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FIG.5B

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50 Asp Thr Lys Val Asn Phe Tyr Ala Tip Lys Arg Met Glu Val Gly
   GAC ACC AAA GTT AAC TTC TAT GCC TGG AAG AGG ATG GAG GTC GGG
60 Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu
   CAG CAG GCT GTA GAA GTC GAG GGC CAG GGC CTG GCC CTG CTC TCA GAA
70 Ala Val Leu Arg Gly Gln Ala Val Leu Ala Asn Ser Ser Gln Pro
   GCT GTC CTG CGG GGC CAG CAG GCC GTG TTG GCC AAC TCT TCC CAG CCT
80 Phe Glu Pro Leu Gln Leu His Met Asp Lys Ala Ile Ser Gly Leu
   TTC GAG CCC CTG CAG CTG CAC ATG GAT AAA GCC ATC AGT GGC CTT
90 Arg Ser Ile Thr Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Glu Ala
   CGC AGC ATC ACC ACT ACT CTG CTT CGG GCG GCG CTG GGA GCC CAG GAA GCC
100 Ile Ser Leu Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
   ATC TCC CTC CCA GAT GCG GCC TCG GCT GCT CCA CTC CGA ACC ATC
110 Thr Ala Asp Thr Phe Cys Lys Leu Phe Arg Val Tyr Ser Asn Phe
   ACT GCT GAC ACT TTC TGC AAA CTC TTC CGA GTC TAC TCC AAT TTC
120
130
140

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## FIG. 5C

150 Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Arg  
 CTC CGG GGA AAG CTG AAG CTG TAC ACG GGG GAG GCC TGC AGG AGA  
 160  
 Gly Asp Arg OP  
 CGG GAC AGA TGA CCAGGTGGTCCAGCTGGGCACATCCACCACCTCCCTCACCACA  
 CTGCCGTGCCACACCCCTCCCTCACCACCTCCCGAACCCTCGAGGGGCTCTCAGCTAAG  
 CGCCAGCCTGTCCCAFGGACACTCCAGTGCCAGCAATGACATCTCAGGGGCCAGAGGAAC  
 TGTCCAGAGCAACTCTGAGATCTAAGGATGTCCAGGGGCCAACTTGAGGGCCCCAGAGC  
 AGGAAGCATTTCAGAGAGCAGCCTTTAAACTCAGGAGCAGAGACAATGCAGGAAACACCTT  
 GAGCTCACTCGGCCACCCTGCAAAATTTGATGCAAGGACACCGCTTTGGAGGCAATTTACCTG  
 TTTTGGCACTACCATCAGGGACAGGATGACTGGAGAACTTAGGTGGCAAGCTGTGACTT  
 CTCAAGGCCCTCAGGGCACTCCCTTGGTGGCAAGAGCCCCCTTGACACTGAGAGAATATT  
 TTGCAATCTGCAGCAGGAAAAATTACGGACAGGTTTGGAGGTTGGAGGGTACTTGACAG  
 GTGfGTGGGAAGCAGGGCGGJAGGGTGGAGCTGGGATGCGAGfGAGAACCCTGAAGAC  
 AGGATGGGGGCTGGCCTCTGGTTCTCGTGGGGTCCAAGCTT  
 HindIII



FIG.6B

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ATTGCCAAGAGGTGGCTGGGTTCAAGGACCGGGGACTTGTCAAGGACCCCGGAAGGGGGGGGGTGGG
GCAGCCYCCACCGTCCCGGGGACTTGGGGAGTTCTTGGGGATGCCA AAAACCTGGCCCTGTTGAGGGGCA
CAGTTGGGGTTGGGGAGGAGGTTTGGGGTTCTGCTGTGCAGTTGTGTGCTGTTGTCAAGTGTCTCG[I.S.]
TTGCACACGCACAGATCAATAAGCCAGAGGCCAGCACCTGAGTGTGCTGATGGTTGGGACAGGAAGGACGAG
CTGGGGCAGAGACGTTGGGGATGAAGGAAGCTGTCTCTCCACAGCCACCCCTTCTCCCCCCCCGCTGACTCT
-23 -20
Glu Cys Pro Ala Trp Leu Trp Leu Trp Leu Leu Ser Leu
CAGCCTGGCTATCTGTTCTAG AA TGT CCT GCC TGG CTG TGG TGG CTT CTC CTG TCC CTG
-10 -1 +1
Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Leu Gly Ala Pro Pro Arg Leu Ile Cys
CTG TCG CTC CCT CCT CTG GGC CTC CCA GTC CTG GGC GGC CCA CCA CGC CTC ATC TGT
10 20 *
Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile
GAC AGC CGA GTC CTG GAG AGG TAC CTC TTG GAG GCC AAG GAG GCC GAG AAT ATC
26
Thr
ACG GTGAGACCCCTTCCCCAGCACATTCACAGAACTCACGGCTCAGGGGCTTCAGGGAACCTCCCTCCAGAT
CCAGGAACCTGGCAGCTTGGTGGGGTGGAGTTGGGAAGCTAGACACTGCCCCCTACATAAGAAATAGTC

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FIG.6C

TGGTGGCCCCAAACCATACCTGAAACTAGGCAAGGAGCAAGCCAGCAGATCCTACGCCCTGTGGCCAGGG

CCAGAGCCTTCAGGGACCCCTTGACTCCCGGGCTGTGTGCATTTTCAG  
27 Thr Gly Cys Ala Glu 30  
ACG GGC TGT GCT GAA

\* 40  
His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr  
CAC TGC AGC TTG AAT GAG AAT ATC ACT GTC CCA GAC ACC AAA GTT AAT TTC TAT

50  
Ala Trp Lys Arg Met Glu 55  
GCC TGG AAG AGG ATG GAG GTGAGTTCCTTTTTTTTTTTTTTTTCTCTTTTGGAGATCTCATT

TGGAGCCTGATTTGGATGAAAGGGAGAAATGATCGGGGAAAGTAAATGGAGCAGCAGAGATGAGGCT  
GCC TGGGCGCAGAGGCTCACGTCTATAATCCCAGGCTGAGATGGCCGAGATGGAGAAATTGCTTGAGCCCT

GGAGTTTCAGACCAACCTAGGCAGCATAGTGAGATCCCCCATCTCTACAACATTTAAAAAATTAGTCAG  
GTGAAGTGGTGCATGGTGGTAGTCCCAGATATTTGGAAGGCTGAGGCGGGAGGATCGCTTGAGCCCAGGAA

TTTGAGGCTGCAGTGAGCTGTGATCACACCCACTGCCACTCCAGCCTCAGTGACAGAGTGAGGCCCTGTCTCA

FIG. 6D

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AAAAAGAAAAGAAAATAATGAGGGCTGTATGGAATACATTTCATTTCACCTCACTCACT
CACTCATTCAATTCATTCAACAAGTCTTATTGCATACCTTCTGTTTGGCTCAGCTTGGTGTGG
GGCTGCTGAGGGCAGGAGGAGGGGTGACATGGGTCAGCTCGACTCCAGAGTCCACTCCCTGTAG
56          60          70          80          90
Val Gly Gln Ala Val Glu Val Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala
GTC GGG CAG CAG GCC GTA GAA GTC TGG CAG GGC CTG GCC CTG TCG TCG GAA GCT

Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu
GTC CTG CGG GGC CAG GCC CTG TTG GTC AAC TCT TCC CAG CCG TGG GAG CCC CTG
          80          *          90

Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu
CAG CTG CAT GTG GAT AAA GCC GTC AGT GGC CTT CGC AGC CTC ACC ACT CTG CTT
110          115
Arg Ala Leu Gly Ala Gln
CGG GCT CTG GGA GCC CAG GTGAGTAGGAGCGGACACTTCTGTGCTTGCCTTCTGTAGAAGGGGA
GAAGGGTCTTGCTAAGGAGTACAGGAACGTGCCGTATTCCTTCCCTTCTGTGGCACTGCAGCGACCTCCT
116          120
Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
GTTTTCTCCTTGGCAG AAG GAA GCC ATC TCC CCT CCA GAT GCG GCC TCA GCT GCT

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## FIG. 6E

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130 Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser
    CCA CTC CGA ACA ATC ACT GCT GAC ACT TTC CGC AAA CTC TTC CGA GTC TAC TCC
    140
    Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly
    AAT TTC CTC CGG GGA AAG CTG AAG CTG TAC ACA GGG GAG GCC TGC AGG ACA GGG
    150
    Asp Arg OP
    GAC AGA TGA CCAGGTGTCCACCCTGGGCATATCCACCCTCCCTCACCACAAATTTGTGCCACA
    CCTTCCCCCGCCACTCCTGAACCCCGTCGAGGGGCTCTCAGCTCAGGCCAGCCTGTCCCATGGACACTCC
    AGTSCCAGCAATGACATCTCAGGGGCCAGAGGAACCTGTCCAGAGAGCAACTCTGAGATCTAAGGATGTAC
    AGGCCAACTTGAAGGGCCAGAGCAGGAAGCATTGAGAGAGCAGCTTTAAACTCAGGGACAGAGCCCATGC
    TGGGAAGACGCCCTGAGCTCAGCTCGGCACCCCTGCAAAATTTGATGCCAGGACACCGCTTTGGAGCGGATTTAC
    CTGTTTTCGCACCTACCATCAGGGACAGGATGACCTGGAGAACTTAGGTGGCAAGCTGTGACTTCTCCAGG
    TCTCACGGGCATGGGCACCTCCCTTGGTGGCAAGAGCCCTTGACACCCGGGTGGTGGGAACCATGAAGAC
    AXGATXGGGGCTGGCCTCTGCTCTCATGGGTCCAAAGTTTTGTGTATTTCTCAACTATTGACAGACTGAA
    ACACAATATGAC

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FIG. 7

		-1 1	
<u>XbaI</u>		<u>MetAla</u>	
CTAG	AAACCATGAG	GGTAATAAAA	TAATGGCTCC
	TTTGGTACTC	CCATTATTTT	ATTACCGAGG
			CGCGCGTCTG
			CGGCGCAGAC
ATCTGCGACT	CGAGAGTTCT	GGAACGTTAC	CTGCTGGAAG
TAGACGCTGA	GCTCTCAAGA	CCTTGCAATG	GACGACCTTC
			GATTTCTTCG
TGAAAACATC	ACCACTGGTT	GTGCTGAACA	CTGTTCTTTG
ACTTTTGTAG	TGGTGACCAA	CACGACTTGT	GACAAGAAAC
			TTGCTTTTGT
TTACGGTACC	AGACACCAAG	GTAACTTCT	ACGCTTGGAA
AATGCCATGG	TCTGTGGTTC	CAATTGAAGA	TGCGAACCTT
			TGCATACCTT
GTTGGTCAAC	AAGCAGTTGA	AGTTTGGCAG	GGTCTGGCAC
CAACCAGTTG	TTCGTCAACT	TCAAACCGTC	CCAGACCGTG
			ACGACTCGCT
GGCTGTACTG	CGTGGCCAGG	CACTGCTGGT	AAACTCCTCT
CCGACATGAC	GCACCGGTCC	GTGACGACCA	TTTGAGGAGA
			GTCGGCACCC
AACCGCTGCA	GCTGCATGTT	GACAAAGCAG	TATCTGGCCT
TTGGCGACGT	CGACGTACAA	CTGTTTCGTC	ATAGACCGGA
			CTCTAGAGAC
ACTACTCTGC	TGCCTGCTCT	GGGTGCACAG	AAAGAGGCTA
TGATGAGACG	ACGCACGAGA	CCCACGTGTC	TTTCTCCGAT
			AGAGAGGCGG
GGATGCTGCA	TCTGCTGCAC	CGCTGCGTAC	CATCACTGCT
CCTACGACGT	AGACGACGTG	GCGACGCATG	GTAGTGACGA
			CTATGGAAGG
GCAAACCTGTT	TCGTGTATAC	TCTAACTTCC	TGCGTGGTAA
CGTTTGACAA	AGCACATATG	AGATTGAAGG	ACGCACCATT
			TGACTTTGAC
TATACTGGCG	AAGCATGCCG	TACTGGTGAC	CGCTAATAG
ATATGACCGC	TTCGTACGGC	ATGACCACTG	GCGATTATCA
			GCT

SalI



FIG. 9

	-20	-10	+1	10	20	30	40
Human	MGVHECPAWLWLLLSLPLGLPVLGAPPRLICDSRVLERLLEAKEAEENITTCGCAEHCSLNENITVPPDTK						
Monkey	MGVHECPAWLWLLLSLPLGLPVPGAPPRLICDSRVLERLLEAKEAENVTMGCSESCSLNENITVPPDTK						
	50	60	70	80	90	100	110
Human	VNFYAWKRMEVGQQAWEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSITLLRALGAQKE						
Monkey	VNFYAWKRMEVGQQAWEVWQGLALLSEAVLRGQAVLANSSQPFEPQLHMDKAVISGLRSITLLRALGAQ-E						
	120	130	140	150	160		
Human	AISPPDAASAAPLRTITADTFRKLFrvysNfLrGKkLkLYTGEACRTGDR						
Monkey	AISLPDAASAAPLRTITADTfckLfrvysNfLrGkLkLYTGEACRRGDR						

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**FIG. 10**

1.           AATTCTAGAAACCATGAGGGTAATAAAAATA  
2.           CCATTATTTTATTACCCTCATGGTTTCTAG  
3.           ATGGCTCCGCCGCGTCTGATCTGCGAC  
4.           CTCGAGTCGCAGATCAGACGCGGCGGAG  
5.           TCGAGAGTTCTGGAACGTTACCTGCTG  
6.           CTTCCAGCAGGTAACGTTCCAGAACT  
7.           GAAGCTAAAGAAGCTGAAAACATC  
8.           GTGGTGATGTTTTTCAGCTTCTTTAG  
9.           ACCACTGGTTGTGCTGAACACTGTTC  
10.          CAAAGAACAGTGTTTCAGCACAACCA  
11.          TTTGAACGAAAACATTACGGTACCG  
12.          GATCCGGTACCGTAATGTTTTTCGTT



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**FIG. 12**

1.           AATTCGGTACCAGACACCAAGGT  
2.           GTTAACCTTGGTGTCTGGTACCG  
3.           TAACTTCTACGCTTGGAAACGTAT  
4.           TTCCATACGTTTCCAAGCGTAGAA  
5.           GGAAGTTGGTCAACAAGCAGTTGAAGT  
6.           CCAAACTTCAACTGCTTGTTGACCAAC  
7.           TTGGCAGGGTCTGGCACTGCTGAGCG  
8.           GCCTCGCTCAGCAGTGCCAGACCCTG  
9.           AGGCTGTACTGCGTGGCCAGGCA  
10.          GCAGTGCCTGGCCACGCAGTACA  
11.          CTGCTGGTAAACTCCTCTCAGCCGT  
12.          TTCCCACGGCTGAGAGGAGTTTACCA  
13.          GGGAACCGCTGCAGCTGCATGTTGAC  
14.          GCTTTGTCAACATGCAGCTGCAGCGG  
15.          AAAGCAGTATCTGGCCTGAGATCTG  
16.          GATCCAGATCTCAGGCCAGATACT

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FIG. 13

ECORI KpnI  
 A ATTGGTACC AGACACCAAG GTTAACTTCT ACGCTTGGAA ACGTATGGAA  
GCCATGG TCTGTGGTTC CAATTGAAGA TGCGAACCTT TGCATACCTT

GTTGGTCAAC AAGCAGTTGA AGTTTGGCAG GGTCTGGCAC TGCTGAGCGA  
CAACCACCTTG TTCGTCAACT TCAAAACCGTC CCAGACCCGTG ACGACTCGCT

GGCTGTACTG CGTGGCCAGG CACGTGCTGGT AAACTCCTCT CAGCCGTGGG  
CCGACATGAC GCACCCGGTCC GTGACGACCA TTTGAGGAGA GTCGGCACCC

AAACCGCTGCA GCTGCATGTT GACAAAGCAG TATCTGGCCT GAGATCTG  
TTGGCGGACGT CGACGTACAA CTGTTTCGTC ATAGACCCGA CTCTAGACCTAC

BamHI