

SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG

<120> CHO cell

<130> 24306 FT

<150> EP07012773.3

<151> 2007-06-29

<160> 11

<170> PatentIn version 3.2

<210> 1

<211> 34

<212> DNA

<213> Artificial

<220>

<223> puro-loxP

<400> 1

ataacttcgt atagcatata ttatacgaag ttat

34

<210> 2

<211> 2097

<212> DNA

<213> Artificial

<220>

<223> transferrin-open reading frame

<400> 2

atgaggctcg ccgtgggagc cctgctggtc tgcgccgtcc tggggctgtg tctggctgtc 60

cctgataaaa ctgtgagatg gtgtgcagtg tcggagcatg aggccactaa gtgccagagt 120

ttccgcgacc atatgaaaag cgtcattcca tccgatggtc ccagtgttgc ttgtgtgaag 180

aaagcctcct accttgattg catcagggcc attgcggcaa acgaagcgga tgctgtgaca 240

ctggatgcag gtttggtgta tgatgcttac ctggctccca ataacctgaa gcctgtggtg 300

gcagagttct atgggtcaaa agaggatcca cagactttct attatgctgt tgctgtggtg 360

aagaaggata gtggcttcca gatgaaccag cttcgaggca agaagtcctg ccacacgggt 420

ctaggcaggt ccgctgggtg gaacatcccc ataggcttac ttactgtga cttacctgag 480

ccacgtaaac ctcttgagaa agcagtggcc aatttcttct cgggcagctg tgccccttgt 540

gcggatggga cggacttccc ccagctgtgt caactgtgtc caggggtgtg ctgctccacc 600

cttaaccaat acttcggcta ctctgggagcc ttcaagtgtc tgaaggatgg tgctggggat 660
gtggcctttg tcaagcactc gactatatatt gagaacttgg caaacaaggc tgacagggac 720
cagtatgagc tgctttgcct ggacaacacc cggaagccgg tagatgaata caaggactgc 780
cacttggecc aggtcccttc tcataccgtc gtggcccgaa gtatgggcgg caaggaggac 840
ttgatctggg agctttctcaa ccaggcccag gaacattttg gcaaagacaa atcaaaagaa 900
ttccaactat tcagctctcc tcatgggaag gacctgtgt ttaaggactc tgcccacggg 960
tttttaaaag tccccccag gatggatgcc aagatgtacc tgggctatga gtatgtcact 1020
gccatccgga atctacggga aggcacatgc ccagaagccc caacagatga atgcaagcct 1080
gtgaagtggg gtgcgctgag ccaccacgag aggtcaagt gtgatgagtg gagtgttaac 1140
agtgtaggga aaatagagtg tgtatcagca gagaccaccg aagactgcat cgccaagatc 1200
atgaatggag aagctgatgc catgagcttg gatggagggg ttgtctacat agcgggcaag 1260
tgtggtctgg tgctgtctt ggagaaaac tacaataaga gcgataattg tgaggataca 1320
ccagaggcag ggtattttgc ttagcagtg gtgaagaaat cagcttctga cctcacctgg 1380
gacaatctga aaggcaagaa gtcctgccat acggcagttg gcagaaccgc tggctggaac 1440
atccccatgg gcctgtctta caataagatc aaccactgca gatttgatga atttttcagt 1500
gaaggttggt cccctgggtc taagaaagac tccagtctct gtaagctgtg tatgggctca 1560
ggcctaaacc tgtgtgaacc caacaacaaa gagggatact acggctacac aggcgctttc 1620
aggtgtctgg ttgagaaggg agatgtggcc tttgtgaaac accagactgt cccacagaac 1680
actgggggaa aaaaccctga tccatgggct aagaatctga atgaaaaaga ctatgagttg 1740
ctgtgccttg atggtaccag gaaacctgtg gaggagtatg cgaactgcca cctggccaga 1800
gccccgaatc acgctgtggg cacacggaaa gataaggaag cttgcgtcca caagatatta 1860
cgtcaacagc agcacctatt tggaagcaac gtaactgact gctcgggcaa cttttgtttg 1920
ttccggtcgg aaaccaagga cttctgttc agagatgaca cagtatgttt ggccaaactt 1980
catgacagaa acacatatga aaaatactta ggagaagaat atgtcaaggc tgttggtaac 2040
ctgagaaaat gctccacctc atcactcctg gaagcctgca ctttccgtag accttaa 2097

<210> 3
<211> 3279
<212> DNA

<213> Artificial

<220>

<223> chimeric receptor ErbB2V>E/IGF-IR

<400> 3

atggagctgg cggccttggtg ccgctggggg ctctctctcg ccctcttgcc ccccgagacc	60
gcgagcacc aagtgtgcac cggcacagac atgaagctgc ggctccctgc cagtcccgag	120
accacactgg acatgctccg ccacctctac cagggctgcc aggtgggtgca gggaaacctg	180
gaactcacct acctgcccac caatgccagc ctgtccttcc tgcaggatat ccaggaggtg	240
cagggctacg tgetcatcgc tcacaaccaa gtgaggcagg tcccactgca gaggctgcgg	300
attgtgcgag gcacccagct ctttgaggac aactatgccc tggccgtgct agacaatgga	360
gaccgcgtga acaataccac ccctgtcaca ggggcctccc caggaggcct gcgggagctg	420
cagcttcgaa gcctcacaga gatcttgaaa ggaggggtct tgatccagcg gaacccccag	480
ctctgctacc aggacacgat tttgtggaag gacatcttcc acaagaacaa ccagctggct	540
ctcacactga tagacaccaa ccgctctcgg gcctgccacc cctgttctcc gatgtgtaag	600
ggctcccgtc gctggggaga gaggctctgag gattgtcaga gcctgacgag cactgtctgt	660
gccggtggct gtgcccgtg caaggggcca ctgcccactg actgctgcca tgagcagtg	720
gctgccggct gcacggggcc caagcactct gactgcctgg cctgcctcca cttcaaccac	780
agtggtcatc gtgagctgca ctgcccagcc ctgggtcacct acaacacaga cacgtttgag	840
tccatgccc aatccgaggg ccggtataca ttccggcgcca gctgtgtgac tgcctgtccc	900
tacaactacc tttctacgga cgtgggatcc tgcaccctcg tctgccccct gcacaaccaa	960
gaggtgacag cagaggatgg aacacagcgg tgtgagaagt gcagcaagcc ctgtgcccga	1020
gtgtgctatg gtctgggcat ggagcacttg cgagaggtga gggcagttac cagtgccaat	1080
atccaggagt ttgctggctg caagaagatc tttgggagcc tggcatttct gccggagagc	1140
tttgatgggg acccagcctc caacactgcc ccgctccagc cagagcagct ccaagtgttt	1200
gagactctgg aagagatcac aggttaccta tacatctcag catggccgga cagcctgcct	1260
gacctcagcg tcttcagaa cctgcaagta atccggggac gaattctgca caatggcgcc	1320
tactcgctga ccctgcaagg gctgggcatc agctggctgg ggctgcgctc actgagggaa	1380
ctgggcagtg gactggccct catccaccat aacaccacc tctgcttcgt gcacacggtg	1440
ccctgggacc agctctttcg gaaccgcac caagctctgc tccacactgc caaccggcca	1500

gaggacgagt gtgtgggcga gggcctggcc tgccaccagc tgtgcgccc agggcactgc 1560
tgggtccag gggccacca gtgtgtcaac tgcagccagt tccttcgggg ccaggagtgc 1620
gtggaggaat gccgagtact gcaggggctc cccaggagat atgtgaatgc caggcactgt 1680
ttgccgtgcc accctgagtg tcagccccag aatggctcag tgacctgttt tggaccggag 1740
gctgaccagt gtgtggcctg tgcccactat aaggaccctc cttctcggt ggcccgctgc 1800
cccagcgggtg tgaacctga cctctcctac atgccatct ggaagttcc agatgaggag 1860
ggcgcagcc agccttgccc catcaactgc accactcct gtgtggacct ggatgacaag 1920
ggctgcccc cggagcagag agccagccct ctgacgtcca tcgtctctgc ggtggaaggc 1980
attctgctgg tcgtggtctt gggggtggtc tttgggatcc tcatcaagcg acggcagcag 2040
aagattgcta gcagaaagag aaataacagc aggctgggga atggagtgt gtatgcctct 2100
gtgaacccgg agtacttcag cgctgctgat gtgtacgttc ctgatgagt ggaggtggct 2160
cgggagaaga tcaccatgag ccgggaactt gggcaggggt cgtttgggat ggtctatgaa 2220
ggagttgcca aggtgtggt gaaagatgaa cctgaaacca gaggggccat taaaacagt 2280
aacgaggccg caagcatgcg tgagaggatt gagtttctca acgaagcttc tgtgatgaag 2340
gagttcaatt gtcaccatgt ggtgcgattg ctgggtgtgg tgtccaagg ccagccaaca 2400
ctggtcatca tggaactgat gacacggggc gatctcaaaa gttatctccg gtctctgagg 2460
ccagaaatgg agaataatcc agtcctagca cctccaagcc tgagcaagat gattcagatg 2520
gccggagaga ttgcagacgg catggcatat ctcaacgcca ataagtctgt ccacagagac 2580
cttgctgccc ggaattgcat ggtagccgaa gatttcacag tcaaaatcgg agattttggt 2640
atgacgcgag atatctatga gacagactat taccggaaag gagggaaagg gctgctgccc 2700
gtgcgctgga tgtctcctga gtccctcaag gatggagtct tcaccactta ctcgacgtc 2760
tggtccttcg gggtcgtcct ctgggagatc gccacactgg ccgagcagcc ctaccagggc 2820
ttgtccaacg agcaagtcct tcgcttcgtc atggagggcg gccttctgga caagccagac 2880
aactgtcctg acatgctgtt tgaactgatg cgcatgtgct ggcagtataa cccaagatg 2940
aggccttcct tcctggagat catcagcagc atcaaagagg agatggagcc tggcttcgg 3000
gaggtctcct tctactacag cgaggagaac aagctgccc agccggagga gctggacctg 3060
gagccagaga acatggagag cgtccccctg gaccctcgg cctcctcgtc ctccctgcca 3120

ctgcccgaca gacactcagg acacaaggcc gagaacggcc ccggccctgg ggtgctggc 3180
ctccgcgcca gcttcgacga gagacagcct tacgcccaca tgaacggggg ccgcaagaac 3240
gagcgggcct tgccgctgcc ccagtcttcg acctgctga 3279

<210> 4
<211> 65
<212> DNA
<213> Artificial

<220>
<223> reverse primer of 56 bp fragment

<400> 4
ttttttcctg caggtattat caccggtgtt ttggcgcgcc aggtggcaact tttcggggaa 60
atgtg 65

<210> 5
<211> 22
<212> DNA
<213> Artificial

<220>
<223> pacF

<400> 5
agctgcaaga actcttcctc ac 22

<210> 6
<211> 15
<212> DNA
<213> Artificial

<220>
<223> pacR

<400> 6
tcaggcaccg ggctt 15

<210> 7
<211> 21
<212> DNA
<213> Artificial

<220>
<223> pacFL - 5'-CCCGCCTTCCTGGAGACCTCC-fluorescein-3'

<400> 7
cccgcccttc tgagacctc c 21

<210> 8
<211> 18
<212> DNA
<213> Artificial

<220>
<223> pacLC - 5'-LC red 640-CGCCCCGCAACCTCCCCT-3'

<400> 8
cgccccgcaa cctcccct

18

<210> 9
<211> 1255
<212> PRT
<213> Homo sapiens

<400> 9

Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu
1 5 10 15

Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys
20 25 30

Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
35 40 45

Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
50 55 60

Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
65 70 75 80

Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu
85 90 95

Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
100 105 110

Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro
115 120 125

Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser
130 135 140

Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
145 150 155 160

Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
165 170 175

Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys
180 185 190

His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
195 200 205

Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
210 215 220

Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
225 230 235 240

Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
245 250 255

His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
260 265 270

Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg
275 280 285

Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu
290 295 300

Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
305 310 315 320

Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
325 330 335

Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu
340 345 350

Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys
355 360 365

Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp
370 375 380

Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe
385 390 395 400

Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro
405 410 415

Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg
420 425 430

Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu
435 440 445

Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly
450 455 460

Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val
465 470 475 480

Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr
485 490 495

Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His
500 505 510

Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys
515 520 525

Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys
530 535 540

Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys
545 550 555 560

Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys
565 570 575

Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp
580 585 590

Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu
595 600 605

Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln
610 615 620

Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys
625 630 635 640

Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser Ile Ile Ser
645 650 655

Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly
660 665 670

Ile Leu Ile Lys Arg Arg Gln Gln Lys Ile Arg Lys Tyr Thr Met Arg
675 680 685

Arg Leu Leu Gln Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly
690 695 700

Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu
705 710 715 720

Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys
725 730 735

Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile
740 745 750

Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu
755 760 765

Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg
770 775 780

Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln Leu
785 790 795 800

Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu Asn Arg Gly Arg
805 810 815

Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala Lys Gly
820 825 830

Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala
835 840 845

Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe
850 855 860

Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp
865 870 875 880

Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg
885 890 895

Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val
900 905 910

Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro Ala
915 920 925

Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro
930 935 940

Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met
945 950 955 960

Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu Phe
965 970 975

Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn Glu
980 985 990

Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr Arg Ser Leu
995 1000 1005

Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala Glu Glu Tyr
1010 1015 1020

Leu Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro Ala Pro Gly
1025 1030 1035

Ala Gly Gly Met Val His His Arg His Arg Ser Ser Ser Thr Arg
1040 1045 1050

Ser Gly Gly Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu
1055 1060 1065

Glu Ala Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser
1070 1075 1080

Asp Val Phe Asp Gly Asp Leu Gly Met Gly Ala Ala Lys Gly Leu
1085 1090 1095

Gln Ser Leu Pro Thr His Asp Pro Ser Pro Leu Gln Arg Tyr Ser
1100 1105 1110

Glu Asp Pro Thr Val Pro Leu Pro Ser Glu Thr Asp Gly Tyr Val
1115 1120 1125

Ala Pro Leu Thr Cys Ser Pro Gln Pro Glu Tyr Val Asn Gln Pro
1130 1135 1140

Asp Val Arg Pro Gln Pro Pro Ser Pro Arg Glu Gly Pro Leu Pro
1145 1150 1155

Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu Arg Pro Lys Thr Leu
1160 1165 1170

Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val Phe Ala Phe Gly
1175 1180 1185

Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln Gly Gly Ala
1190 1195 1200

Ala Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala Phe Asp
1205 1210 1215

Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala Pro
1220 1225 1230

Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu Tyr
1235 1240 1245

Leu Gly Leu Asp Val Pro Val
1250 1255

<210> 10

<211> 1367

<212> PRT

<213> Homo sapiens

<400> 10

Met Lys Ser Gly Ser Gly Gly Gly Ser Pro Thr Ser Leu Trp Gly Leu
1 5 10 15

Leu Phe Leu Ser Ala Ala Leu Ser Leu Trp Pro Thr Ser Gly Glu Ile
20 25 30

Cys Gly Pro Gly Ile Asp Ile Arg Asn Asp Tyr Gln Gln Leu Lys Arg
35 40 45

Leu Glu Asn Cys Thr Val Ile Glu Gly Tyr Leu His Ile Leu Leu Ile
50 55 60

Ser Lys Ala Glu Asp Tyr Arg Ser Tyr Arg Phe Pro Lys Leu Thr Val
65 70 75 80

Ile Thr Glu Tyr Leu Leu Leu Phe Arg Val Ala Gly Leu Glu Ser Leu
85 90 95

Gly Asp Leu Phe Pro Asn Leu Thr Val Ile Arg Gly Trp Lys Leu Phe
100 105 110

Tyr Asn Tyr Ala Leu Val Ile Phe Glu Met Thr Asn Leu Lys Asp Ile
115 120 125

Gly Leu Tyr Asn Leu Arg Asn Ile Thr Arg Gly Ala Ile Arg Ile Glu
130 135 140

Lys Asn Ala Asp Leu Cys Tyr Leu Ser Thr Val Asp Trp Ser Leu Ile
145 150 155 160

Leu Asp Ala Val Ser Asn Asn Tyr Ile Val Gly Asn Lys Pro Pro Lys
165 170 175

Glu Cys Gly Asp Leu Cys Pro Gly Thr Met Glu Glu Lys Pro Met Cys
180 185 190

Glu Lys Thr Thr Ile Asn Asn Glu Tyr Asn Tyr Arg Cys Trp Thr Thr
195 200 205

Asn Arg Cys Gln Lys Met Cys Pro Ser Thr Cys Gly Lys Arg Ala Cys
210 215 220

Thr Glu Asn Asn Glu Cys Cys His Pro Glu Cys Leu Gly Ser Cys Ser
225 230 235 240

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

Ala Gly Val Cys Val Pro Ala Cys Pro Pro Asn Thr Tyr Arg Phe Glu
260 265 270

Gly Trp Arg Cys Val Asp Arg Asp Phe Cys Ala Asn Ile Leu Ser Ala
275 280 285

Glu Ser Ser Asp Ser Glu Gly Phe Val Ile His Asp Gly Glu Cys Met
290 295 300

Gln Glu Cys Pro Ser Gly Phe Ile Arg Asn Gly Ser Gln Ser Met Tyr
305 310 315 320

Cys Ile Pro Cys Glu Gly Pro Cys Pro Lys Val Cys Glu Glu Glu Lys
325 330 335

Lys Thr Lys Thr Ile Asp Ser Val Thr Ser Ala Gln Met Leu Gln Gly
340 345 350

Cys Thr Ile Phe Lys Gly Asn Leu Leu Ile Asn Ile Arg Arg Gly Asn
355 360 365

Asn Ile Ala Ser Glu Leu Glu Asn Phe Met Gly Leu Ile Glu Val Val
370 375 380

Thr Gly Tyr Val Lys Ile Arg His Ser His Ala Leu Val Ser Leu Ser
385 390 395 400

Phe Leu Lys Asn Leu Arg Leu Ile Leu Gly Glu Glu Gln Leu Glu Gly
405 410 415

Asn Tyr Ser Phe Tyr Val Leu Asp Asn Gln Asn Leu Gln Gln Leu Trp
420 425 430

Asp Trp Asp His Arg Asn Leu Thr Ile Lys Ala Gly Lys Met Tyr Phe
435 440 445

Ala Phe Asn Pro Lys Leu Cys Val Ser Glu Ile Tyr Arg Met Glu Glu
450 455 460

Val Thr Gly Thr Lys Gly Arg Gln Ser Lys Gly Asp Ile Asn Thr Arg
465 470 475 480

Asn Asn Gly Glu Arg Ala Ser Cys Glu Ser Asp Val Leu His Phe Thr
485 490 495

Ser Thr Thr Thr Ser Lys Asn Arg Ile Ile Ile Thr Trp His Arg Tyr
500 505 510

Arg Pro Pro Asp Tyr Arg Asp Leu Ile Ser Phe Thr Val Tyr Tyr Lys
515 520 525

Glu Ala Pro Phe Lys Asn Val Thr Glu Tyr Asp Gly Gln Asp Ala Cys
530 535 540

Gly Ser Asn Ser Trp Asn Met Val Asp Val Asp Leu Pro Pro Asn Lys
545 550 555 560

Asp Val Glu Pro Gly Ile Leu Leu His Gly Leu Lys Pro Trp Thr Gln
565 570 575

Tyr Ala Val Tyr Val Lys Ala Val Thr Leu Thr Met Val Glu Asn Asp
580 585 590

His Ile Arg Gly Ala Lys Ser Glu Ile Leu Tyr Ile Arg Thr Asn Ala
595 600 605

Ser Val Pro Ser Ile Pro Leu Asp Val Leu Ser Ala Ser Asn Ser Ser
610 615 620

Ser Gln Leu Ile Val Lys Trp Asn Pro Pro Ser Leu Pro Asn Gly Asn
625 630 635 640

Leu Ser Tyr Tyr Ile Val Arg Trp Gln Arg Gln Pro Gln Asp Gly Tyr
645 650 655

Leu Tyr Arg His Asn Tyr Cys Ser Lys Asp Lys Ile Pro Ile Arg Lys
660 665 670

Tyr Ala Asp Gly Thr Ile Asp Ile Glu Glu Val Thr Glu Asn Pro Lys
675 680 685

Thr Glu Val Cys Gly Gly Glu Lys Gly Pro Cys Cys Ala Cys Pro Lys
690 695 700

Thr Glu Ala Glu Lys Gln Ala Glu Lys Glu Glu Ala Glu Tyr Arg Lys
705 710 715 720

Val Phe Glu Asn Phe Leu His Asn Ser Ile Phe Val Pro Arg Pro Glu
725 730 735

Arg Lys Arg Arg Asp Val Met Gln Val Ala Asn Thr Thr Met Ser Ser
740 745 750

Arg Ser Arg Asn Thr Thr Ala Ala Asp Thr Tyr Asn Ile Thr Asp Pro
755 760 765

Glu Glu Leu Glu Thr Glu Tyr Pro Phe Phe Glu Ser Arg Val Asp Asn
770 775 780

Lys Glu Arg Thr Val Ile Ser Asn Leu Arg Pro Phe Thr Leu Tyr Arg
785 790 795 800

Ile Asp Ile His Ser Cys Asn His Glu Ala Glu Lys Leu Gly Cys Ser
805 810 815

Ala Ser Asn Phe Val Phe Ala Arg Thr Met Pro Ala Glu Gly Ala Asp
820 825 830

Asp Ile Pro Gly Pro Val Thr Trp Glu Pro Arg Pro Glu Asn Ser Ile
835 840 845

Phe Leu Lys Trp Pro Glu Pro Glu Asn Pro Asn Gly Leu Ile Leu Met
850 855 860

Tyr Glu Ile Lys Tyr Gly Ser Gln Val Glu Asp Gln Arg Glu Cys Val
865 870 875 880

Ser Arg Gln Glu Tyr Arg Lys Tyr Gly Gly Ala Lys Leu Asn Arg Leu
885 890 895

Asn Pro Gly Asn Tyr Thr Ala Arg Ile Gln Ala Thr Ser Leu Ser Gly
900 905 910

Asn Gly Ser Trp Thr Asp Pro Val Phe Phe Tyr Val Gln Ala Lys Thr
915 920 925

Gly Tyr Glu Asn Phe Ile His Leu Ile Ile Ala Leu Pro Val Ala Val
930 935 940

Leu Leu Ile Val Gly Gly Leu Val Ile Met Leu Tyr Val Phe His Arg
945 950 955 960

Lys Arg Asn Asn Ser Arg Leu Gly Asn Gly Val Leu Tyr Ala Ser Val
965 970 975

Asn Pro Glu Tyr Phe Ser Ala Ala Asp Val Tyr Val Pro Asp Glu Trp
980 985 990

Glu Val Ala Arg Glu Lys Ile Thr Met Ser Arg Glu Leu Gly Gln Gly
995 1000 1005

Ser Phe Gly Met Val Tyr Glu Gly Val Ala Lys Gly Val Val Lys
1010 1015 1020

Asp Glu Pro Glu Thr Arg Val Ala Ile Lys Thr Val Asn Glu Ala
1025 1030 1035

Ala Ser Met Arg Glu Arg Ile Glu Phe Leu Asn Glu Ala Ser Val
1040 1045 1050

Met Lys Glu Phe Asn Cys His His Val Val Arg Leu Leu Gly Val
1055 1060 1065

Val Ser Gln Gly Gln Pro Thr Leu Val Ile Met Glu Leu Met Thr
1070 1075 1080

Arg Gly Asp Leu Lys Ser Tyr Leu Arg Ser Leu Arg Pro Glu Met
1085 1090 1095

Glu Asn Asn Pro Val Leu Ala Pro Pro Ser Leu Ser Lys Met Ile
1100 1105 1110

Gln Met Ala Gly Glu Ile Ala Asp Gly Met Ala Tyr Leu Asn Ala
1115 1120 1125

Asn Lys Phe Val His Arg Asp Leu Ala Ala Arg Asn Cys Met Val
1130 1135 1140

Ala Glu Asp Phe Thr Val Lys Ile Gly Asp Phe Gly Met Thr Arg
1145 1150 1155

Asp Ile Tyr Glu Thr Asp Tyr Tyr Arg Lys Gly Gly Lys Gly Leu
1160 1165 1170

Leu Pro Val Arg Trp Met Ser Pro Glu Ser Leu Lys Asp Gly Val
1175 1180 1185

Phe Thr Thr Tyr Ser Asp Val Trp Ser Phe Gly Val Val Leu Trp
1190 1195 1200

Glu Ile Ala Thr Leu Ala Glu Gln Pro Tyr Gln Gly Leu Ser Asn
1205 1210 1215

Glu Gln Val Leu Arg Phe Val Met Glu Gly Gly Leu Leu Asp Lys
1220 1225 1230

Pro Asp Asn Cys Pro Asp Met Leu Phe Glu Leu Met Arg Met Cys
1235 1240 1245

Trp Gln Tyr Asn Pro Lys Met Arg Pro Ser Phe Leu Glu Ile Ile
1250 1255 1260

Ser Ser Ile Lys Glu Glu Met Glu Pro Gly Phe Arg Glu Val Ser
1265 1270 1275

Phe Tyr Tyr Ser Glu Glu Asn Lys Leu Pro Glu Pro Glu Glu Leu
1280 1285 1290

Asp Leu Glu Pro Glu Asn Met Glu Ser Val Pro Leu Asp Pro Ser
1295 1300 1305

Ala Ser Ser Ser Ser Leu Pro Leu Pro Asp Arg His Ser Gly His
1310 1315 1320

Lys Ala Glu Asn Gly Pro Gly Pro Gly Val Leu Val Leu Arg Ala
1325 1330 1335

Ser Phe Asp Glu Arg Gln Pro Tyr Ala His Met Asn Gly Gly Arg
1340 1345 1350

Lys Asn Glu Arg Ala Leu Pro Leu Pro Gln Ser Ser Thr Cys
1355 1360 1365

<210> 11

<211> 61

<212> DNA

<213> Artificial

<220>

<223> forward primer for 56 bp fragment

<400> 11

ataataacctg caggaaaagg ccggccaaag gatccctgtg gaatgtgtgt cagttagggt 60

g

61