTAAA	AGTTAAAATT	TCTTCAAATA	180
TTCCCATCAA	GGCCTTGTAG	CCTCTGAGAT	TGGTTTACTA	TTTGCCCACT	TATTTAAAGC	240
TCTCTGCATT	CCTTCCTGAT	TTAATATTGC	TATGGCCAGG	ACAATGTGTA	GAAGTAAAAA	300
GGATATCATA	TTTACAGGTG	TAACGC				326

I claim:

1. A method for identifying a sequence expressed in a metastasis comprising the steps of:

[a)] transfecting an oncogenic sequence into a mammalian cell to form a population of transfected cells;

[b)] administering transfected cells to a primary site of a host mammal to form a primary tumor;

[c)] maintaining said mammal for a period of time sufficient to develop a metastasis at a secondary site;

[d)] amplifying expressed RNA sequences of the transfected cells and expressed RNA sequences of the metastasis by differential-display PCR; and

[e)] comparing the amplified expressed RNA sequences of the transfected cells with the amplified expressed RNA sequences of the metastasis and identifying the sequence expressed at a higher level in the metastasis as compared to the expressed RNA sequences of the transfected cells.

2. The method of claim 1 wherein the mammalian cell is transfected by calcium phosphate transfection, viral transduction, lipofection, dextran sulfate transfection or electroporation.

3. The method of claim 1 wherein the oncogenic sequence is a sequence of the gene that [erodes] *encodes* the oncoproteins p21, p34, *mutant* p53, myc, ras or src.

4. The method of claim 1 wherein the oncogenic sequence is a sequence that enhances metastatic potential.

5. The method of claim 4 wherein the oncogenic sequence is a sequence of the gene that encodes cyclin D1, caveolin or TGF- β 1.

6. The method of claim 1 wherein the mammalian cell is treated with an agent that alters gene expression prior to the administration of said cell to said host mammal.

7. The method of claim 6 wherein the agent is benzantracene (BA), dimethyl benzantracene (DMBA) or 5-azacytidine.

8. The method of claim 1 wherein the mammalian cell is a primary cell or an established cell line.

9. The method of claim 1 wherein the mammalian cell is [isolate] *isolated* from urogenital sinus tissue.

10. The method of claim 1 wherein the mammalian cell is a fetal cell.

11. The method of claim 1 wherein the mammalian cell contains a gene selected from the group consisting of TGF- β 1, cyclin D1, p21, p34, *mutant* p53, ras, and myc.

12. The method of claim 1 wherein the mammalian cell is isolated from the same species as the host mammal.

13. The method of claim 1 wherein the mammalian cell and the host mammal are histocompatible.

14. The method of claim 1 wherein the mammalian cell and the host mammal are syngeneic.

15. The method of claim 1 wherein the transfected cell is isolated and maintained in vivo or in vitro for a period of time prior to introduction of said cell to the host mammal.

16. The method of claim 1 wherein the expressed sequences of the transfected cells are obtained from a cell line of immortalized transfected cells.

17. The method of claim 1 wherein the transfected cells are administered to the primary site by subcutaneous implantation.

18. The method of claim 1 wherein the host mammal is a mouse, a rabbit or a primate.

19. The method of claim 1 wherein the host mammal is a syngeneic, xenogeneic, immunocompromised or transgenic host mammal.

20. The method of claim 1 further comprising suppressing expression of TGF- β in the host mammal prior to the introduction of transfected cells into said host mammal.

21. The method of claim 1 wherein the primary site is the renal capsule, the prostate or the testis.

22. The method of claim 1 wherein the secondary site is selected from the group of sites consisting of lung, kidney, liver, lymph nodes, brain, bone, testis, spleen, ovaries and mammary.

23. The method of claim 1 wherein differential display PCR is performed with an anchor primer and a variable primer.

24. The method of claim 22 wherein the anchor primer comprises a polythymidine sequence and a dinucleotide sequence connected to a 3'-terminus.

25. The method of claim 24 wherein the polythymidine sequence comprises between about 5 to about 30 thymidines.

26. The method of claim 24 wherein the dinucleotide sequence is selected from the group of sequences consisting of AA, AG, AC, AT, GA, GG, GC, GT, CA, CG, CC and CT.

27. The method of claim 23 wherein the anchor primer or the variable primer comprise a detectable moiety selected from the group consisting of radioactive moieties, phosphorescent moieties, magnetic moieties, luminescent moieties and conjugatable moieties.

28. The method of claim 23 wherein the anchor primer and the variable primer have a common sequence.

29. The method of claim 7 wherein the agent is a retinoid.

30. A method for identifying a sequence expressed in metastasis comprising the steps of:

[a)] pretreating a mammalian cell with an agent that enhances metastatic potential to form a population of cells predisposed to metastasis;

[b)] introducing the pretreated cells to a primary site of a host mammal;

[c)] maintaining said mammal for a period of time sufficient to develop a metastasis at a secondary site;

[d)] amplifying expressed RNA sequences of pretreated cells and expressed RNA sequences of the metastasis by differential-display PCR; and

[e) identifyg] *identifying* the sequence expressed at a higher level in the metastasis as compared to expressed RNA sequences of the pretreated cells.

31. The method of claim 30 further comprising the step of treating cells of the primary or secondary sites with a genotoxic agent prior to amplification.

32. The method of claim 31 wherein the genotoxic agent is benzenanthracene (BA), dimethyl benzanthracene (DMBA) or 5-azacytidine.
33. The method of claim 30 further comprising the step of comparing the expressed sequences amplified from the metastasis with expressed sequences amplified from mam-
malian cells before pretreatment to identify the sequence selectively expressed in the metastasis.
34. The method of claim 30 wherein the chemical com-
pound is a benzenanthracene, dimethyl benzanthracene, or
5-azacytidine.
35. The method of claim 30 wherein the mammalian cell is transfected, prior to the administration of said cell to the host mammal, with an oncogenic sequence before or after
treatment of said cell with the agent that enhances metastatic
potential.
36. The method of claim 30 wherein the mammalian cell is a cell line.
37. The method of claim 30 wherein the mammalian cell is isolated from lymphatic tissue, hematopoietic cells, repro-
ductive tissues or urogenital sinus tissue.
38. The method of claim 30 wherein the mammalian cell is a fetal cell.
39. The method of claim 30 wherein the mammalian cell is isolated from a transgenic animal.
40. The method of claim 30 wherein the primary site is the renal capsule, the prostate or the testis.

41. The method of claim 30 wherein the secondary site is selected from the group of sites consisting of lung, kidney, liver, lymph nodes, brain, bone, testis, spleen, ovaries and mammary.
42. The method of claim 30 wherein differential display PCR is performed using an anchor primer and a variable primer.
43. A method of identifying a sequence expressed in metastasis comprising the steps of:
- pretreating a population of mamalian cells with an agent that enhances metastatic potential to form a population of cells predisposed to metastasis;*
- introducing the pretreated cells to a primary site of a host mammal;*
- maintaining said mammal for a period of time sufficient to develop a metastasis at a secondary site;*
- amplifying expressed RNA sequences of the mammalian cells before pretreatment and expressed RNA sequences of the metastasis by differential-display PCR; and*
- comparing the expressed sequences amplified from the metastasis with expressed sequences amplified from mammalian cells before pretreatment to identify the sequence selectively expressed in the metastasis.*

* * * * *

UNITED STATES PATENT AND TRADEMARK OFFICE
CERTIFICATE OF CORRECTION

PATENT NO. : RE. 38,392 E
DATED : January 20, 2004
INVENTOR(S) : Timothy C. Thompson

Page 1 of 1

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

Column 163,

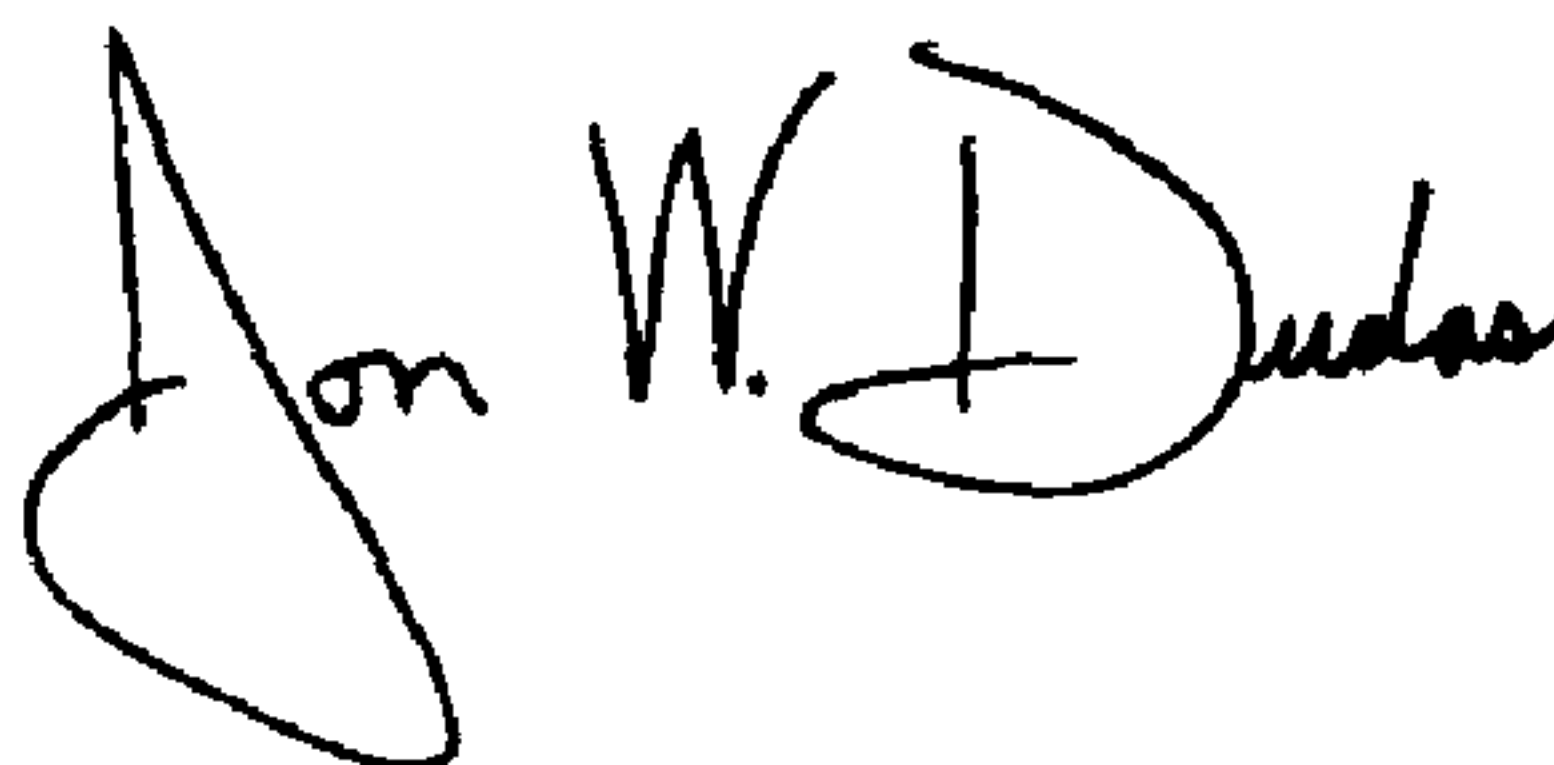
Lines 44-45, delete "benzantracene" please insert -- benzanthracene --.

Column 165,

Lines 2 and 10, delete "benzenthracene" please insert -- benzanthracene --.

Signed and Sealed this

Sixteenth Day of March, 2004

A handwritten signature in black ink, reading "Jon W. Dudas". The signature is stylized, with a large loop for the "J" and a cursive "Dudas".

JON W. DUDAS
Acting Director of the United States Patent and Trademark Office