SEQUENCE LISTING

<110> Geneuro

<120> Antiretroviral drug targeting human endogenous retrovirus

<130>

<160> 28

<170> BiSSAP 1.3

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<213> Mus musculus

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<210> 2
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Arg Thr Ser Asn Leu Ala Ser
1 5

<210> 3
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Gln Gln Tyr Gln Ser Leu Pro Leu Thr
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Asp Tyr Glu Met His
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Tyr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Trp Ile Tyr
        35   40   45
Arg Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
65   70   75   80
Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Gln Ser Leu Pro Leu Thr
                85   90   95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

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<211> 116
<212> PRT
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<220>
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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20   25   30
Glu Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Ala Val Ala Pro Glu Thr Gly Gly Thr Ala Tyr Asn Gln Lys Phe
    50   55   60
Lys Gly Arg Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65   70   75   80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Thr Ser Thr Val Val Pro Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
            100   105   110
Thr Val Ser Ser
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<211> 443
<212> PRT
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<220>
<223> HC

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20   25   30
Glu Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Ala Val Ala Pro Glu Thr Gly Gly Thr Ala Tyr Asn Gln Lys Phe
    50   55   60
Lys Gly Arg Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65   70   75   80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Thr Ser Thr Val Val Pro Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
            100   105   110
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        115   120   125
Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu

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Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145                 150                 155                 160
Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                165                 170                 175
Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            180                 185                 190
Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr
        195                 200                 205
Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
    210                 215                 220
Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
225                 230                 235                 240
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
                245                 250                 255
Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
            260                 265                 270
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
        275                 280                 285
Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
    290                 295                 300
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305                 310                 315                 320
Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
                325                 330                 335
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
            340                 345                 350
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
        355                 360                 365
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
    370                 375                 380
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
385                 390                 395                 400
Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
                405                 410                 415
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
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Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
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<220>
<223> LC

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Tyr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Trp Ile Tyr
35 40 45
Arg Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60
Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
65 70 75 80
Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Gln Ser Leu Pro Leu Thr
85 90 95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205
Asn Arg Gly Glu Cys
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<210> 11
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 11
cttccagaat tgaagctgta aagc 24

<210> 12
<211> 22
<212> DNA
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<400> 12
gggttgtgca gttgagattt cc 22

<210> 13
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<223> PROBE / FAM in 5' position and TAMRA in 3' position

<400> 13
ttcttcaaat ggagccccag atgcag 26

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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<400> 14
actttgtctc ttccagaatc 20

<210> 15
<211> 20
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<220>
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<400> 15
gcggtagatc ttagtcttgg 20

<210> 16
<211> 17
<212> DNA
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<223> PROBE / FAM in position 5' and TAMRA in position 3'

<400> 16
atggagccca agatgca 17

<210> 17
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<220>
<223> primer

<400> 17
ggcggttagc aagtctaaag 20

<210> 18
<211> 21
<212> DNA
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<220>
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<400> 18
atggaacagg tcactgactc c 21

<210> 19
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<220>
<223> primer

<400> 19
gtatgtctga tgggggtgga g 21

<210> 20
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<223> primer

<400> 20
ctagtccttt gtaggggcta gag 23

<210> 21
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<400> 21
tgccccatcg tataggagtc t 21

<210> 22
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<400> 22
catgtacccg ggtgagttgg 20

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cctgtacgtc ctgactctc 19

<210> 24
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<223> primer

<400> 24
cttgggctaa tgcctggcc 19

<210> 25
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<220>
<223> PROBE/ FAM in position 5' and TAMRA in position 3'

<400> 25
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<210> 26
<211> 24
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<220>
<223> primer

<400> 26
ggtgtgaacc atgagaagta tgac 24

<210> 27
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<213> Artificial Sequence

<220>
<223> primer

<400> 27
tggcatggac tgtggtcatg 20

<210> 28
<211> 27
<212> DNA
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<220>

eolf-seql

<223> PROBE / VIC in position 5' and TAMRA in position 3'

<400> 28

agcctcaaga tcatcagcaa tgcctcc 27