

EXHIBIT 6

Part 2 of 5

FIG. 2

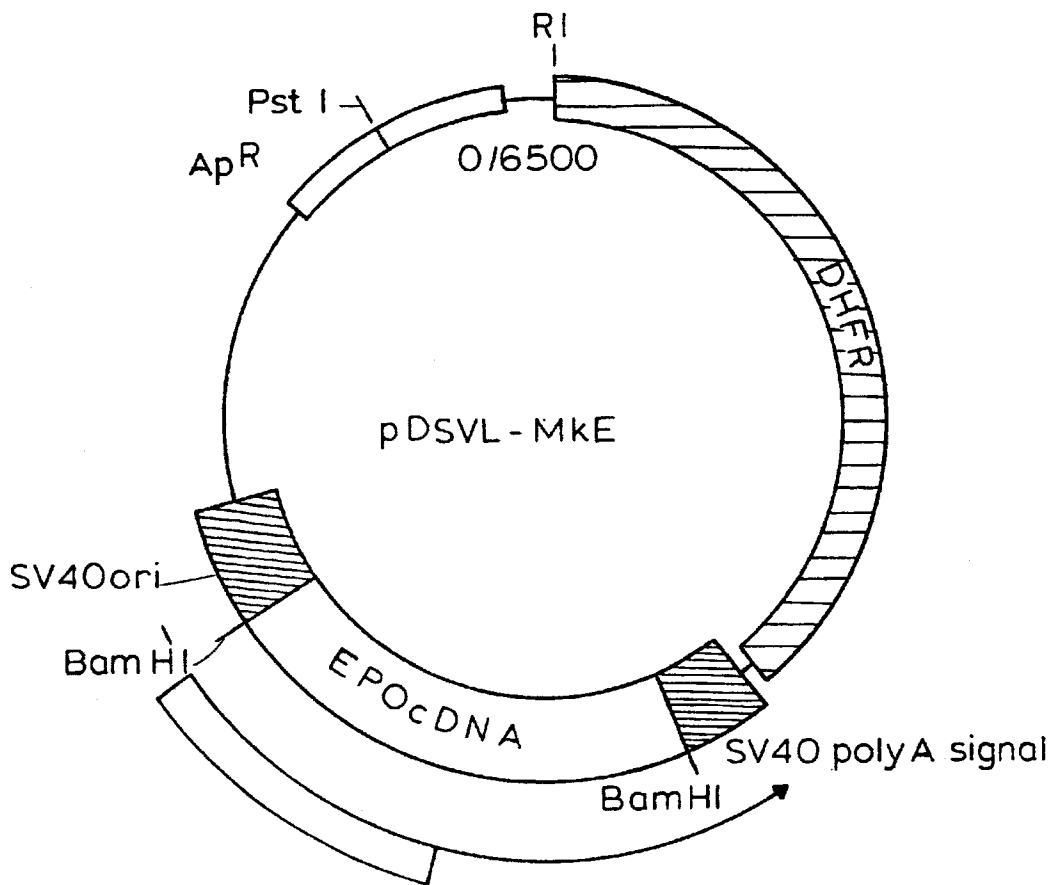


FIG. 3

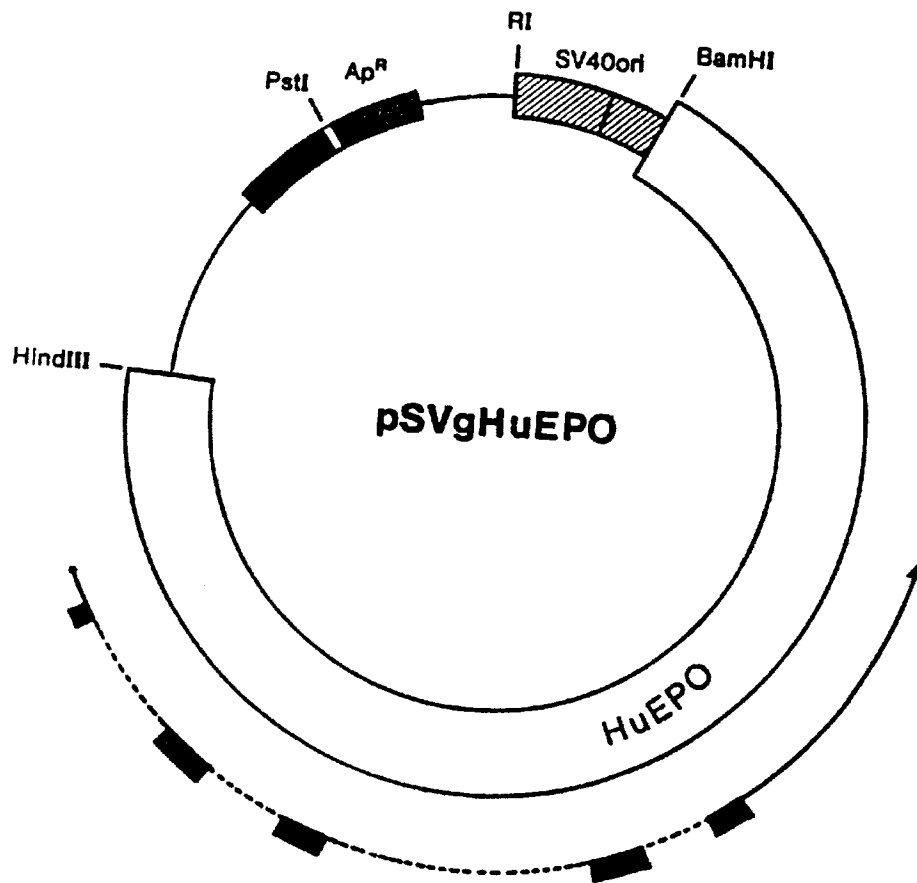


FIG. 4

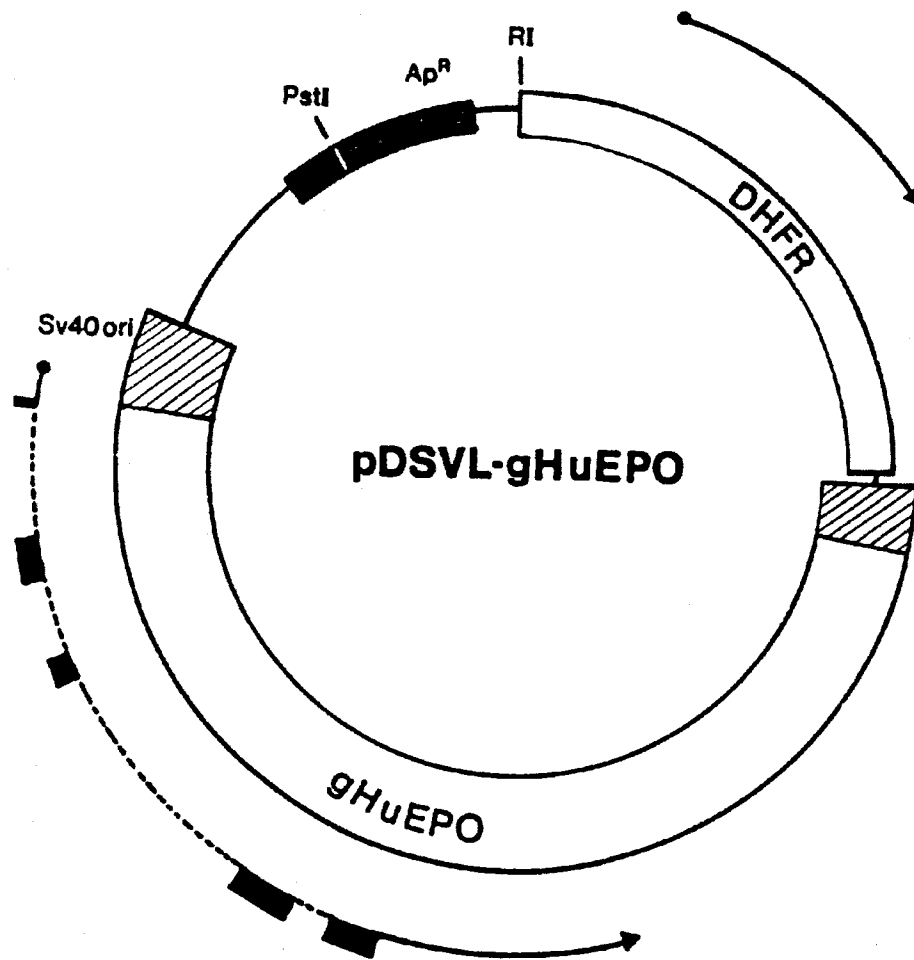


FIG. 5A

Sau3A
 GATCCGGCCCCCTGGACAGCCCTCTCCTCCAGGCCCGTGGGGCTGGCCCCCTGCC
 CGCTGAACCTCCCGGATGAGGACTCCCGGTGTGGTCAACCGCGCCTAGGTCGCTGAG

-27
 Met Gly Val His Glu Cys Pro Ala Trp
 GGACCCCGCCAGCGCGGAGATG GGG GTG CAC GAA TGT CCT GCC TGG

-10
 Leu Trp Leu Leu Ser Leu Val Ser Leu Pro Leu Gly Leu Pro
 CTG TGG CTT CTC CTG TCT CTC GTG TCG TCG CTC CCT CTG GGC CTC CCA

-1 +1 10
 Val Pro Gly Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu
 GTC CCG GGC GCC CCA CCA CGC CTC ATC TGT GAC AGC CGA GTC CTG

20 *
 Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Val Thr Met
 GAG AGG TAC CTC TTG GAG GCC AAG GAG GCC GAG AAT GTC ACG ATG

30 40
 Gly Cys Ser Glu Ser Cys Ser Leu Asn Glu Asn Ile Thr Val Pro
 GGC TGT TCC GAA AGC TGC AGC TTG AAT GAG AAT ATC ACC GTC CCA

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FIG.5B

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

FIG. 5C

150 Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Ala Cys Arg Arg
 CTC CGG GGA AAG CTG AAG CTG TAC ACG GGG GAG GCC TGC AGG AGA
 160
 Gly Asp Arg OP
 GGG GAC AGA TGA CCAGGTGCGTCCAGCTGGGCACATCCACCACCTCCCTCACCACA
 CTGCCCTGTGCCACACCCCTCCCTCACCCACTCCCAGAACCCCATCGAGGGGCTCTCAGCTAAG
 CGCCAGCCTGTCCCATGGACACTCCAGTGCCAGCAATGACATCTCAGGGGCCAGAGGAAC
 TGTCCAGAGCACAACTCTGAGATCTAAGGATGTCGACGGGCCAACTTGAGGGCCAGAGC
 AGGAGCATTTCAGAGAGCAGCTTTAAACTCAGGAGCAGAGACAATGCAGGGAAAACACCTT
 GAGCTCACTCGGCCACCTGCAAAATTTGATGCAGGACACGCTTTGGAGGCAATTTACCTG
 TTTTTCACCCTACCATCAGGGACAGGATGACTGGAGAACTTAGGTGGCAAGCTGTGACTT
 CTCAGGCCCTCAGGGCACTCCCTTGGTGGCAAGAGCCCCCTTGACACTGAGAGAAATATT
 TTGCAATCTGCAGCAGGAAAATACGGACAGGTTTGGAGGTTGGAGGTTACTTTGACAG
 GTGTGTGGGAAGCAGGGCGGTAGGGGTGGAGCTGGGATGCGAGTGAACAACCGTGAAGAC
 AGGATGGGGCTGGCCCTCGGTTCTCGTGGGGTCCAAGCTT
 HindIII

FIG.6A

AAGCTTCTGGGCTTCCAGACCAGCTACTTTGGGAACTCAGCAACCAGGCACTCTGAGTCTCCGCCCA
AGACCGGATGCCCCCCAGGGAGGTGTCCGGGAGCCAGCCCTTCCAGATAGCACGCTCCGCCAGTCCC
AAGGTGCGCAACC GGCTGCAC TCCCTCCCGGACCCAGGGCCCGGAGCAGCCCCCATGACCCACACGC
ACGTCTGCAGAGCCCGCTCAGCCCGGCGAGCCTCAACCAGGGTCTCTGCCCTGCTGACCCCGG
GTGGCCCTACCCCTGGCGACCCCTCACGCACACAGCCTCTCCCCACCCCGGCACGCACACATG
CAGATAACAGCCCGACCCCGGCGAGCCGXAGAGTCCCTGGGCCACCCCGGCGCTCGCTGCGCGTG
CGCCGCACCGGCTGTCTCCCGGAGCCGGACCCGGGCCACCCGCGCTCTGCTCCGACACCCGGCCC
CTTGGACAGCCCTCTCTTAGGCCGTGGGCTGGCCCTGCACCCCGGAGCTTCCCGGGATGAGGXX

CCCGGTGACCGGCGGCCCAAGTCGCTGAGGGACCCCGGCCAAGCGCGGAG ATG GGG GTG CAC G
GTGAGTACTCGGGGCTGGGCGCTCCCGGCGCCGGGTTCTGTTGAGCGGGGATTTAGCGCCCGCGCT

-27 -24

Met Gly Val His

FIG.6B

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ATTGCCAAGAGGTTGGCTGGGTTCAAGGACCGGGACTTGTCAAGGACCCCGGAAGGGGGAGGGGGTGGG
GCAGCCTCCACGTGCCGGGGACTTGGGGAGTTCCTGGGATGGCAAACCTGGCCTGTGTGAGGGGCA
CAGTTGGGGTGGGAGGAGGTTTGGGGTTCTGCTGTGCAGTTGTGTGTGTCAGTGTCTCG[I.S.]
TTGCACACGCACAGATCAATAAGCCAGAGGACACCTGAGTGTTCATGGTTGGGACAGGAAAGGACGAG
CTGGGCGAGAGACGTGGGGATGAAGGAAGCTGTCCCTCCACAGCCACCCCTTCTCCCCCCCCCGCTGACTCT
-23          -20          +1
Glu Cys Pro Ala Trp Leu Trp Leu Trp Leu Trp 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 CTC CTG GGC GGC CCA CCA CTC ATC TGT
10          *
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 GTGAGACCCCTTCCCAGCACATTCACAGAACTCACGGCTCAGGGCTTCAGGGAACTCCTCCCAGAT
CCAGGAACCTGGCACCTTGGTTTGGGGTGGAGTTGGGAAGCTAGACACTGCCCTACATAAGAATAAGTC

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FIG.6C

TGGTGGCCCAACCATACCTGAAACTAGGCAAGGAGCAAAAGCCAGCAGATCCTACGCCCTGTGGCCAGGG

27 30

Thr Gly Cys Ala Glu
ACG GGC TGT GCT GAA

CCAGAGCCTTCAGGGACCCCTTGACTCCCGGGCTGTGTGCATTTTCAG

* 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

GCC TGG AAG AGG ATG GAG GTGAGTTCCTTTTTTTTTTTTTTTTTTTTTTTTCCCTTTCTTTTGGAGAACTCAT

55

TGCGAGCCTGATTTTGGATGAAAGGGAGAAATGATCGGGGAAAGGTAATAATGGAGCAGCAGAGATGAGGCT

GCCTGGCGCAGAGGCTCACGTCTATAATCCAGGCTGAGATGGCCGAGATGGGAGAAATTGCTTGAGCCCT

GGAGTTTCAGACCAACCTAGGCAGCATAGTGAGATCCCCCATCTCTACAAACATTTAAAAAATTAGTCAG

GTGAAGTGGTGCATGGTGTAGTCCAGATATTGGAAGGCTGAGCGGGAGGATCGCTTGAGCCAGGAA

TTTGAGGCTGCAGTGAGCTGTGATCACACCACTGCCACTCCAGCCCTCAGTGACAGAGTGAGGCCCTGTCTCA

FIG. 6D

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AAAAAGAAAAGAAAAGAAAATAATGAGGGCTGTATGGAATACATTTCATTTCACCTCACTCACTCACT
CACTCATTTCATTTCATTTCATTTCATCAACAAGTCATTATTGCATACCTTCTGTTTGTCTCAGCTTGGTGTGG
GGTGTGAGGGGAGGAGGAGGGGTGACATGGGTGAGCTCGACTCCAGAGTCCACTCCCTCCCTGTAG
56          60          70
Val Gly Gln Gln Ala Val Glu Val Val Trip Gln Gly Leu Ala Leu Leu Ser Glu Ala
GTC GGG CAG CAG GCC GTA GAA GTC TGG CAG GGC CTG GCC CTG CTG TCG GAA GCT

Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trip Glu Pro Leu
GTC CTG CGG GGC CAG GCC CAG GTC 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
100

Arg Ala Leu Gly Ala Gln
CGG GCT CTG GGA GCC CAG GTGAGTAGGAGCGGACACTTCTGCTTGCCCTTCTGTAAGAAGGGA
110          115

GAAGGGTCTTGCTAAGGAGTACAGGAACCTGCTCCGTATTCTTCCCTTCTGTGGCACTGCAGCGACCTCCT
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
150 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

160
166 Asp Arg OP
    GAC AGA TGA CCAGGTGTGCCACCTGGGCAATATCCACCACCTCCCTCACCACATTTGTTGCCACA
    CCTCCCCGCCACTCCTGAACCCCGTCGAGGGCTCTCAGCTCAGCGCCAGCCTGTCCCATGGACACTCC
    AGTSCCAGCAATGACATCTCAGGGGCCAGAGGAACCTGTCCAGAGAGCAACTTGAGATCTAAGGATGTCAC
    AGGGCCAACTTGAAGGGCCAGAGCAGGAAGCATTCAGAGAGCAGCTTTAAACTCAGGGACAGAGCCCATGC
    TGGGAAGACGCCCTGAGCTCACTCGGCACCCTGC AAAAATTTGATGCCAGGACACCGCTTTGGAGGCCGATTAC
    CTGTTTTGCCACCCTACCATCAGGGACAGGATGACCCTGGAGAACTTAGGTGGCAAGCTGTGACTTCTCCAGG
    TCTCAGGGCATGGCCACTCCCTTGGTGGCAAGAGCCCTTGACACCGGGTGGTGGGAACCATGAAGAC
    AXGATXGGGGCTGGCCTCTCATGGGTC CAAGTTTGTGTATCTCAACCTATTGACAGACTGAA
    ACACAATATGAC
    
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FIG. 7

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