SEQUENCE LISTING

<110> NATIONAL UNIVERSITY CORPORATION KOBE UNIVERSITY

<120> Method of modifying nucleic acid sequence of cell comprising specifically converting nucleobase in targeted DNA using endogenous DNA qualification enzyme in cell, and molecular complex used therefor

<130> 092729

<150> JP 2017-056727
<151> 2017-03-22

<160> 37

<170> PatentIn version 3.5

<210> 1
<211> 549
<212> DNA
<213> Human immunodeficiency virus

<220>
<221> CDS
<222> (1)..(549)

<220>
<221> misc_difference
<222> (406)..(408)
<223> artificial mutation

<400> 1

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gtg tgg caa gta gac agg atg agg att aga aca tgg aac agt tta gta         48
Val Trp Gln Val Asp Arg Met Arg Ile Arg Thr Trp Asn Ser Leu Val
1               5                   10                  15

aaa cat cac atg tat atc tca aag aaa gca aaa aat tgg ttt tat aga         96
Lys His His Met Tyr Ile Ser Lys Lys Ala Lys Asn Trp Phe Tyr Arg
            20                  25                  30

cat cac ttt gaa agc agt cat cca aga gta agt tca gaa gta cac atc        144
His His Phe Glu Ser Ser His Pro Arg Val Ser Ser Glu Val His Ile
        35                  40                  45

cca cta ggg gat gct aga tta gta gta aga aca tat tgg ggt ctg cat        192
Pro Leu Gly Asp Ala Arg Leu Val Val Arg Thr Tyr Trp Gly Leu His
    50                  55                  60

aca gga gaa aaa gat tgg cac ttg ggt aat ggg gtg tcc ata gaa tgg        240
Thr Gly Glu Lys Asp Trp His Leu Gly Asn Gly Val Ser Ile Glu Trp
65                  70                  75                  80

aga cta aga aga tat agc aca caa ata gat cct gac ctg gca gac caa        288
Arg Leu Arg Arg Tyr Ser Thr Gln Ile Asp Pro Asp Leu Ala Asp Gln
                85                  90                  95
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```
cta att cat ctg cat tat ttt aat tgt ttt tca gac tct gcc ata agg        336
Leu Ile His Leu His Tyr Phe Asn Cys Phe Ser Asp Ser Ala Ile Arg
            100                 105                 110

aaa gcc ata tta gga caa gta gtt aga cct aga tgt gac tat caa gca        384
Lys Ala Ile Leu Gly Gln Val Val Arg Pro Arg Cys Asp Tyr Gln Ala
        115                 120                 125

gga cat aac aag gta gga tct gct caa tat ttg gca ctg aaa gca tta        432
Gly His Asn Lys Val Gly Ser Ala Gln Tyr Leu Ala Leu Lys Ala Leu
    130                 135                 140

gta aca cca gta agg aca agg cca cct ttg cct agt gtt agg aaa tta        480
Val Thr Pro Val Arg Thr Arg Pro Pro Leu Pro Ser Val Arg Lys Leu
145                 150                 155                 160

gca gag gac aga tgg aac aag ccc cag aaa acc agg ggt ccc aga ggg        528
Ala Glu Asp Arg Trp Asn Lys Pro Gln Lys Thr Arg Gly Pro Arg Gly
                165                 170                 175

agc cat aca atg aat gga cat                                           549
Ser His Thr Met Asn Gly His
            180
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<210> 2
<211> 183
<212> PRT
<213> Human immunodeficiency virus

<400> 2

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Val Trp Gln Val Asp Arg Met Arg Ile Arg Thr Trp Asn Ser Leu Val
1               5                   10                  15

Lys His His Met Tyr Ile Ser Lys Lys Ala Lys Asn Trp Phe Tyr Arg
            20                  25                  30

His His Phe Glu Ser Ser His Pro Arg Val Ser Ser Glu Val His Ile
        35                  40                  45

Pro Leu Gly Asp Ala Arg Leu Val Val Arg Thr Tyr Trp Gly Leu His
    50                  55                  60

Thr Gly Glu Lys Asp Trp His Leu Gly Asn Gly Val Ser Ile Glu Trp
65                  70                  75                  80

Arg Leu Arg Arg Tyr Ser Thr Gln Ile Asp Pro Asp Leu Ala Asp Gln
                85                  90                  95

Leu Ile His Leu His Tyr Phe Asn Cys Phe Ser Asp Ser Ala Ile Arg
            100                 105                 110
```

Lys Ala Ile Leu Gly Gln Val Val Arg Pro Arg Cys Asp Tyr Gln Ala
115 120 125

Gly His Asn Lys Val Gly Ser Ala Gln Tyr Leu Ala Leu Lys Ala Leu
130 135 140

Val Thr Pro Val Arg Thr Arg Pro Pro Leu Pro Ser Val Arg Lys Leu
145 150 155 160

Ala Glu Asp Arg Trp Asn Lys Pro Gln Lys Thr Arg Gly Pro Arg Gly
165 170 175

Ser His Thr Met Asn Gly His
180

<210> 3
<211> 573
<212> DNA
<213> Artificial Sequence

<220>
<223> Vif variant construct

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cctaggggta ccgaaatggt gtggcaagta gacaggatga ggattagaac atggaacagt 60

ttagtaaaac atcacatgta tatctcaaag aaagcaaaaa attggtttta tagacatcac 120

tttgaaagca gtcatccaag agtaagttca gaagtacaca tcccactagg ggatgctaga 180

ttagtagtaa gaacatattg gggtctgcat acaggagaaa aagattggca cttgggtaat 240

ggggtgtcca tagaatggag actaagaaga tatagcacac aaatagatcc tgacctggca 300

gaccaactaa ttcatctgca ttattttaat tgtttttcag actctgccat aaggaaagcc 360

atattaggac aagtagttag acctagatgt gactatcaag caggacataa caaggtagga 420

tctgctcaat atttggcact gaaagcatta gtaacaccag taaggacaag gccacctttg 480

cctagtgtta ggaaattagc agaggacaga tggaacaagc cccagaaaac caggggtccc 540

agagggagcc atacaatgaa tggacatgct agc 573

<210> 4
<211> 4116
<212> DNA
<213> Artificial Sequence

<220>

<223> Cas9 codon-optimized for human.

<220>
<221> CDS
<222> (1)..(4116)

<400> 4

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atg gac aag aag tac tcc att ggg ctc gmt atc ggc aca aac agc gtc        48
Met Asp Lys Lys Tyr Ser Ile Gly Leu Xaa Ile Gly Thr Asn Ser Val
1               5                  10                  15

ggt tgg gcc gtc att acg gac gag tac aag gtg ccg agc aaa aaa ttc        96
Gly Trp Ala Val Ile Thr Asp Glu Tyr Lys Val Pro Ser Lys Lys Phe
            20                  25                  30

aaa gtt ctg ggc aat acc gat cgc cac agc ata aag aag aac ctc att       144
Lys Val Leu Gly Asn Thr Asp Arg His Ser Ile Lys Lys Asn Leu Ile
        35                  40                  45

ggc gcc ctc ctg ttc gac tcc ggg gag acg gcc gaa gcc acg cgg ctc       192
Gly Ala Leu Leu Phe Asp Ser Gly Glu Thr Ala Glu Ala Thr Arg Leu
    50                  55                  60

aaa aga aca gca cgg cgc aga tat acc cgc aga aag aat cgg atc tgc       240
Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg Ile Cys
65                  70                  75                  80

tac ctg cag gag atc ttt agt aat gag atg gct aag gtg gat gac tct       288
Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met Ala Lys Val Asp Asp Ser
                85                  90                  95

ttc ttc cat agg ctg gag gag tcc ttt ttg gtg gag gag gat aaa aag       336
Phe Phe His Arg Leu Glu Glu Ser Phe Leu Val Glu Glu Asp Lys Lys
            100                 105                 110

cac gag cgc cac cca atc ttt ggc aat atc gtg gac gag gtg gcg tac       384
His Glu Arg His Pro Ile Phe Gly Asn Ile Val Asp Glu Val Ala Tyr
        115                 120                 125

cat gaa aag tac cca acc ata tat cat ctg agg aag aag ctt gta gac       432
His Glu Lys Tyr Pro Thr Ile Tyr His Leu Arg Lys Lys Leu Val Asp
    130                 135                 140

agt act gat aag gct gac ttg cgg ttg atc tat ctc gcg ctg gcg cat       480
Ser Thr Asp Lys Ala Asp Leu Arg Leu Ile Tyr Leu Ala Leu Ala His
145                 150                 155                 160

atg atc aaa ttt cgg gga cac ttc ctc atc gag ggg gac ctg aac cca       528
Met Ile Lys Phe Arg Gly His Phe Leu Ile Glu Gly Asp Leu Asn Pro
                165                 170                 175

gac aac agc gat gtc gac aaa ctc ttt atc caa ctg gtt cag act tac       576
Asp Asn Ser Asp Val Asp Lys Leu Phe Ile Gln Leu Val Gln Thr Tyr
            180                 185                 190

aat cag ctt ttc gaa gag aac ccg atc aac gca tcc gga gtt gac gcc       624
Asn Gln Leu Phe Glu Glu Asn Pro Ile Asn Ala Ser Gly Val Asp Ala
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        195                 200                 205

aaa gca atc ctg agc gct agg ctg tcc aaa tcc cgg cgg ctc gaa aac        672
Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn
    210                 215                 220

ctc atc gca cag ctc cct ggg gag aag aag aac ggc ctg ttt ggt aat        720
Leu Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn
225                 230                 235                 240

ctt atc gcc ctg tca ctc ggg ctg acc ccc aac ttt aaa tct aac ttc        768
Leu Ile Ala Leu Ser Leu Gly Leu Thr Pro Asn Phe Lys Ser Asn Phe
                245                 250                 255

gac ctg gcc gaa gat gcc aag ctt caa ctg agc aaa gac acc tac gat        816
Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser Lys Asp Thr Tyr Asp
            260                 265                 270

gat gat ctc gac aat ctg ctg gcc cag atc ggc gac cag tac gca gac        864
Asp Asp Leu Asp Asn Leu Leu Ala Gln Ile Gly Asp Gln Tyr Ala Asp
        275                 280                 285

ctt ttt ttg gcg gca aag aac ctg tca gac gcc att ctg ctg agt gat        912
Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp Ala Ile Leu Leu Ser Asp
    290                 295                 300

att ctg cga gtg aac acg gag atc acc aaa gct ccg ctg agc gct agt        960
Ile Leu Arg Val Asn Thr Glu Ile Thr Lys Ala Pro Leu Ser Ala Ser
305                 310                 315                 320

atg atc aag cgc tat gat gag cac cac caa gac ttg act ttg ctg aag       1008
Met Ile Lys Arg Tyr Asp Glu His His Gln Asp Leu Thr Leu Leu Lys
                325                 330                 335

gcc ctt gtc aga cag caa ctg cct gag aag tac aag gaa att ttc ttc       1056
Ala Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile Phe Phe
            340                 345                 350

gat cag tct aaa aat ggc tac gcc gga tac att gac ggc gga gca agc       1104
Asp Gln Ser Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Gly Ala Ser
        355                 360                 365

cag gag gaa ttt tac aaa ttt att aag ccc atc ttg gaa aaa atg gac       1152
Gln Glu Glu Phe Tyr Lys Phe Ile Lys Pro Ile Leu Glu Lys Met Asp
    370                 375                 380

ggc acc gag gag ctg ctg gta aag ctt aac aga gaa gat ctg ttg cgc       1200
Gly Thr Glu Glu Leu Leu Val Lys Leu Asn Arg Glu Asp Leu Leu Arg
385                 390                 395                 400

aaa cag cgc act ttc gac aat gga agc atc ccc cac cag att cac ctg       1248
Lys Gln Arg Thr Phe Asp Asn Gly Ser Ile Pro His Gln Ile His Leu
                405                 410                 415

ggc gaa ctg cac gct atc ctc agg cgg caa gag gat ttc tac ccc ttt       1296
Gly Glu Leu His Ala Ile Leu Arg Arg Gln Glu Asp Phe Tyr Pro Phe
            420                 425                 430
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ttg aaa gat aac agg gaa aag att gag aaa atc ctc aca ttt cgg ata       1344
Leu Lys Asp Asn Arg Glu Lys Ile Glu Lys Ile Leu Thr Phe Arg Ile
        435                 440                 445

ccc tac tat gta ggc ccc ctc gcc cgg gga aat tcc aga ttc gcg tgg       1392
Pro Tyr Tyr Val Gly Pro Leu Ala Arg Gly Asn Ser Arg Phe Ala Trp
    450                 455                 460

atg act cgc aaa tca gaa gag acc atc act ccc tgg aac ttc gag gaa       1440
Met Thr Arg Lys Ser Glu Glu Thr Ile Thr Pro Trp Asn Phe Glu Glu
465                 470                 475                 480

gtc gtg gat aag ggg gcc tct gcc cag tcc ttc atc gaa agg atg act       1488
Val Val Asp Lys Gly Ala Ser Ala Gln Ser Phe Ile Glu Arg Met Thr
                485                 490                 495

aac ttt gat aaa aat ctg cct aac gaa aag gtg ctt cct aaa cac tct       1536
Asn Phe Asp Lys Asn Leu Pro Asn Glu Lys Val Leu Pro Lys His Ser
            500                 505                 510

ctg ctg tac gag tac ttc aca gtt tat aac gag ctc acc aag gtc aaa       1584
Leu Leu Tyr Glu Tyr Phe Thr Val Tyr Asn Glu Leu Thr Lys Val Lys
        515                 520                 525

tac gtc aca gaa ggg atg aga aag cca gca ttc ctg tct gga gag cag       1632
Tyr Val Thr Glu Gly Met Arg Lys Pro Ala Phe Leu Ser Gly Glu Gln
    530                 535                 540

aag aaa gct atc gtg gac ctc ctc ttc aag acg aac cgg aaa gtt acc       1680
Lys Lys Ala Ile Val Asp Leu Leu Phe Lys Thr Asn Arg Lys Val Thr
545                 550                 555                 560

gtg aaa cag ctc aaa gaa gac tat ttc aaa aag att gaa tgt ttc gac       1728
Val Lys Gln Leu Lys Glu Asp Tyr Phe Lys Lys Ile Glu Cys Phe Asp
                565                 570                 575

tct gtt gaa atc agc gga gtg gag gat cgc ttc aac gca tcc ctg gga       1776
Ser Val Glu Ile Ser Gly Val Glu Asp Arg Phe Asn Ala Ser Leu Gly
            580                 585                 590

acg tat cac gat ctc ctg aaa atc att aaa gac aag gac ttc ctg gac       1824
Thr Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys Asp Phe Leu Asp
        595                 600                 605

aat gag gag aac gag gac att ctt gag gac att gtc ctc acc ctt acg       1872
Asn Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr
    610                 615                 620

ttg ttt gaa gat agg gag atg att gaa gaa cgc ttg aaa act tac gct       1920
Leu Phe Glu Asp Arg Glu Met Ile Glu Glu Arg Leu Lys Thr Tyr Ala
625                 630                 635                 640

cat ctc ttc gac gac aaa gtc atg aaa cag ctc aag agg cgc cga tat       1968
His Leu Phe Asp Asp Lys Val Met Lys Gln Leu Lys Arg Arg Arg Tyr
                645                 650                 655

aca gga tgg ggg cgg ctg tca aga aaa ctg atc aat ggg atc cga gac       2016
Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu Ile Asn Gly Ile Arg Asp
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            660                 665                 670

aag cag agt gga aag aca atc ctg gat ttt ctt aag tcc gat gga ttt      2064
Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe
        675                 680                 685

gcc aac cgg aac ttc atg cag ttg atc cat gat gac tct ctc acc ttt      2112
Ala Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe
    690                 695                 700

aag gag gac atc cag aaa gca caa gtt tct ggc cag ggg gac agt ctt      2160
Lys Glu Asp Ile Gln Lys Ala Gln Val Ser Gly Gln Gly Asp Ser Leu
705                 710                 715                 720

cac gag cac atc gct aat ctt gca ggt agc cca gct atc aaa aag gga      2208
His Glu His Ile Ala Asn Leu Ala Gly Ser Pro Ala Ile Lys Lys Gly
                725                 730                 735

ata ctg cag acc gtt aag gtc gtg gat gaa ctc gtc aaa gta atg gga      2256
Ile Leu Gln Thr Val Lys Val Val Asp Glu Leu Val Lys Val Met Gly
            740                 745                 750

agg cat aag ccc gag aat atc gtt atc gag atg gcc cga gag aac caa      2304
Arg His Lys Pro Glu Asn Ile Val Ile Glu Met Ala Arg Glu Asn Gln
        755                 760                 765

act acc cag aag gga cag aag aac agt agg gaa agg atg aag agg att      2352
Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg Glu Arg Met Lys Arg Ile
    770                 775                 780

gaa gag ggt ata aaa gaa ctg ggg tcc caa atc ctt aag gaa cac cca      2400
Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln Ile Leu Lys Glu His Pro
785                 790                 795                 800

gtt gaa aac acc cag ctt cag aat gag aag ctc tac ctg tac tac ctg      2448
Val Glu Asn Thr Gln Leu Gln Asn Glu Lys Leu Tyr Leu Tyr Tyr Leu
                805                 810                 815

cag aac ggc agg gac atg tac gtg gat cag gaa ctg gac atc aat cgg      2496
Gln Asn Gly Arg Asp Met Tyr Val Asp Gln Glu Leu Asp Ile Asn Arg
            820                 825                 830

ctc tcc gac tac gac gtg gat smt atc gtg ccc cag tct ttt ctc aaa      2544
Leu Ser Asp Tyr Asp Val Asp Xaa Ile Val Pro Gln Ser Phe Leu Lys
        835                 840                 845

gat gat tct att gat aat aaa gtg ttg aca aga tcc gat aaa aat aga      2592
Asp Asp Ser Ile Asp Asn Lys Val Leu Thr Arg Ser Asp Lys Asn Arg
    850                 855                 860

ggg aag agt gat aac gtc ccc tca gaa gaa gtt gtc aag aaa atg aaa      2640
Gly Lys Ser Asp Asn Val Pro Ser Glu Glu Val Val Lys Lys Met Lys
865                 870                 875                 880

aat tat tgg cgg cag ctg ctg aac gcc aaa ctg atc aca caa cgg aag      2688
Asn Tyr Trp Arg Gln Leu Leu Asn Ala Lys Leu Ile Thr Gln Arg Lys
                885                 890                 895
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ttc gat aat ctg act aag gct gaa cga ggt ggc ctg tct gag ttg gat       2736
Phe Asp Asn Leu Thr Lys Ala Glu Arg Gly Gly Leu Ser Glu Leu Asp
            900                 905                 910

aaa gcc ggc ttc atc aaa agg cag ctt gtt gag aca cgc cag atc acc       2784
Lys Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr
        915                 920                 925

aag cac gtg gcc caa att ctc gat tca cgc atg aac acc aag tac gat       2832
Lys His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp
    930                 935                 940

gaa aat gac aaa ctg att cga gag gtg aaa gtt att act ctg aag tct       2880
Glu Asn Asp Lys Leu Ile Arg Glu Val Lys Val Ile Thr Leu Lys Ser
945                 950                 955                 960

aag ctg gtc tca gat ttc aga aag gac ttt cag ttt tat aag gtg aga       2928
Lys Leu Val Ser Asp Phe Arg Lys Asp Phe Gln Phe Tyr Lys Val Arg
                965                 970                 975

gag atc aac aat tac cac cat gcg cat gat gcc tac ctg aat gca gtg       2976
Glu Ile Asn Asn Tyr His His Ala His Asp Ala Tyr Leu Asn Ala Val
            980                 985                 990

gta ggc act gca ctt atc aaa aaa  tat ccc aag ctt gaa  tct gaa ttt     3024
Val Gly Thr Ala Leu Ile Lys Lys  Tyr Pro Lys Leu Glu  Ser Glu Phe
        995                 1000                1005

gtt tac  gga gac tat aaa gtg  tac gat gtt agg aaa  atg atc gca       3069
Val Tyr  Gly Asp Tyr Lys Val  Tyr Asp Val Arg Lys  Met Ile Ala
    1010                1015                1020

aag tct  gag cag gaa ata ggc  aag gcc acc gct aag  tac ttc ttt       3114
Lys Ser  Glu Gln Glu Ile Gly  Lys Ala Thr Ala Lys  Tyr Phe Phe
    1025                1030                1035

tac agc  aat att atg aat ttt  ttc aag acc gag att  aca ctg gcc       3159
Tyr Ser  Asn Ile Met Asn Phe  Phe Lys Thr Glu Ile  Thr Leu Ala
    1040                1045                1050

aat gga  gag att cgg aag cga  cca ctt atc gaa aca  aac gga gaa       3204
Asn Gly  Glu Ile Arg Lys Arg  Pro Leu Ile Glu Thr  Asn Gly Glu
    1055                1060                1065

aca gga  gaa atc gtg tgg gac  aag ggt agg gat ttc  gcg aca gtc       3249
Thr Gly  Glu Ile Val Trp Asp  Lys Gly Arg Asp Phe  Ala Thr Val
    1070                1075                1080

cgg aag  gtc ctg tcc atg ccg  cag gtg aac atc gtt  aaa aag acc       3294
Arg Lys  Val Leu Ser Met Pro  Gln Val Asn Ile Val  Lys Lys Thr
    1085                1090                1095

gaa gta  cag acc gga ggc ttc  tcc aag gaa agt atc  ctc ccg aaa       3339
Glu Val  Gln Thr Gly Gly Phe  Ser Lys Glu Ser Ile  Leu Pro Lys
    1100                1105                1110

agg aac  agc gac aag ctg atc  gca cgc aaa aaa gat  tgg gac ccc       3384
Arg Asn  Ser Asp Lys Leu Ile  Ala Arg Lys Lys Asp  Trp Asp Pro
```

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    1115                1120                1125

aag aaa  tac ggc gga ttc gat  tct cct aca gtc gct  tac agt gta        3429
Lys Lys  Tyr Gly Gly Phe Asp  Ser Pro Thr Val Ala  Tyr Ser Val
    1130                1135                1140

ctg gtt  gtg gcc aaa gtg gag  aaa ggg aag tct aaa  aaa ctc aaa        3474
Leu Val  Val Ala Lys Val Glu  Lys Gly Lys Ser Lys  Lys Leu Lys
    1145                1150                1155

agc gtc  aag gaa ctg ctg ggc  atc aca atc atg gag  cga tca agc        3519
Ser Val  Lys Glu Leu Leu Gly  Ile Thr Ile Met Glu  Arg Ser Ser
    1160                1165                1170

ttc gaa  aaa aac ccc atc gac  ttt ctc gag gcg aaa  gga tat aaa        3564
Phe Glu  Lys Asn Pro Ile Asp  Phe Leu Glu Ala Lys  Gly Tyr Lys
    1175                1180                1185

gag gtc  aaa aaa gac ctc atc  att aag ctt ccc aag  tac tct ctc        3609
Glu Val  Lys Lys Asp Leu Ile  Ile Lys Leu Pro Lys  Tyr Ser Leu
    1190                1195                1200

ttt gag  ctt gaa aac ggc cgg  aaa cga atg ctc gct  agt gcg ggc        3654
Phe Glu  Leu Glu Asn Gly Arg  Lys Arg Met Leu Ala  Ser Ala Gly
    1205                1210                1215

gag ctg  cag aaa ggt aac gag  ctg gca ctg ccc tct  aaa tac gtt        3699
Glu Leu  Gln Lys Gly Asn Glu  Leu Ala Leu Pro Ser  Lys Tyr Val
    1220                1225                1230

aat ttc  ttg tat ctg gcc agc  cac tat gaa aag ctc  aaa ggg tct        3744
Asn Phe  Leu Tyr Leu Ala Ser  His Tyr Glu Lys Leu  Lys Gly Ser
    1235                1240                1245

ccc gaa  gat aat gag cag aag  cag ctg ttc gtg gaa  caa cac aaa        3789
Pro Glu  Asp Asn Glu Gln Lys  Gln Leu Phe Val Glu  Gln His Lys
    1250                1255                1260

cac tac  ctt gat gag atc atc  gag caa ata agc gaa  ttc tcc aaa        3834
His Tyr  Leu Asp Glu Ile Ile  Glu Gln Ile Ser Glu  Phe Ser Lys
    1265                1270                1275

aga gtg  atc ctc gcc gac gct  aac ctc gat aag gtg  ctt tct gct        3879
Arg Val  Ile Leu Ala Asp Ala  Asn Leu Asp Lys Val  Leu Ser Ala
    1280                1285                1290

tac aat  aag cac agg gat aag  ccc atc agg gag cag  gca gaa aac        3924
Tyr Asn  Lys His Arg Asp Lys  Pro Ile Arg Glu Gln  Ala Glu Asn
    1295                1300                1305

att atc  cac ttg ttt act ctg  acc aac ttg ggc gcg  cct gca gcc        3969
Ile Ile  His Leu Phe Thr Leu  Thr Asn Leu Gly Ala  Pro Ala Ala
    1310                1315                1320

ttc aag  tac ttc gac acc acc  ata gac aga aag cgg  tac acc tct        4014
Phe Lys  Tyr Phe Asp Thr Thr  Ile Asp Arg Lys Arg  Tyr Thr Ser
    1325                1330                1335
```

```
aca aag  gag gtc ctg gac gcc  aca ctg att cat cag  tca att acg        4059
Thr Lys  Glu Val Leu Asp Ala  Thr Leu Ile His Gln  Ser Ile Thr
    1340                 1345                 1350

ggg ctc  tat gaa aca aga atc  gac ctc tct cag ctc  ggt gga gac        4104
Gly Leu  Tyr Glu Thr Arg Ile  Asp Leu Ser Gln Leu  Gly Gly Asp
    1355                 1360                 1365

agc agg  gct gac                                                    4116
Ser Arg  Ala Asp
    1370
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<210> 5
<211> 1372
<212> PRT
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (10)..(10)
<223> The 'Xaa' at location 10 stands for Asp, or Ala.

<220>
<221> misc_feature
<222> (840)..(840)
<223> The 'Xaa' at location 840 stands for Asp, Ala, His, or Pro.

<220>
<223> Synthetic Construct

<400> 5

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Met Asp Lys Lys Tyr Ser Ile Gly Leu Xaa Ile Gly Thr Asn Ser Val
1               5                  10                  15

Gly Trp Ala Val Ile Thr Asp Glu Tyr Lys Val Pro Ser Lys Lys Phe
            20                  25                  30

Lys Val Leu Gly Asn Thr Asp Arg His Ser Ile Lys Lys Asn Leu Ile
        35                  40                  45

Gly Ala Leu Leu Phe Asp Ser Gly Glu Thr Ala Glu Ala Thr Arg Leu
    50                  55                  60

Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg Ile Cys
65                  70                  75                  80

Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met Ala Lys Val Asp Asp Ser
                85                  90                  95

Phe Phe His Arg Leu Glu Glu Ser Phe Leu Val Glu Glu Asp Lys Lys
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```
            100                 105                 110

His Glu Arg His Pro Ile Phe Gly Asn Ile Val Asp Glu Val Ala Tyr
        115                 120                 125

His Glu Lys Tyr Pro Thr Ile Tyr His Leu Arg Lys Lys Leu Val Asp
    130                 135                 140

Ser Thr Asp Lys Ala Asp Leu Arg Leu Ile Tyr Leu Ala Leu Ala His
145                 150                 155                 160

Met Ile Lys Phe Arg Gly His Phe Leu Ile Glu Gly Asp Leu Asn Pro
                165                 170                 175

Asp Asn Ser Asp Val Asp Lys Leu Phe Ile Gln Leu Val Gln Thr Tyr
            180                 185                 190

Asn Gln Leu Phe Glu Glu Asn Pro Ile Asn Ala Ser Gly Val Asp Ala
        195                 200                 205

Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn
    210                 215                 220

Leu Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn
225                 230                 235                 240

Leu Ile Ala Leu Ser Leu Gly Leu Thr Pro Asn Phe Lys Ser Asn Phe
                245                 250                 255

Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser Lys Asp Thr Tyr Asp
            260                 265                 270

Asp Asp Leu Asp Asn Leu Leu Ala Gln Ile Gly Asp Gln Tyr Ala Asp
        275                 280                 285

Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp Ala Ile Leu Leu Ser Asp
    290                 295                 300

Ile Leu Arg Val Asn Thr Glu Ile Thr Lys Ala Pro Leu Ser Ala Ser
305                 310                 315                 320

Met Ile Lys Arg Tyr Asp Glu His His Gln Asp Leu Thr Leu Leu Lys
                325                 330                 335
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Ala Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile Phe Phe
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Asp Gln Ser Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Gly Ala Ser
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Gln Glu Glu Phe Tyr Lys Phe Ile Lys Pro Ile Leu Glu Lys Met Asp
    370                 375                 380

Gly Thr Glu Glu Leu Leu Val Lys Leu Asn Arg Glu Asp Leu Leu Arg
385                 390                 395                 400

Lys Gln Arg Thr Phe Asp Asn Gly Ser Ile Pro His Gln Ile His Leu
                405                 410                 415

Gly Glu Leu His Ala Ile Leu Arg Arg Gln Glu Asp Phe Tyr Pro Phe
            420                 425                 430

Leu Lys Asp Asn Arg Glu Lys Ile Glu Lys Ile Leu Thr Phe Arg Ile
        435                 440                 445

Pro Tyr Tyr Val Gly Pro Leu Ala Arg Gly Asn Ser Arg Phe Ala Trp
    450                 455                 460

Met Thr Arg Lys Ser Glu Glu Thr Ile Thr Pro Trp Asn Phe Glu Glu
465                 470                 475                 480

Val Val Asp Lys Gly Ala Ser Ala Gln Ser Phe Ile Glu Arg Met Thr
                485                 490                 495

Asn Phe Asp Lys Asn Leu Pro Asn Glu Lys Val Leu Pro Lys His Ser
            500                 505                 510

Leu Leu Tyr Glu Tyr Phe Thr Val Tyr Asn Glu Leu Thr Lys Val Lys
        515                 520                 525

Tyr Val Thr Glu Gly Met Arg Lys Pro Ala Phe Leu Ser Gly Glu Gln
    530                 535                 540

Lys Lys Ala Ile Val Asp Leu Leu Phe Lys Thr Asn Arg Lys Val Thr
545                 550                 555                 560

Val Lys Gln Leu Lys Glu Asp Tyr Phe Lys Lys Ile Glu Cys Phe Asp
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Ser Val Glu Ile Ser Gly Val Glu Asp Arg Phe Asn Ala Ser Leu Gly
580 585 590

Thr Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys Asp Phe Leu Asp
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Asn Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr
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Leu Phe Glu Asp Arg Glu Met Ile Glu Glu Arg Leu Lys Thr Tyr Ala
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His Leu Phe Asp Asp Lys Val Met Lys Gln Leu Lys Arg Arg Arg Tyr
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Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu Ile Asn Gly Ile Arg Asp
660 665 670

Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe
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Ala Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe
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Lys Glu Asp Ile Gln Lys Ala Gln Val Ser Gly Gln Gly Asp Ser Leu
705 710 715 720

His Glu His Ile Ala Asn Leu Ala Gly Ser Pro Ala Ile Lys Lys Gly
725 730 735

Ile Leu Gln Thr Val Lys Val Val Asp Glu Leu Val Lys Val Met Gly
740 745 750

Arg His Lys Pro Glu Asn Ile Val Ile Glu Met Ala Arg Glu Asn Gln
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Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg Glu Arg Met Lys Arg Ile
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Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln Ile Leu Lys Glu His Pro
785 790 795 800

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Val Glu Asn Thr Gln Leu Gln Asn Glu Lys Leu Tyr Leu Tyr Tyr Leu
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Gln Asn Gly Arg Asp Met Tyr Val Asp Gln Glu Leu Asp Ile Asn Arg
            820                 825                 830

Leu Ser Asp Tyr Asp Val Asp Xaa Ile Val Pro Gln Ser Phe Leu Lys
        835                 840                 845

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

Gly Lys Ser Asp Asn Val Pro Ser Glu Glu Val Val Lys Lys Met Lys
865                 870                 875                 880

Asn Tyr Trp Arg Gln Leu Leu Asn Ala Lys Leu Ile Thr Gln Arg Lys
                885                 890                 895

Phe Asp Asn Leu Thr Lys Ala Glu Arg Gly Gly Leu Ser Glu Leu Asp
            900                 905                 910

Lys Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr
        915                 920                 925

Lys His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp
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Glu Asn Asp Lys Leu Ile Arg Glu Val Lys Val Ile Thr Leu Lys Ser
945                 950                 955                 960

Lys Leu Val Ser Asp Phe Arg Lys Asp Phe Gln Phe Tyr Lys Val Arg
                965                 970                 975

Glu Ile Asn Asn Tyr His His Ala His Asp Ala Tyr Leu Asn Ala Val
            980                 985                 990

Val Gly Thr Ala Leu Ile Lys Lys  Tyr Pro Lys Leu Glu  Ser Glu Phe
        995                 1000                1005

Val Tyr  Gly Asp Tyr Lys Val  Tyr Asp Val Arg Lys  Met Ile Ala
    1010                1015                1020

Lys Ser  Glu Gln Glu Ile Gly  Lys Ala Thr Ala Lys  Tyr Phe Phe
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Tyr Ser Asn Ile Met Asn Phe Phe Lys Thr Glu Ile Thr Leu Ala
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Asn Gly Glu Ile Arg Lys Arg Pro Leu Ile Glu Thr Asn Gly Glu
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Thr Gly Glu Ile Val Trp Asp Lys Gly Arg Asp Phe Ala Thr Val
1070 1075 1080

Arg Lys Val Leu Ser Met Pro Gln Val Asn Ile Val Lys Lys Thr
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Glu Val Gln Thr Gly Gly Phe Ser Lys Glu Ser Ile Leu Pro Lys
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Arg Asn Ser Asp Lys Leu Ile Ala Arg Lys Lys Asp Trp Asp Pro
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Lys Lys Tyr Gly Gly Phe Asp Ser Pro Thr Val Ala Tyr Ser Val
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Leu Val Val Ala Lys Val Glu Lys Gly Lys Ser Lys Lys Leu Lys
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Ser Val Lys Glu Leu Leu Gly Ile Thr Ile Met Glu Arg Ser Ser
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Glu Val Lys Lys Asp Leu Ile Ile Lys Leu Pro Lys Tyr Ser Leu
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Phe Glu Leu Glu Asn Gly Arg Lys Arg Met Leu Ala Ser Ala Gly
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Glu Leu Gln Lys Gly Asn Glu Leu Ala Leu Pro Ser Lys Tyr Val
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Asn Phe Leu Tyr Leu Ala Ser His Tyr Glu Lys Leu Lys Gly Ser
1235 1240 1245

Pro Glu Asp Asn Glu Gln Lys Gln Leu Phe Val Glu Gln His Lys
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His Tyr Leu Asp Glu Ile Ile Glu Gln Ile Ser Glu Phe Ser Lys
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Arg Val Ile Leu Ala Asp Ala Asn Leu Asp Lys Val Leu Ser Ala
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Tyr Asn Lys His Arg Asp Lys Pro Ile Arg Glu Gln Ala Glu Asn
1295 1300 1305

Ile Ile His Leu Phe Thr Leu Thr Asn Leu Gly Ala Pro Ala Ala
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Phe Lys Tyr Phe Asp Thr Thr Ile Asp Arg Lys Arg Tyr Thr Ser
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Thr Lys Glu Val Leu Asp Ala Thr Leu Ile His Gln Ser Ile Thr
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Ala

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1 5 10 15

Ala

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cagctcggtg gagacagcag ggctgacccc aagaagaaga ggaaggtggg tggaggaggt 7440

acccctagga ccgaaggcag gggaagcctt ctgacttgtg gggatgtgga agaaaaccct 7500

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ccaaactcat caatgtatct tagc 8604

<210> 14
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 14
attccagaat atctccatgt agattttggt 30

<210> 15
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 15
aattccagga ggtccagatc ttcagggccc 30

<210> 16
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 16
tctttcccta cacgacgctc ttccgatcta ttccagaata tctccatgta gattttggt 59

<210> 17
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 17
gtgactggag ttcagacgtg tgctcttccg atctttaggc aaggaagtga ctgtaattat 60

gagc 64

<210> 18
<211> 26
<212> DNA
<213> Homo sapiens

<400> 18
acaatgcaga ctttgctttc cttggt 26

<210> 19
<211> 252
<212> DNA
<213> Artificial Sequence

<220>
<223> PBS2-derived Ugi CDS optimized for eucaryotic cell expression

<220>
<221> CDS
<222> (1)..(252)

<400> 19
atg acc aac ctt tcc gac atc ata gag aag gaa aca ggc aaa cag ttg 48
Met Thr Asn Leu Ser Asp Ile Ile Glu Lys Glu Thr Gly Lys Gln Leu
1 5 10 15

```
gtc atc caa gag tcg ata ctc atg ctt cct gaa gaa gtt gag gag gtc          96
Val Ile Gln Glu Ser Ile Leu Met Leu Pro Glu Glu Val Glu Glu Val
            20                  25                  30

att ggg aat aag ccg gaa agt gac att ctc gta cac act gcg tat gat         144
Ile Gly Asn Lys Pro Glu Ser Asp Ile Leu Val His Thr Ala Tyr Asp
        35                  40                  45

gag agc acc gat gag aac gtg atg ctg ctc acg tca gat gcc cca gag         192
Glu Ser Thr Asp Glu Asn Val Met Leu Leu Thr Ser Asp Ala Pro Glu
    50                  55                  60

tac aaa ccc tgg gct ctg gtg att cag gac tct aat gga gag aac aag         240
Tyr Lys Pro Trp Ala Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys
65                  70                  75                  80

atc aag atg cta                                                        252
Ile Lys Met Leu
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<210> 20
<211> 84
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 20

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Met Thr Asn Leu Ser Asp Ile Ile Glu Lys Glu Thr Gly Lys Gln Leu
1               5                   10                  15

Val Ile Gln Glu Ser Ile Leu Met Leu Pro Glu Glu Val Glu Glu Val
            20                  25                  30

Ile Gly Asn Lys Pro Glu Ser Asp Ile Leu Val His Thr Ala Tyr Asp
        35                  40                  45

Glu Ser Thr Asp Glu Asn Val Met Leu Leu Thr Ser Asp Ala Pro Glu
    50                  55                  60

Tyr Lys Pro Trp Ala Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys
65                  70                  75                  80

Ile Lys Met Leu
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<210> 21
<211> 420
<212> DNA

<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(420)
<223> fragment of TopBv2 (452-591)

<400> 21
aaa ggt att ccc aaa ctg gat gat gct aat gat gct ggt ggt aaa cat 48
Lys Gly Ile Pro Lys Leu Asp Asp Ala Asn Asp Ala Gly Gly Lys His
1 5 10 15

tcc ctg gag tgt aca ctg ata tta aca gag gga gac tct gcc aaa tca 96
Ser Leu Glu Cys Thr Leu Ile Leu Thr Glu Gly Asp Ser Ala Lys Ser
20 25 30

ctg gct gtg tct gga tta ggt gtg att gga cga gac aga tac gga gtt 144
Leu Ala Val Ser Gly Leu Gly Val Ile Gly Arg Asp Arg Tyr Gly Val
35 40 45

ttt cca ctc agg ggc aaa att ctt aat gta cgg gaa gct tct cat aaa 192
Phe Pro Leu Arg Gly Lys Ile Leu Asn Val Arg Glu Ala Ser His Lys
50 55 60

cag atc atg gaa aat gct gaa ata aat aat att att aaa ata gtt ggt 240
Gln Ile Met Glu Asn Ala Glu Ile Asn Asn Ile Ile Lys Ile Val Gly
65 70 75 80

cta caa tat aag aaa agt tac gat gat gca gaa tct ctg aaa acc tta 288
Leu Gln Tyr Lys Lys Ser Tyr Asp Asp Ala Glu Ser Leu Lys Thr Leu
85 90 95

cgc tat gga aag att atg att atg acc gat cag gat caa gat ggt tct 336
Arg Tyr Gly Lys Ile Met Ile Met Thr Asp Gln Asp Gln Asp Gly Ser
100 105 110

cac ata aaa ggc ctg ctt att aat ttc atc cat cac aat tgg cca tca 384
His Ile Lys Gly Leu Leu Ile Asn Phe Ile His His Asn Trp Pro Ser
115 120 125

ctt ttg aag cat ggt ttt ctt gaa gag ttc att act 420
Leu Leu Lys His Gly Phe Leu Glu Glu Phe Ile Thr
130 135 140

<210> 22
<211> 140
<212> PRT
<213> Homo sapiens

<400> 22

Lys Gly Ile Pro Lys Leu Asp Asp Ala Asn Asp Ala Gly Gly Lys His
1 5 10 15

Ser Leu Glu Cys Thr Leu Ile Leu Thr Glu Gly Asp Ser Ala Lys Ser

```
            20                  25                  30

Leu Ala Val Ser Gly Leu Gly Val Ile Gly Arg Asp Arg Tyr Gly Val
        35                  40                  45

Phe Pro Leu Arg Gly Lys Ile Leu Asn Val Arg Glu Ala Ser His Lys
    50                  55                  60

Gln Ile Met Glu Asn Ala Glu Ile Asn Asn Ile Ile Lys Ile Val Gly
65                  70                  75                  80

Leu Gln Tyr Lys Lys Ser Tyr Asp Asp Ala Glu Ser Leu Lys Thr Leu
                85                  90                  95

Arg Tyr Gly Lys Ile Met Ile Met Thr Asp Gln Asp Gln Asp Gly Ser
            100                 105                 110

His Ile Lys Gly Leu Leu Ile Asn Phe Ile His His Asn Trp Pro Ser
        115                 120                 125

Leu Leu Lys His Gly Phe Leu Glu Glu Phe Ile Thr
    130                 135                 140
```

<210> 23
<211> 246
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(246)
<223> fragment of IQGAP2 (466-547)

<400> 23

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gaa ggg aat cct ttg agg act tta gaa act ttg ctc cta cct act gcg        48
Glu Gly Asn Pro Leu Arg Thr Leu Glu Thr Leu Leu Leu Pro Thr Ala
1               5                   10                  15

aat att agt gat gtg gac cca gcc cat gcc cag cac tac cag gat gtt        96
Asn Ile Ser Asp Val Asp Pro Ala His Ala Gln His Tyr Gln Asp Val
            20                  25                  30

tta tac cat gct aaa tca cag aaa ctc gga gac tct gag agt gtt tcc       144
Leu Tyr His Ala Lys Ser Gln Lys Leu Gly Asp Ser Glu Ser Val Ser
        35                  40                  45

aaa gtg ctt tgg ctg gat gag ata cag caa gcc gtc gat gat gcc aac       192
Lys Val Leu Trp Leu Asp Glu Ile Gln Gln Ala Val Asp Asp Ala Asn
    50                  55                  60
```

```
gtg gac aag gac aga gca aaa caa tgg gtt act ctg gtg gtt gat gtt        240
Val Asp Lys Asp Arg Ala Lys Gln Trp Val Thr Leu Val Val Asp Val
65                  70                  75                  80

aat cag                                                              246
Asn Gln
```

<210> 24
<211> 82
<212> PRT
<213> Homo sapiens

<400> 24

```
Glu Gly Asn Pro Leu Arg Thr Leu Glu Thr Leu Leu Leu Pro Thr Ala
1               5                   10                  15

Asn Ile Ser Asp Val Asp Pro Ala His Ala Gln His Tyr Gln Asp Val
            20                  25                  30

Leu Tyr His Ala Lys Ser Gln Lys Leu Gly Asp Ser Glu Ser Val Ser
        35                  40                  45

Lys Val Leu Trp Leu Asp Glu Ile Gln Gln Ala Val Asp Asp Ala Asn
    50                  55                  60

Val Asp Lys Asp Arg Ala Lys Gln Trp Val Thr Leu Val Val Asp Val
65                  70                  75                  80

Asn Gln
```

<210> 25
<211> 447
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(447)
<223> fragment of NIF-ZFN335_745-893 (466-547)

<400> 25

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agt tcc cca gga cct cct gag ata ccc cca gag gcg aca act ttc cag         48
Ser Ser Pro Gly Pro Pro Glu Ile Pro Pro Glu Ala Thr Thr Phe Gln
1               5                   10                  15

tca tct gag gct ccc tca ttg ctc tgt tct gac acc ctg ggc ggc gcc         96
```

```
Ser Ser Glu Ala Pro Ser Leu Leu Cys Ser Asp Thr Leu Gly Gly Ala
            20                  25                  30

acc atc atc tac cag caa gga gct gag gag tcg aca gcg atg gcc acg        144
Thr Ile Ile Tyr Gln Gln Gly Ala Glu Glu Ser Thr Ala Met Ala Thr
        35                  40                  45

cag aca gcc ttg gat ctt ctg ctg aac atg agt gct cag cgg gaa ctg        192
Gln Thr Ala Leu Asp Leu Leu Leu Asn Met Ser Ala Gln Arg Glu Leu
    50                  55                  60

ggg ggc aca gcc ctg cag gtg gct gtg gtg aag tcg gaa gat gtg gaa        240
Gly Gly Thr Ala Leu Gln Val Ala Val Val Lys Ser Glu Asp Val Glu
65                  70                  75                  80

gca ggg tta gca tcc cct ggt ggg cag ccc tcc cct gaa ggt gcc act        288
Ala Gly Leu Ala Ser Pro Gly Gly Gln Pro Ser Pro Glu Gly Ala Thr
                85                  90                  95

cca cag gtc gtc acc ctc cac gtg gca gag cca ggg ggc ggt gca gca        336
Pro Gln Val Val Thr Leu His Val Ala Glu Pro Gly Gly Gly Ala Ala
            100                 105                 110

gcc gag agc cag cta ggc cct cct gac cta ccg cag atc acc ctg gca        384
Ala Glu Ser Gln Leu Gly Pro Pro Asp Leu Pro Gln Ile Thr Leu Ala
        115                 120                 125

cct ggt cca ttt ggt ggg act ggc tac agt gtc atc aca gca ccc cct        432
Pro Gly Pro Phe Gly Gly Thr Gly Tyr Ser Val Ile Thr Ala Pro Pro
    130                 135                 140

atg gag gag gga aca                                                    447
Met Glu Glu Gly Thr
145
```

<210> 26
<211> 149
<212> PRT
<213> Homo sapiens

<400> 26

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Ser Ser Pro Gly Pro Pro Glu Ile Pro Pro Glu Ala Thr Thr Phe Gln
1               5                   10                  15


Ser Ser Glu Ala Pro Ser Leu Leu Cys Ser Asp Thr Leu Gly Gly Ala
            20                  25                  30


Thr Ile Ile Tyr Gln Gln Gly Ala Glu Glu Ser Thr Ala Met Ala Thr
        35                  40                  45


Gln Thr Ala Leu Asp Leu Leu Leu Asn Met Ser Ala Gln Arg Glu Leu
    50                  55                  60
```

Gly Gly Thr Ala Leu Gln Val Ala Val Val Lys Ser Glu Asp Val Glu
65 70 75 80

Ala Gly Leu Ala Ser Pro Gly Gly Gln Pro Ser Pro Glu Gly Ala Thr
85 90 95

Pro Gln Val Val Thr Leu His Val Ala Glu Pro Gly Gly Gly Ala Ala
100 105 110

Ala Glu Ser Gln Leu Gly Pro Pro Asp Leu Pro Gln Ile Thr Leu Ala
115 120 125

Pro Gly Pro Phe Gly Gly Thr Gly Tyr Ser Val Ile Thr Ala Pro Pro
130 135 140

Met Glu Glu Gly Thr
145

<210> 27
<211> 20
<212> DNA
<213> Homo sapiens

<400> 27
tcgagatgtg atgaaggaga 20

<210> 28
<211> 9228
<212> DNA
<213> Artificial Sequence

<220>
<223> Complete nucleotide sequence of vector 1923-2

<220>
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<222> (167)..(188)
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<220>
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<222> (476)..(1064)
<223> ori

<220>
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<223> AmpR

<220>
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<222> (2096)..(2200)
<223> AmpR promoter

<220>
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<223> H1 promoter

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<223> Target (HPRT site 1)

<220>
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<222> (2482)..(2557)
<223> tracrRNA

<220>
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<223> CMV enhancer

<220>
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<222> (2952)..(3155)
<223> CMV promoter

<220>
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<222> (3200)..(3218)
<223> T7 promoter

<220>
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<222> (3247)..(3498)
<223> UGI

<220>
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<222> (3502)..(3504)
<223> kozac

<220>
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<222> (3505)..(3555)
<223> NLS unit

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<222> (3511)..(3531)
<223> SV40 NLS

<220>
<221> gene
<222> (3556)..(7692)

<223> nCas9 (D10A)

<220>
<221> misc_feature
<222> (7672)..(7692)
<223> SV40 NLS

<220>
<221> gene
<222> (7714)..(8262)
<223> dVif

<220>
<221> misc_feature
<222> (7714)..(7722)
<223> CBF beta binding

<220>
<221> misc_feature
<222> (8272)..(8325)
<223> T2A

<220>
<221> gene
<222> (8332)..(8931)
<223> PuroR

<220>
<221> polyA_signal
<222> (9105)..(9226)
<223> SV40 poly(A) signal

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ggccgccacc gcggtggagc tccagctttt gttcccttta gtgagggtta attgcgcgct 60

tggcgtaatc atggtcatag ctgtttcctg tgtgaaattg ttatccgctc acaattccac 120

acaacatacg agccggaagc ataaagtgta aagcctgggg tgcctaatga gtgagctaac 180

tcacattaat tgcgttgcgc tcactgcccg ctttccagtc gggaaacctg tcgtgccagc 240

tgcattaatg aatcggccaa cgcgcgggga gaggcggttt gcgtattggg cgctcttccg 300

cttcctcgct cactgactcg ctgcgctcgg tcgttcggct gcggcgagcg gtatcagctc 360

actcaaaggc ggtaatacgg ttatccacag aatcagggga taacgcagga aagaacatgt 420

gagcaaaagg ccagcaaaag gccaggaacc gtaaaaaggc cgcgttgctg gcgtttttcc 480

ataggctccg ccccccctgac gagcatcaca aaaatcgacg ctcaagtcag aggtggcgaa 540

acccgacagg actataaaga taccaggcgt ttcccccctgg aagctccctc gtgcgctctc 600

ctgttccgac cctgccgctt accggatacc tgtccgcctt tctcccttcg ggaagcgtgg 660

cgctttctca tagctcacgc tgtaggtatc tcagttcggt gtaggtcgtt cgctccaagc 720

tgggctgtgt gcacgaaccc cccgttcagc ccgaccgctg cgccttatcc ggtaactatc 780

gtcttgagtc caacccggta agacacgact tatcgccact ggcagcagcc actggtaaca 840

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gaaaactctc aaggatctta ccgctgttga gatccagttc gatgtaaccc actcgtgcac 1980

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