SEQUENCE LISTING

<110> Transgene SA
MARTIN, Perrine
MARCHAND, Jean-Baptiste
SILVESTRE, Nathalie

<120> HBV polymerase mutant

<130> 361194D31275

<150> EP11305909.1
<151> 2011-07-12

<150> EP12305450.4
<151> 2012-04-18

<160> 26

<170> PatentIn version 3.3

<210> 1
<211> 344
<212> PRT
<213> Hepatitis B virus

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa (7) can be Thr (T) or Ala (A)

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> Xaa (13) can be Asn (N), Arg (R) or His (H)

<220>
<221> MISC_FEATURE
<222> (16)..(16)
<223> Xaa (16) can be Ile (I) or Thr (T)

<220>
<221> MISC_FEATURE
<222> (38)..(38)
<223> Xaa (38) can be Thr (T) or Ala (A)

<220>
<221> MISC_FEATURE
<222> (53)..(53)
<223> Xaa (53) can be Ser (S) or Asn (N)

<220>
<221> MISC_FEATURE
<222> (54)..(54)
<223> Xaa (54) can be Thr (T) or Tyr (Y)

<220>
<221> MISC_FEATURE
<222> (55)..(55)
<223> Xaa (55) can be His (H) or Arg (R)

<220>
<221> MISC_FEATURE
<222> (91)..(91)
<223> Xaa (91) can be Ile (I) or Leu (L)

<220>

<221> MISC_FEATURE
<222> (109)..(109)
<223> Xaa (109) can be Pro (P) or Ser (S)

<220>
<221> MISC_FEATURE
<222> (118)..(118)
<223> Xaa (118) can be Thr (T) or Asn (N)

<220>
<221> MISC_FEATURE
<222> (121)..(121)
<223> Xaa (121) can be Asn (N) or Ile (I)

<220>
<221> MISC_FEATURE
<222> (122)..(122)
<223> Xaa (122) can be Ile (I) or Phe (F)

<220>
<221> MISC_FEATURE
<222> (124)..(124)
<223> Xaa (124) can be Tyr (Y) or Asn (N)

<220>
<221> MISC_FEATURE
<222> (127)..(127)
<223> Xaa (127) can be Gly (G) or Arg (R)

<220>
<221> MISC_FEATURE
<222> (131)..(131)
<223> Xaa (131) can be Asp (D) or Asn (N)

<220>
<221> MISC_FEATURE
<222> (134)..(134)
<223> Xaa (134) can be Asp (D) or Asn (N)

<220>
<221> MISC_FEATURE
<222> (145)..(145)
<223> Xaa (145) can be Leu (L) or Met (M)

<220>
<221> MISC_FEATURE
<222> (149)..(149)
<223> Xaa (149) can be Lys (K) or Gln (Q)

<220>
<221> MISC_FEATURE
<222> (151)..(151)
<223> Xaa (151) can be Phe (F) or Tyr (Y)

<220>
<221> MISC_FEATURE
<222> (221)..(221)
<223> Xaa (221) can be Phe (F) or Tyr (Y)

<220>
<221> MISC_FEATURE
<222> (222)..(222)
<223> Xaa (222) can be Thr (T) or Ala (A)

<220>
<221> MISC_FEATURE
<222> (223)..(223)
<223> Xaa (223) can be Ser (S) or Ala (A)

<220>
<221> MISC_FEATURE
<222> (224)..(224)
<223> Xaa (224) can be Ile (I) or Val (V)

<220>
<221> MISC_FEATURE
<222> (238)..(238)
<223> Xaa (238) can be Asn (N) or His (H)

<220>
<221> MISC_FEATURE
<222> (248)..(248)
<223> Xaa (248) can be Asn (N) or His (H)

<220>
<221> MISC_FEATURE
<222> (256)..(256)
<223> Xaa (256) can be Ser (S) or Cys (C)

<220>
<221> MISC_FEATURE
<222> (257)..(257)
<223> Xaa (257) can be Trp (W) or Tyr (Y)

<220>
<221> MISC_FEATURE
<222> (259)..(259)
<223> Xaa (259) can be Thr (T) or Ser (S)

<220>
<221> MISC_FEATURE
<222> (263)..(263)
<223> Xaa (263) can be Glu (E) or Asp (D)

<220>
<221> MISC_FEATURE
<222> (266)..(266)
<223> Xaa (266) can be Val (V) or Ile (I)

<220>
<221> MISC_FEATURE
<222> (267)..(267)
<223> Xaa (267) can be Leu (L) or Gln (Q)

<220>
<221> MISC_FEATURE
<222> (271)..(271)
<223> Xaa (271) can be Gln (Q), Met (M) or Glu (E)

<220>
<221> MISC_FEATURE
<222> (317)..(317)
<223> Xaa (317) can be Ser (S) or Ala (A)

<220>
<221> MISC_FEATURE
<222> (317)..(317)
<223> Xaa (317) can be Ser (S) or Ala (A)

<220>
<221> MISC_FEATURE
<222> (332)..(332)
<223> Xaa (332) can be Cys (C) or Ser (S)

<400> 1

eolf-seql

```
Glu Asp Trp Gly Pro Cys Xaa Glu His Gly Glu His Xaa Ile Arg Xaa
1               5                  10                  15

Pro Arg Thr Pro Ala Arg Val Thr Gly Gly Val Phe Leu Val Asp Lys
            20                  25                  30

Asn Pro His Asn Thr Xaa Glu Ser Arg Leu Val Val Asp Phe Ser Gln
        35                  40                  45

Phe Ser Arg Gly Xaa Xaa Xaa Val Ser Trp Pro Lys Phe Ala Val Pro
    50                  55                  60

Asn Leu Gln Ser Leu Thr Asn Leu Leu Ser Ser Asn Leu Ser Trp Leu
65                  70                  75                  80

Ser Leu Asp Val Ser Ala Ala Phe Tyr His Xaa Pro Leu His Pro Ala
                85                  90                  95

Ala Met Pro His Leu Leu Val Gly Ser Ser Gly Leu Xaa Arg Tyr Val
            100                 105                 110

Ala Arg Leu Ser Ser Xaa Ser Arg Xaa Xaa Asn Xaa Gln His Xaa Thr
        115                 120                 125

Met Gln Xaa Leu His Xaa Ser Cys Ser Arg Asn Leu Tyr Val Ser Leu
    130                 135                 140

Xaa Leu Leu Tyr Xaa Thr Xaa Gly Arg Lys Leu His Leu Tyr Ser His
145                 150                 155                 160

Pro Ile Ile Leu Gly Phe Arg Lys Ile Pro Met Gly Val Gly Leu Ser
                165                 170                 175

Pro Phe Leu Leu Ala Gln Phe Thr Ser Ala Ile Cys Ser Val Val Arg
            180                 185                 190

Arg Ala Phe Pro His Cys Leu Ala Phe Ser Tyr Met Asp Asp Val Val
        195                 200                 205

Leu Gly Ala Lys Ser Val Gln His Leu Glu Ser Leu Xaa Xaa Xaa Xaa
    210                 215                 220

Thr Asn Phe Leu Leu Ser Leu Gly Ile His Leu Asn Pro Xaa Lys Thr
225                 230                 235                 240

Lys Arg Trp Gly Tyr Ser Leu Xaa Phe Met Gly Tyr Val Ile Gly Xaa
                245                 250                 255

Xaa Gly Xaa Leu Pro Gln Xaa His Ile Xaa Xaa Lys Ile Lys Xaa Cys
            260                 265                 270
```

```
Phe Arg Lys Leu Pro Val Asn Arg Pro Ile Asp Trp Lys Val Cys Gln
        275                 280                 285

Arg Ile Val Gly Leu Leu Gly Phe Ala Ala Pro Phe Thr Gln Cys Gly
    290                 295                 300

Tyr Pro Ala Leu Met Pro Leu Tyr Ala Cys Ile Gln Xaa Lys Gln Ala
305                 310                 315                 320

Phe Thr Phe Ser Pro Thr Tyr Lys Ala Phe Leu Xaa Lys Gln Tyr Leu
                325                 330                 335

Asn Leu Tyr Pro Val Ala Arg Gln
            340
```

<210> 2
<211> 337
<212> PRT
<213> artificial sequence

<220>
<223> mutated Y07587 polymerase domain (del YMDDVVL)

<400> 2

```
Glu Asp Trp Gly Pro Cys Ala Glu His Gly Glu His His Ile Arg Ile
1               5                   10                  15

Pro Arg Thr Pro Ala Arg Val Thr Gly Gly Val Phe Leu Val Asp Lys
            20                  25                  30

Asn Pro His Asn Thr Ala Glu Ser Arg Leu Val Val Asp Phe Ser Gln
        35                  40                  45

Phe Ser Arg Gly Asn Tyr Arg Val Ser Trp Pro Lys Phe Ala Val Pro
    50                  55                  60

Asn Leu Gln Ser Leu Thr Asn Leu Leu Ser Ser Asn Leu Ser Trp Leu
65                  70                  75                  80

Ser Leu Asp Val Ser Ala Ala Phe Tyr His Leu Pro Leu His Pro Ala
                85                  90                  95

Ala Met Pro His Leu Leu Val Gly Ser Ser Gly Leu Ser Arg Tyr Val
            100                 105                 110

Ala Arg Leu Ser Ser Asn Ser Arg Ile Phe Asn Tyr Gln His Gly Thr
        115                 120                 125

Met Gln Asn Leu His Asp Ser Cys Ser Arg Asn Leu Tyr Val Ser Leu
    130                 135                 140

Leu Leu Leu Tyr Gln Thr Phe Gly Arg Lys Leu His Leu Tyr Ser His
145                 150                 155                 160
```

```
Pro Ile Ile Leu Gly Phe Arg Lys Ile Pro Met Gly Val Gly Leu Ser
                165                 170                 175

Pro Phe Leu Leu Ala Gln Phe Thr Ser Ala Ile Cys Ser Val Val Arg
            180                 185                 190

Arg Ala Phe Pro His Cys Leu Ala Phe Ser Gly Ala Lys Ser Val Gln
        195                 200                 205

His Leu Glu Ser Leu Phe Thr Ala Val Thr Asn Phe Leu Leu Ser Leu
    210                 215                 220

Gly Ile His Leu Asn Pro Asn Lys Thr Lys Arg Trp Gly Tyr Ser Leu
225                 230                 235                 240

His Phe Met Gly Tyr Val Ile Gly Cys Tyr Gly Ser Leu Pro Gln Asp
                245                 250                 255

His Ile Ile Gln Lys Ile Lys Glu Cys Phe Arg Lys Leu Pro Val Asn
            260                 265                 270

Arg Pro Ile Asp Trp Lys Val Cys Gln Arg Ile Val Gly Leu Leu Gly
        275                 280                 285

Phe Ala Ala Pro Phe Thr Gln Cys Gly Tyr Pro Ala Leu Met Pro Leu
    290                 295                 300

Tyr Ala Cys Ile Gln Ser Lys Gln Ala Phe Thr Phe Ser Pro Thr Tyr
305                 310                 315                 320

Lys Ala Phe Leu Cys Lys Gln Tyr Leu Asn Leu Tyr Pro Val Ala Arg
                325                 330                 335

Gln
```

<210> 3
<211> 153
<212> PRT
<213> Hepatitis B virus

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa (2) can be Ser (S) or Pro (P)

<220>
<221> MISC_FEATURE
<222> (19)..(19)
<223> Xaa (19) can be Ala (A) or Val (V)

<220>
<221> MISC_FEATURE

<222> (20)..(20)
<223> Xaa (20) can be Ile (I) or Met (M)

<220>
<221> MISC_FEATURE
<222> (30)..(30)
<223> Xaa (30) can be Val (V) or Leu (L)

<220>
<221> MISC_FEATURE
<222> (31)..(31)
<223> Xaa (31) can be Ala (A) or Ser (S)

<220>
<221> MISC_FEATURE
<222> (53)..(53)
<223> Xaa (53) can be Lys (K) or Asn (N)

<220>
<221> MISC_FEATURE
<222> (54)..(54)
<223> Xaa (54) can be Leu (L) or Ile (I)

<220>
<221> MISC_FEATURE
<222> (55)..(55)
<223> Xaa (55) can be Leu (L) or Ile (I)

<220>
<221> MISC_FEATURE
<222> (97)..(97)
<223> Xaa (97) can be Ala (A) or Thr (T)

<220>
<221> MISC_FEATURE
<222> (108)..(108)
<223> Xaa (108) can be Tyr (Y) or Ser (S)

<220>
<221> MISC_FEATURE
<222> (115)..(115)
<223> Xaa (115) can be Pro (P) or Leu (L)

<220>
<221> MISC_FEATURE
<222> (116)..(116)
<223> Xaa (116) can be Phe (F) or Tyr (Y)

<220>
<221> MISC_FEATURE
<222> (128)..(128)
<223> Xaa (128) can be Val (V) or Asp (D)

<400> 3

Arg Xaa Gly Leu Cys Gln Val Phe Ala Asp Ala Thr Pro Thr Gly Trp
1 5 10 15

Gly Leu Xaa Xaa Gly His Gln Arg Met Arg Gly Thr Phe Xaa Xaa Pro
20 25 30

Leu Pro Ile His Thr Ala Glu Leu Leu Ala Ala Cys Phe Ala Arg Ser
35 40 45

Arg Ser Gly Ala Xaa Xaa Xaa Gly Thr Asp Asn Ser Val Val Leu Ser

50 55 60

Arg Lys Tyr Thr Ser Phe Pro Trp Leu Leu Gly Cys Ala Ala Asn Trp
65 70 75 80

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

Xaa Asp Asp Pro Ser Arg Gly Arg Leu Gly Leu Xaa Arg Pro Leu Leu
100 105 110

Arg Leu Xaa Xaa Arg Pro Thr Thr Gly Arg Thr Ser Leu Tyr Ala Xaa
115 120 125

Ser Pro Ser Val Pro Ser His Leu Pro Asp Arg Val His Phe Ala Ser
130 135 140

Pro Leu His Val Ala Trp Arg Pro Pro
145 150

<210> 4
<211> 120
<212> PRT
<213> artificial sequence

<220>
<223> mutated Y07587 RNaseH domain (deletion 710-742 ; subsittution D689H V769Y V776Y D777H)

<400> 4

Arg Pro Gly Leu Cys Gln Val Phe Ala His Ala Thr Pro Thr Gly Trp
1 5 10 15

Gly Leu Val Met Gly His Gln Arg Met Arg Gly Thr Phe Leu Ser Arg
20 25 30

Lys Tyr Thr Ser Phe Pro Trp Leu Leu Gly Cys Ala Ala Asn Trp Ile
35 40 45

Leu Arg Gly Thr Ser Phe Val Tyr Tyr Pro Ser Ala Leu Asn Pro Tyr
50 55 60

His Asp Pro Ser Arg Gly Arg Leu Gly Leu Ser Arg Pro Leu Leu Arg
65 70 75 80

Leu Pro Phe Arg Pro Thr Thr Gly Arg Thr Ser Leu Tyr Ala Asp Ser
85 90 95

Pro Ser Val Pro Ser His Leu Pro Asp Arg Val His Phe Ala Ser Pro
100 105 110

Leu His Val Ala Trp Arg Pro Pro
115 120

<210> 5
<211> 792
<212> PRT
<213> artificial sequence

<220>
<223> Y07587 polymerase with mutated polymerase and RNaseH domains

<400> 5

Met Pro Leu Ser Tyr Gln His Phe Arg Arg Leu Leu Leu Leu Asp Asp
1 5 10 15

Glu Ala Gly Pro Leu Glu Glu Glu Leu Pro Arg Leu Ala Asp Glu Gly
20 25 30

Leu Asn Arg Arg Val Ala Glu Asp Leu Asn Leu Gly Asn Leu Asn Val
35 40 45

Ser Ile Pro Trp Thr His Lys Val Gly Asn Phe Thr Gly Leu Tyr Ser
50 55 60

Ser Thr Val Pro Val Phe Asn Pro His Trp Lys Thr Pro Ser Phe Pro
65 70 75 80

Asn Ile His Leu His Gln Asp Ile Ile Lys Lys Cys Glu Gln Phe Val
85 90 95

Gly Pro Leu Thr Val Asn Glu Lys Arg Arg Leu Gln Leu Ile Met Pro
100 105 110

Ala Arg Phe Tyr Pro Asn Val Thr Lys Tyr Leu Pro Leu Asp Lys Gly
115 120 125

Ile Lys Pro Tyr Tyr Pro Glu His Leu Val Asn His Tyr Phe Gln Thr
130 135 140

Arg His Tyr Leu His Thr Leu Trp Lys Ala Gly Ile Leu Tyr Lys Arg
145 150 155 160

Glu Thr Thr His Ser Ala Ser Phe Cys Gly Ser Pro Tyr Ser Trp Glu
165 170 175

Gln Lys Leu Gln His Gly Ala Glu Ser Phe His Gln Gln Ser Ser Gly
180 185 190

Ile Leu Ser Arg Pro Pro Val Gly Ser Ser Leu Gln Ser Lys His Arg
195 200 205

Lys Ser Arg Leu Gly Leu Gln Ser Gln Gln Gly His Leu Ala Arg Arg
210 215 220

```
Gln Gln Gly Arg Ser Trp Ser Ile Arg Ala Gly Ile His Pro Thr Ala
225                 230                 235                 240

Arg Arg Ser Phe Gly Val Glu Pro Ser Gly Ser Gly His Ser Thr Asn
                245                 250                 255

Leu Ala Ser Lys Ser Ala Ser Cys Leu Tyr Gln Ser Pro Val Arg Lys
            260                 265                 270

Ala Ala Tyr Pro Ala Val Ser Thr Phe Glu Lys His Ser Ser Ser Gly
        275                 280                 285

His Ala Val Glu Leu His Asn Leu Pro Pro Asn Ser Ala Arg Ser Gln
    290                 295                 300

Ser Glu Arg Pro Val Phe Pro Cys Trp Trp Leu Gln Phe Arg Asn Ser
305                 310                 315                 320

Lys Pro Cys Ser Asp Tyr Cys Leu Ser His Ile Val Asn Leu Leu Glu
                325                 330                 335

Asp Trp Gly Pro Cys Ala Glu His Gly Glu His His Ile Arg Ile Pro
            340                 345                 350

Arg Thr Pro Ala Arg Val Thr Gly Gly Val Phe Leu Val Asp Lys Asn
        355                 360                 365

Pro His Asn Thr Ala Glu Ser Arg Leu Val Val Asp Phe Ser Gln Phe
    370                 375                 380

Ser Arg Gly Asn Tyr Arg Val Ser Trp Pro Lys Phe Ala Val Pro Asn
385                 390                 395                 400

Leu Gln Ser Leu Thr Asn Leu Leu Ser Ser Asn Leu Ser Trp Leu Ser
                405                 410                 415

Leu Asp Val Ser Ala Ala Phe Tyr His Leu Pro Leu His Pro Ala Ala
            420                 425                 430

Met Pro His Leu Leu Val Gly Ser Ser Gly Leu Ser Arg Tyr Val Ala
        435                 440                 445

Arg Leu Ser Ser Asn Ser Arg Ile Phe Asn Tyr Gln His Gly Thr Met
    450                 455                 460

Gln Asn Leu His Asp Ser Cys Ser Arg Asn Leu Tyr Val Ser Leu Leu
465                 470                 475                 480

Leu Leu Tyr Gln Thr Phe Gly Arg Lys Leu His Leu Tyr Ser His Pro
                485                 490                 495
```

```
Ile Ile Leu Gly Phe Arg Lys Ile Pro Met Gly Val Gly Leu Ser Pro
            500                 505                 510

Phe Leu Leu Ala Gln Phe Thr Ser Ala Ile Cys Ser Val Val Arg Arg
        515                 520                 525

Ala Phe Pro His Cys Leu Ala Phe Ser Gly Ala Lys Ser Val Gln His
    530                 535                 540

Leu Glu Ser Leu Phe Thr Ala Val Thr Asn Phe Leu Leu Ser Leu Gly
545                 550                 555                 560

Ile His Leu Asn Pro Asn Lys Thr Lys Arg Trp Gly Tyr Ser Leu His
                565                 570                 575

Phe Met Gly Tyr Val Ile Gly Cys Tyr Gly Ser Leu Pro Gln Asp His
            580                 585                 590

Ile Ile Gln Lys Ile Lys Glu Cys Phe Arg Lys Leu Pro Val Asn Arg
        595                 600                 605

Pro Ile Asp Trp Lys Val Cys Gln Arg Ile Val Gly Leu Leu Gly Phe
    610                 615                 620

Ala Ala Pro Phe Thr Gln Cys Gly Tyr Pro Ala Leu Met Pro Leu Tyr
625                 630                 635                 640

Ala Cys Ile Gln Ser Lys Gln Ala Phe Thr Phe Ser Pro Thr Tyr Lys
                645                 650                 655

Ala Phe Leu Cys Lys Gln Tyr Leu Asn Leu Tyr Pro Val Ala Arg Gln
            660                 665                 670

Arg Pro Gly Leu Cys Gln Val Phe Ala His Ala Thr Pro Thr Gly Trp
        675                 680                 685

Gly Leu Val Met Gly His Gln Arg Met Arg Gly Thr Phe Leu Ser Arg
    690                 695                 700

Lys Tyr Thr Ser Phe Pro Trp Leu Leu Gly Cys Ala Ala Asn Trp Ile
705                 710                 715                 720

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

His Asp Pro Ser Arg Gly Arg Leu Gly Leu Ser Arg Pro Leu Leu Arg
            740                 745                 750

Leu Pro Phe Arg Pro Thr Thr Gly Arg Thr Ser Leu Tyr Ala Asp Ser
        755                 760                 765
```

Pro Ser Val Pro Ser His Leu Pro Asp Arg Val His Phe Ala Ser Pro
770 775 780

Leu His Val Ala Trp Arg Pro Pro
785 790

<210> 6
<211> 939
<212> PRT
<213> artificial sequence

<220>
<223> fusion between a trunctaed version of HBc (1-148) and the mutated Y07587 polymerase

<400> 6

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Pro Leu Ser Tyr Gln His Phe Arg Arg Leu Leu Leu
145 150 155 160

Leu Asp Asp Glu Ala Gly Pro Leu Glu Glu Glu Leu Pro Arg Leu Ala
165 170 175

Asp Glu Gly Leu Asn Arg Arg Val Ala Glu Asp Leu Asn Leu Gly Asn
180 185 190

Leu Asn Val Ser Ile Pro Trp Thr His Lys Val Gly Asn Phe Thr Gly

195 200 205

Leu Tyr Ser Ser Thr Val Pro Val Phe Asn Pro His Trp Lys Thr Pro
210 215 220

Ser Phe Pro Asn Ile His Leu His Gln Asp Ile Ile Lys Lys Cys Glu
225 230 235 240

Gln Phe Val Gly Pro Leu Thr Val Asn Glu Lys Arg Arg Leu Gln Leu
245 250 255

Ile Met Pro Ala Arg Phe Tyr Pro Asn Val Thr Lys Tyr Leu Pro Leu
260 265 270

Asp Lys Gly Ile Lys Pro Tyr Tyr Pro Glu His Leu Val Asn His Tyr
275 280 285

Phe Gln Thr Arg His Tyr Leu His Thr Leu Trp Lys Ala Gly Ile Leu
290 295 300

Tyr Lys Arg Glu Thr Thr His Ser Ala Ser Phe Cys Gly Ser Pro Tyr
305 310 315 320

Ser Trp Glu Gln Lys Leu Gln His Gly Ala Glu Ser Phe His Gln Gln
325 330 335

Ser Ser Gly Ile Leu Ser Arg Pro Pro Val Gly Ser Ser Leu Gln Ser
340 345 350

Lys His Arg Lys Ser Arg Leu Gly Leu Gln Ser Gln Gln Gly His Leu
355 360 365

Ala Arg Arg Gln Gln Gly Arg Ser Trp Ser Ile Arg Ala Gly Ile His
370 375 380

Pro Thr Ala Arg Arg Ser Phe Gly Val Glu Pro Ser Gly Ser Gly His
385 390 395 400

Ser Thr Asn Leu Ala Ser Lys Ser Ala Ser Cys Leu Tyr Gln Ser Pro
405 410 415

Val Arg Lys Ala Ala Tyr Pro Ala Val Ser Thr Phe Glu Lys His Ser
420 425 430

Ser Ser Gly His Ala Val Glu Leu His Asn Leu Pro Pro Asn Ser Ala
435 440 445

Arg Ser Gln Ser Glu Arg Pro Val Phe Pro Cys Trp Trp Leu Gln Phe
450 455 460

Arg Asn Ser Lys Pro Cys Ser Asp Tyr Cys Leu Ser His Ile Val Asn

```
465                 470                 475                 480

Leu Leu Glu Asp Trp Gly Pro Cys Ala Glu His Gly Glu His His Ile
                485                 490                 495

Arg Ile Pro Arg Thr Pro Ala Arg Val Thr Gly Gly Val Phe Leu Val
            500                 505                 510

Asp Lys Asn Pro His Asn Thr Ala Glu Ser Arg Leu Val Val Asp Phe
        515                 520                 525

Ser Gln Phe Ser Arg Gly Asn Tyr Arg Val Ser Trp Pro Lys Phe Ala
    530                 535                 540

Val Pro Asn Leu Gln Ser Leu Thr Asn Leu Leu Ser Ser Asn Leu Ser
545                 550                 555                 560

Trp Leu Ser Leu Asp Val Ser Ala Ala Phe Tyr His Leu Pro Leu His
                565                 570                 575

Pro Ala Ala Met Pro His Leu Leu Val Gly Ser Ser Gly Leu Ser Arg
            580                 585                 590

Tyr Val Ala Arg Leu Ser Ser Asn Ser Arg Ile Phe Asn Tyr Gln His
        595                 600                 605

Gly Thr Met Gln Asn Leu His Asp Ser Cys Ser Arg Asn Leu Tyr Val
    610                 615                 620

Ser Leu Leu Leu Leu Tyr Gln Thr Phe Gly Arg Lys Leu His Leu Tyr
625                 630                 635                 640

Ser His Pro Ile Ile Leu Gly Phe Arg Lys Ile Pro Met Gly Val Gly
                645                 650                 655

Leu Ser Pro Phe Leu Leu Ala Gln Phe Thr Ser Ala Ile Cys Ser Val
            660                 665                 670

Val Arg Arg Ala Phe Pro His Cys Leu Ala Phe Ser Gly Ala Lys Ser
        675                 680                 685

Val Gln His Leu Glu Ser Leu Phe Thr Ala Val Thr Asn Phe Leu Leu
    690                 695                 700

Ser Leu Gly Ile His Leu Asn Pro Asn Lys Thr Lys Arg Trp Gly Tyr
705                 710                 715                 720

Ser Leu His Phe Met Gly Tyr Val Ile Gly Cys Tyr Gly Ser Leu Pro
                725                 730                 735

Gln Asp His Ile Ile Gln Lys Ile Lys Glu Cys Phe Arg Lys Leu Pro
```

740 745 750

Val Asn Arg Pro Ile Asp Trp Lys Val Cys Gln Arg Ile Val Gly Leu
755 760 765

Leu Gly Phe Ala Ala Pro Phe Thr Gln Cys Gly Tyr Pro Ala Leu Met
770 775 780

Pro Leu Tyr Ala Cys Ile Gln Ser Lys Gln Ala Phe Thr Phe Ser Pro
785 790 795 800

Thr Tyr Lys Ala Phe Leu Cys Lys Gln Tyr Leu Asn Leu Tyr Pro Val
805 810 815

Ala Arg Gln Arg Pro Gly Leu Cys Gln Val Phe Ala His Ala Thr Pro
820 825 830

Thr Gly Trp Gly Leu Val Met Gly His Gln Arg Met Arg Gly Thr Phe
835 840 845

Leu Ser Arg Lys Tyr Thr Ser Phe Pro Trp Leu Leu Gly Cys Ala Ala
850 855 860

Asn Trp Ile Leu Arg Gly Thr Ser Phe Val Tyr Tyr Pro Ser Ala Leu
865 870 875 880

Asn Pro Tyr His Asp Pro Ser Arg Gly Arg Leu Gly Leu Ser Arg Pro
885 890 895

Leu Leu Arg Leu Pro Phe Arg Pro Thr Thr Gly Arg Thr Ser Leu Tyr
900 905 910

Ala Asp Ser Pro Ser Val Pro Ser His Leu Pro Asp Arg Val His Phe
915 920 925

Ala Ser Pro Leu His Val Ala Trp Arg Pro Pro
930 935

<210> 7
<211> 860
<212> PRT
<213> artificial sequence

<220>
<223> fusion mutated Y07587 polymerase with env1 and env2 immunogenic domains

<400> 7

Met Pro Leu Ser Tyr Gln His Phe Arg Arg Leu Leu Leu Leu Asp Asp
1 5 10 15

Glu Ala Gly Pro Leu Glu Glu Glu Leu Pro Arg Leu Ala Asp Glu Gly
20 25 30

Leu Asn Arg Arg Val Ala Glu Asp Leu Asn Leu Gly Asn Leu Asn Val
35 40 45

Ser Ile Pro Trp Thr His Lys Val Gly Asn Phe Thr Gly Leu Tyr Ser
50 55 60

Ser Thr Val Pro Val Phe Asn Pro His Trp Lys Thr Pro Ser Phe Pro
65 70 75 80

Asn Ile His Leu His Gln Asp Ile Ile Lys Lys Cys Glu Gln Phe Val
85 90 95

Gly Pro Leu Thr Val Asn Glu Lys Arg Arg Leu Gln Leu Ile Met Pro
100 105 110

Ala Arg Phe Tyr Pro Asn Val Thr Lys Tyr Leu Pro Leu Asp Lys Gly
115 120 125

Ile Lys Pro Tyr Tyr Pro Glu His Leu Val Asn His Tyr Phe Gln Thr
130 135 140

Arg His Tyr Leu His Thr Leu Trp Lys Ala Gly Ile Leu Tyr Lys Arg
145 150 155 160

Glu Thr Thr His Ser Ala Ser Phe Cys Gly Ser Pro Tyr Ser Trp Glu
165 170 175

Gln Lys Leu Gln His Gly Ala Glu Ser Phe His Gln Gln Ser Ser Gly
180 185 190

Ile Leu Ser Arg Pro Pro Val Gly Ser Ser Leu Gln Ser Lys His Arg
195 200 205

Lys Ser Arg Leu Gly Leu Gln Ser Gln Gln Gly His Leu Ala Arg Arg
210 215 220

Gln Gln Gly Arg Ser Trp Ser Ile Arg Ala Gly Ile His Pro Thr Ala
225 230 235 240

Arg Arg Ser Phe Gly Val Glu Pro Ser Gly Ser Gly His Ser Thr Asn
245 250 255

Leu Ala Ser Lys Ser Ala Ser Cys Leu Tyr Gln Ser Pro Val Arg Lys
260 265 270

Ala Ala Tyr Pro Ala Val Ser Thr Phe Glu Lys His Ser Ser Ser Gly
275 280 285

His Ala Val Glu Leu His Asn Leu Pro Pro Asn Ser Ala Arg Ser Gln
290 295 300

Ser Glu Arg Pro Val Phe Pro Cys Trp Trp Leu Gln Phe Arg Asn Ser
305 310 315 320

Lys Pro Cys Ser Asp Tyr Cys Leu Ser His Ile Val Asn Leu Leu Glu
325 330 335

Asp Trp Gly Pro Cys Ala Glu His Gly Glu His His Ile Arg Ile Pro
340 345 350

Arg Thr Pro Ala Arg Val Thr Gly Gly Val Phe Leu Val Asp Lys Asn
355 360 365

Pro His Asn Thr Ala Glu Ser Arg Leu Val Val Asp Phe Ser Gln Phe
370 375 380

Ser Arg Gly Asn Tyr Arg Val Ser Trp Pro Lys Phe Ala Val Pro Asn
385 390 395 400

Leu Gln Ser Leu Thr Asn Leu Leu Ser Ser Asn Leu Ser Trp Leu Ser
405 410 415

Leu Asp Val Ser Ala Ala Phe Tyr His Leu Pro Leu His Pro Ala Ala
420 425 430

Met Pro His Leu Leu Val Gly Ser Ser Gly Leu Ser Arg Tyr Val Ala
435 440 445

Arg Leu Ser Ser Asn Ser Arg Ile Phe Asn Tyr Gln His Gly Thr Met
450 455 460

Gln Asn Leu His Asp Ser Cys Ser Arg Asn Leu Tyr Val Ser Leu Leu
465 470 475 480

Leu Leu Tyr Gln Thr Phe Gly Arg Lys Leu His Leu Tyr Ser His Pro
485 490 495

Ile Ile Leu Gly Phe Arg Lys Ile Pro Met Gly Val Gly Leu Ser Pro
500 505 510

Phe Leu Leu Ala Gln Phe Thr Ser Ala Ile Cys Ser Val Val Arg Arg
515 520 525

Ala Phe Pro His Cys Leu Ala Phe Ser Val Leu Gln Ala Gly Phe Phe
530 535 540

Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp
545 550 555 560

Thr Ser Leu Asn Phe Leu Gly Gly Thr Thr Val Cys Leu Gly Gln Gly
565 570 575

```
Ala Lys Ser Val Gln His Leu Glu Ser Leu Phe Thr Ala Val Thr Asn
            580                 585                 590

Phe Leu Leu Ser Leu Gly Ile His Leu Asn Pro Asn Lys Thr Lys Arg
        595                 600                 605

Trp Gly Tyr Ser Leu His Phe Met Gly Tyr Val Ile Gly Cys Tyr Gly
    610                 615                 620

Ser Leu Pro Gln Asp His Ile Ile Gln Lys Ile Lys Glu Cys Phe Arg
625                 630                 635                 640

Lys Leu Pro Val Asn Arg Pro Ile Asp Trp Lys Val Cys Gln Arg Ile
                645                 650                 655

Val Gly Leu Leu Gly Phe Ala Ala Pro Phe Thr Gln Cys Gly Tyr Pro
            660                 665                 670

Ala Leu Met Pro Leu Tyr Ala Cys Ile Gln Ser Lys Gln Ala Phe Thr
        675                 680                 685

Phe Ser Pro Thr Tyr Lys Ala Phe Leu Cys Lys Gln Tyr Leu Asn Leu
    690                 695                 700

Tyr Pro Val Ala Arg Gln Arg Pro Gly Leu Cys Gln Val Phe Ala His
705                 710                 715                 720

Ala Thr Pro Thr Gly Trp Gly Leu Val Met Gly His Gln Arg Met Arg
                725                 730                 735

Gly Thr Phe Leu Trp Ala Ser Ala Arg Phe Ser Trp Leu Ser Leu Leu
            740                 745                 750

Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
        755                 760                 765

Ser Val Ser Arg Lys Tyr Thr Ser Phe Pro Trp Leu Leu Gly Cys Ala
    770                 775                 780

Ala Asn Trp Ile Leu Arg Gly Thr Ser Phe Val Tyr Tyr Pro Ser Ala
785                 790                 795                 800

Leu Asn Pro Tyr His Asp Pro Ser Arg Gly Arg Leu Gly Leu Ser Arg
                805                 810                 815

Pro Leu Leu Arg Leu Pro Phe Arg Pro Thr Thr Gly Arg Thr Ser Leu
            820                 825                 830

Tyr Ala Asp Ser Pro Ser Val Pro Ser His Leu Pro Asp Arg Val His
        835                 840                 845
```

```
Phe Ala Ser Pro Leu His Val Ala Trp Arg Pro Pro
    850                 855                 860
```

<210> 8
<211> 1007
<212> PRT
<213> artificial sequence

<220>
<223> fusion between truncated core (1-148)- mutated Y07587 polymerase - env1 and env2

<400> 8

```
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1               5                  10                  15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
            20                  25                  30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
        35                  40                  45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
    50                  55                  60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile
65                  70                  75                  80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
                85                  90                  95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
            100                 105                 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
        115                 120                 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
    130                 135                 140

Glu Thr Thr Val Pro Leu Ser Tyr Gln His Phe Arg Arg Leu Leu Leu
145                 150                 155                 160

Leu Asp Asp Glu Ala Gly Pro Leu Glu Glu Glu Leu Pro Arg Leu Ala
                165                 170                 175

Asp Glu Gly Leu Asn Arg Arg Val Ala Glu Asp Leu Asn Leu Gly Asn
            180                 185                 190

Leu Asn Val Ser Ile Pro Trp Thr His Lys Val Gly Asn Phe Thr Gly
        195                 200                 205
```

```
Leu Tyr Ser Ser Thr Val Pro Val Phe Asn Pro His Trp Lys Thr Pro
    210                 215                 220

Ser Phe Pro Asn Ile His Leu His Gln Asp Ile Ile Lys Lys Cys Glu
225                 230                 235                 240

Gln Phe Val Gly Pro Leu Thr Val Asn Glu Lys Arg Arg Leu Gln Leu
                245                 250                 255

Ile Met Pro Ala Arg Phe Tyr Pro Asn Val Thr Lys Tyr Leu Pro Leu
            260                 265                 270

Asp Lys Gly Ile Lys Pro Tyr Tyr Pro Glu His Leu Val Asn His Tyr
        275                 280                 285

Phe Gln Thr Arg His Tyr Leu His Thr Leu Trp Lys Ala Gly Ile Leu
    290                 295                 300

Tyr Lys Arg Glu Thr Thr His Ser Ala Ser Phe Cys Gly Ser Pro Tyr
305                 310                 315                 320

Ser Trp Glu Gln Lys Leu Gln His Gly Ala Glu Ser Phe His Gln Gln
                325                 330                 335

Ser Ser Gly Ile Leu Ser Arg Pro Pro Val Gly Ser Ser Leu Gln Ser
            340                 345                 350

Lys His Arg Lys Ser Arg Leu Gly Leu Gln Ser Gln Gln Gly His Leu
        355                 360                 365

Ala Arg Arg Gln Gln Gly Arg Ser Trp Ser Ile Arg Ala Gly Ile His
    370                 375                 380

Pro Thr Ala Arg Arg Ser Phe Gly Val Glu Pro Ser Gly Ser Gly His
385                 390                 395                 400

Ser Thr Asn Leu Ala Ser Lys Ser Ala Ser Cys Leu Tyr Gln Ser Pro
                405                 410                 415

Val Arg Lys Ala Ala Tyr Pro Ala Val Ser Thr Phe Glu Lys His Ser
            420                 425                 430

Ser Ser Gly His Ala Val Glu Leu His Asn Leu Pro Pro Asn Ser Ala
        435                 440                 445

Arg Ser Gln Ser Glu Arg Pro Val Phe Pro Cys Trp Trp Leu Gln Phe
    450                 455                 460

Arg Asn Ser Lys Pro Cys Ser Asp Tyr Cys Leu Ser His Ile Val Asn
465                 470                 475                 480
```

Leu Leu Glu Asp Trp Gly Pro Cys Ala Glu His Gly Glu His His Ile
485 490 495

Arg Ile Pro Arg Thr Pro Ala Arg Val Thr Gly Gly Val Phe Leu Val
500 505 510

Asp Lys Asn Pro His Asn Thr Ala Glu Ser Arg Leu Val Val Asp Phe
515 520 525

Ser Gln Phe Ser Arg Gly Asn Tyr Arg Val Ser Trp Pro Lys Phe Ala
530 535 540

Val Pro Asn Leu Gln Ser Leu Thr Asn Leu Leu Ser Ser Asn Leu Ser
545 550 555 560

Trp Leu Ser Leu Asp Val Ser Ala Ala Phe Tyr His Leu Pro Leu His
565 570 575

Pro Ala Ala Met Pro His Leu Leu Val Gly Ser Ser Gly Leu Ser Arg
580 585 590

Tyr Val Ala Arg Leu Ser Ser Asn Ser Arg Ile Phe Asn Tyr Gln His
595 600 605

Gly Thr Met Gln Asn Leu His Asp Ser Cys Ser Arg Asn Leu Tyr Val
610 615 620

Ser Leu Leu Leu Leu Tyr Gln Thr Phe Gly Arg Lys Leu His Leu Tyr
625 630 635 640

Ser His Pro Ile Ile Leu Gly Phe Arg Lys Ile Pro Met Gly Val Gly
645 650 655

Leu Ser Pro Phe Leu Leu Ala Gln Phe Thr Ser Ala Ile Cys Ser Val
660 665 670

Val Arg Arg Ala Phe Pro His Cys Leu Ala Phe Ser Val Leu Gln Ala
675 680 685

Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp
690 695 700

Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Thr Thr Val Cys Leu
705 710 715 720

Gly Gln Gly Ala Lys Ser Val Gln His Leu Glu Ser Leu Phe Thr Ala
725 730 735

Val Thr Asn Phe Leu Leu Ser Leu Gly Ile His Leu Asn Pro Asn Lys
740 745 750

Thr Lys Arg Trp Gly Tyr Ser Leu His Phe Met Gly Tyr Val Ile Gly
755 760 765

Cys Tyr Gly Ser Leu Pro Gln Asp His Ile Ile Gln Lys Ile Lys Glu
770 775 780

Cys Phe Arg Lys Leu Pro Val Asn Arg Pro Ile Asp Trp Lys Val Cys
785 790 795 800

Gln Arg Ile Val Gly Leu Leu Gly Phe Ala Ala Pro Phe Thr Gln Cys
805 810 815

Gly Tyr Pro Ala Leu Met Pro Leu Tyr Ala Cys Ile Gln Ser Lys Gln
820 825 830

Ala Phe Thr Phe Ser Pro Thr Tyr Lys Ala Phe Leu Cys Lys Gln Tyr
835 840 845

Leu Asn Leu Tyr Pro Val Ala Arg Gln Arg Pro Gly Leu Cys Gln Val
850 855 860

Phe Ala His Ala Thr Pro Thr Gly Trp Gly Leu Val Met Gly His Gln
865 870 875 880

Arg Met Arg Gly Thr Phe Leu Trp Ala Ser Ala Arg Phe Ser Trp Leu
885 890 895

Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr
900 905 910

Val Trp Leu Ser Val Ser Arg Lys Tyr Thr Ser Phe Pro Trp Leu Leu
915 920 925

Gly Cys Ala Ala Asn Trp Ile Leu Arg Gly Thr Ser Phe Val Tyr Tyr
930 935 940

Pro Ser Ala Leu Asn Pro Tyr His Asp Pro Ser Arg Gly Arg Leu Gly
945 950 955 960

Leu Ser Arg Pro Leu Leu Arg Leu Pro Phe Arg Pro Thr Thr Gly Arg
965 970 975

Thr Ser Leu Tyr Ala Asp Ser Pro Ser Val Pro Ser His Leu Pro Asp
980 985 990

Arg Val His Phe Ala Ser Pro Leu His Val Ala Trp Arg Pro Pro
995 1000 1005

<210> 9
<211> 1042
<212> PRT

<213> artificial sequence

<220>
<223> fusion between native core (1-183) - mutated Y07587 polymerase - env1 and env2

<400> 9

```
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1               5                  10                  15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
            20                  25                  30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
        35                  40                  45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
    50                  55                  60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile
65                  70                  75                  80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
                85                  90                  95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
            100                 105                 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
        115                 120                 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
    130                 135                 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145                 150                 155                 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
                165                 170                 175

Gln Ser Arg Glu Ser Gln Cys Pro Leu Ser Tyr Gln His Phe Arg Arg
            180                 185                 190

Leu Leu Leu Leu Asp Asp Glu Ala Gly Pro Leu Glu Glu Glu Leu Pro
        195                 200                 205

Arg Leu Ala Asp Glu Gly Leu Asn Arg Arg Val Ala Glu Asp Leu Asn
    210                 215                 220

Leu Gly Asn Leu Asn Val Ser Ile Pro Trp Thr His Lys Val Gly Asn
225                 230                 235                 240
```

```
Phe Thr Gly Leu Tyr Ser Ser Thr Val Pro Val Phe Asn Pro His Trp
                245                 250                 255

Lys Thr Pro Ser Phe Pro Asn Ile His Leu His Gln Asp Ile Ile Lys
            260                 265                 270

Lys Cys Glu Gln Phe Val Gly Pro Leu Thr Val Asn Glu Lys Arg Arg
        275                 280                 285

Leu Gln Leu Ile Met Pro Ala Arg Phe Tyr Pro Asn Val Thr Lys Tyr
    290                 295                 300

Leu Pro Leu Asp Lys Gly Ile Lys Pro Tyr Tyr Pro Glu His Leu Val
305                 310                 315                 320

Asn His Tyr Phe Gln Thr Arg His Tyr Leu His Thr Leu Trp Lys Ala
                325                 330                 335

Gly Ile Leu Tyr Lys Arg Glu Thr Thr His Ser Ala Ser Phe Cys Gly
            340                 345                 350

Ser Pro Tyr Ser Trp Glu Gln Lys Leu Gln His Gly Ala Glu Ser Phe
        355                 360                 365

His Gln Gln Ser Ser Gly Ile Leu Ser Arg Pro Pro Val Gly Ser Ser
    370                 375                 380

Leu Gln Ser Lys His Arg Lys Ser Arg Leu Gly Leu Gln Ser Gln Gln
385                 390                 395                 400

Gly His Leu Ala Arg Arg Gln Gln Gly Arg Ser Trp Ser Ile Arg Ala
                405                 410                 415

Gly Ile His Pro Thr Ala Arg Arg Ser Phe Gly Val Glu Pro Ser Gly
            420                 425                 430

Ser Gly His Ser Thr Asn Leu Ala Ser Lys Ser Ala Ser Cys Leu Tyr
        435                 440                 445

Gln Ser Pro Val Arg Lys Ala Ala Tyr Pro Ala Val Ser Thr Phe Glu
    450                 455                 460

Lys His Ser Ser Ser Gly His Ala Val Glu Leu His Asn Leu Pro Pro
465                 470                 475                 480

Asn Ser Ala Arg Ser Gln Ser Glu Arg Pro Val Phe Pro Cys Trp Trp
                485                 490                 495

Leu Gln Phe Arg Asn Ser Lys Pro Cys Ser Asp Tyr Cys Leu Ser His
            500                 505                 510
```

```
Ile Val Asn Leu Leu Glu Asp Trp Gly Pro Cys Ala Glu His Gly Glu
        515                 520                 525

His His Ile Arg Ile Pro Arg Thr Pro Ala Arg Val Thr Gly Gly Val
    530                 535                 540

Phe Leu Val Asp Lys Asn Pro His Asn Thr Ala Glu Ser Arg Leu Val
545                 550                 555                 560

Val Asp Phe Ser Gln Phe Ser Arg Gly Asn Tyr Arg Val Ser Trp Pro
                565                 570                 575

Lys Phe Ala Val Pro Asn Leu Gln Ser Leu Thr Asn Leu Leu Ser Ser
            580                 585                 590

Asn Leu Ser Trp Leu Ser Leu Asp Val Ser Ala Ala Phe Tyr His Leu
        595                 600                 605

Pro Leu His Pro Ala Ala Met Pro His Leu Leu Val Gly Ser Ser Gly
    610                 615                 620

Leu Ser Arg Tyr Val Ala Arg Leu Ser Ser Asn Ser Arg Ile Phe Asn
625                 630                 635                 640

Tyr Gln His Gly Thr Met Gln Asn Leu His Asp Ser Cys Ser Arg Asn
                645                 650                 655

Leu Tyr Val Ser Leu Leu Leu Leu Tyr Gln Thr Phe Gly Arg Lys Leu
            660                 665                 670

His Leu Tyr Ser His Pro Ile Ile Leu Gly Phe Arg Lys Ile Pro Met
        675                 680                 685

Gly Val Gly Leu Ser Pro Phe Leu Leu Ala Gln Phe Thr Ser Ala Ile
    690                 695                 700

Cys Ser Val Val Arg Arg Ala Phe Pro His Cys Leu Ala Phe Ser Val
705                 710                 715                 720

Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln
                725                 730                 735

Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Thr Thr
            740                 745                 750

Val Cys Leu Gly Gln Gly Ala Lys Ser Val Gln His Leu Glu Ser Leu
        755                 760                 765

Phe Thr Ala Val Thr Asn Phe Leu Leu Ser Leu Gly Ile His Leu Asn
    770                 775                 780
```

```
Pro Asn Lys Thr Lys Arg Trp Gly Tyr Ser Leu His Phe Met Gly Tyr
785                 790                 795                 800

Val Ile Gly Cys Tyr Gly Ser Leu Pro Gln Asp His Ile Ile Gln Lys
                805                 810                 815

Ile Lys Glu Cys Phe Arg Lys Leu Pro Val Asn Arg Pro Ile Asp Trp
            820                 825                 830

Lys Val Cys Gln Arg Ile Val Gly Leu Leu Gly Phe Ala Ala Pro Phe
        835                 840                 845

Thr Gln Cys Gly Tyr Pro Ala Leu Met Pro Leu Tyr Ala Cys Ile Gln
    850                 855                 860

Ser Lys Gln Ala Phe Thr Phe Ser Pro Thr Tyr Lys Ala Phe Leu Cys
865                 870                 875                 880

Lys Gln Tyr Leu Asn Leu Tyr Pro Val Ala Arg Gln Arg Pro Gly Leu
                885                 890                 895

Cys Gln Val Phe Ala His Ala Thr Pro Thr Gly Trp Gly Leu Val Met
            900                 905                 910

Gly His Gln Arg Met Arg Gly Thr Phe Leu Trp Ala Ser Ala Arg Phe
        915                 920                 925

Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu
    930                 935                 940

Ser Pro Thr Val Trp Leu Ser Val Ser Arg Lys Tyr Thr Ser Phe Pro
945                 950                 955                 960

Trp Leu Leu Gly Cys Ala Ala Asn Trp Ile Leu Arg Gly Thr Ser Phe
                965                 970                 975

Val Tyr Tyr Pro Ser Ala Leu Asn Pro Tyr His Asp Pro Ser Arg Gly
            980                 985                 990

Arg Leu Gly Leu Ser Arg Pro Leu  Leu Arg Leu Pro Phe  Arg Pro Thr
        995                 1000                1005

Thr Gly  Arg Thr Ser Leu Tyr  Ala Asp Ser Pro Ser  Val Pro Ser
    1010                1015                1020

His Leu  Pro Asp Arg Val His  Phe Ala Ser Pro Leu  His Val Ala
    1025                1030                1035

Trp Arg  Pro Pro
    1040
```

<210> 10
<211> 880
<212> PRT
<213> artificial sequence

<220>
<223> fusion between signal sequence -mutated Y07587 polymerase and transmembrane sequence

<400> 10

Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe Pro Leu
1 5 10 15

Cys Phe Gly Lys Phe Pro Ile Pro Leu Ser Tyr Gln His Phe Arg Arg
20 25 30

Leu Leu Leu Leu Asp Asp Glu Ala Gly Pro Leu Glu Glu Glu Leu Pro
35 40 45

Arg Leu Ala Asp Glu Gly Leu Asn Arg Arg Val Ala Glu Asp Leu Asn
50 55 60

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

Phe Thr Gly Leu Tyr Ser Ser Thr Val Pro Val Phe Asn Pro His Trp
85 90 95

Lys Thr Pro Ser Phe Pro Asn Ile His Leu His Gln Asp Ile Ile Lys
100 105 110

Lys Cys Glu Gln Phe Val Gly Pro Leu Thr Val Asn Glu Lys Arg Arg
115 120 125

Leu Gln Leu Ile Met Pro Ala Arg Phe Tyr Pro Asn Val Thr Lys Tyr
130 135 140

Leu Pro Leu Asp Lys Gly Ile Lys Pro Tyr Tyr Pro Glu His Leu Val
145 150 155 160

Asn His Tyr Phe Gln Thr Arg His Tyr Leu His Thr Leu Trp Lys Ala
165 170 175

Gly Ile Leu Tyr Lys Arg Glu Thr Thr His Ser Ala Ser Phe Cys Gly
180 185 190

Ser Pro Tyr Ser Trp Glu Gln Lys Leu Gln His Gly Ala Glu Ser Phe
195 200 205

His Gln Gln Ser Ser Gly Ile Leu Ser Arg Pro Pro Val Gly Ser Ser
210 215 220

Leu Gln Ser Lys His Arg Lys Ser Arg Leu Gly Leu Gln Ser Gln Gln

225 230 235 240

Gly His Leu Ala Arg Arg Gln Gln Gly Arg Ser Trp Ser Ile Arg Ala
245 250 255

Gly Ile His Pro Thr Ala Arg Arg Ser Phe Gly Val Glu Pro Ser Gly
260 265 270

Ser Gly His Ser Thr Asn Leu Ala Ser Lys Ser Ala Ser Cys Leu Tyr
275 280 285

Gln Ser Pro Val Arg Lys Ala Ala Tyr Pro Ala Val Ser Thr Phe Glu
290 295 300

Lys His Ser Ser Ser Gly His Ala Val Glu Leu His Asn Leu Pro Pro
305 310 315 320

Asn Ser Ala Arg Ser Gln Ser Glu Arg Pro Val Phe Pro Cys Trp Trp
325 330 335

Leu Gln Phe Arg Asn Ser Lys Pro Cys Ser Asp Tyr Cys Leu Ser His
340 345 350

Ile Val Asn Leu Leu Glu Asp Trp Gly Pro Cys Ala Glu His Gly Glu
355 360 365

His His Ile Arg Ile Pro Arg Thr Pro Ala Arg Val Thr Gly Gly Val
370 375 380

Phe Leu Val Asp Lys Asn Pro His Asn Thr Ala Glu Ser Arg Leu Val
385 390 395 400

Val Asp Phe Ser Gln Phe Ser Arg Gly Asn Tyr Arg Val Ser Trp Pro
405 410 415

Lys Phe Ala Val Pro Asn Leu Gln Ser Leu Thr Asn Leu Leu Ser Ser
420 425 430

Asn Leu Ser Trp Leu Ser Leu Asp Val Ser Ala Ala Phe Tyr His Leu
435 440 445

Pro Leu His Pro Ala Ala Met Pro His Leu Leu Val Gly Ser Ser Gly
450 455 460

Leu Ser Arg Tyr Val Ala Arg Leu Ser Ser Asn Ser Arg Ile Phe Asn
465 470 475 480

Tyr Gln His Gly Thr Met Gln Asn Leu His Asp Ser Cys Ser Arg Asn
485 490 495

Leu Tyr Val Ser Leu Leu Leu Leu Tyr Gln Thr Phe Gly Arg Lys Leu

500 505 510

His Leu Tyr Ser His Pro Ile Ile Leu Gly Phe Arg Lys Ile Pro Met
515 520 525

Gly Val Gly Leu Ser Pro Phe Leu Leu Ala Gln Phe Thr Ser Ala Ile
530 535 540

Cys Ser Val Val Arg Arg Ala Phe Pro His Cys Leu Ala Phe Ser Gly
545 550 555 560

Ala Lys Ser Val Gln His Leu Glu Ser Leu Phe Thr Ala Val Thr Asn
565 570 575

Phe Leu Leu Ser Leu Gly Ile His Leu Asn Pro Asn Lys Thr Lys Arg
580 585 590

Trp Gly Tyr Ser Leu His Phe Met Gly Tyr Val Ile Gly Cys Tyr Gly
595 600 605

Ser Leu Pro Gln Asp His Ile Ile Gln Lys Ile Lys Glu Cys Phe Arg
610 615 620

Lys Leu Pro Val Asn Arg Pro Ile Asp Trp Lys Val Cys Gln Arg Ile
625 630 635 640

Val Gly Leu Leu Gly Phe Ala Ala Pro Phe Thr Gln Cys Gly Tyr Pro
645 650 655

Ala Leu Met Pro Leu Tyr Ala Cys Ile Gln Ser Lys Gln Ala Phe Thr
660 665 670

Phe Ser Pro Thr Tyr Lys Ala Phe Leu Cys Lys Gln Tyr Leu Asn Leu
675 680 685

Tyr Pro Val Ala Arg Gln Arg Pro Gly Leu Cys Gln Val Phe Ala His
690 695 700

Ala Thr Pro Thr Gly Trp Gly Leu Val Met Gly His Gln Arg Met Arg
705 710 715 720

Gly Thr Phe Leu Ser Arg Lys Tyr Thr Ser Phe Pro Trp Leu Leu Gly
725 730 735

Cys Ala Ala Asn Trp Ile Leu Arg Gly Thr Ser Phe Val Tyr Tyr Pro
740 745 750

Ser Ala Leu Asn Pro Tyr His Asp Pro Ser Arg Gly Arg Leu Gly Leu
755 760 765

Ser Arg Pro Leu Leu Arg Leu Pro Phe Arg Pro Thr Thr Gly Arg Thr

770 775 780

Ser Leu Tyr Ala Asp Ser Pro Ser Val Pro Ser His Leu Pro Asp Arg
785 790 795 800

Val His Phe Ala Ser Pro Leu His Val Ala Trp Arg Pro Pro Tyr Val
805 810 815

Leu Leu Ser Ala Gly Ala Leu Thr Ala Leu Met Leu Ile Ile Phe Leu
820 825 830

Met Thr Cys Cys Arg Arg Val Asn Arg Ser Glu Pro Thr Gln His Asn
835 840 845

Leu Arg Gly Thr Gly Arg Glu Val Ser Val Thr Pro Gln Ser Gly Lys
850 855 860

Ile Ile Ser Ser Trp Glu Ser His Lys Ser Gly Gly Glu Thr Arg Leu
865 870 875 880

<210> 11
<211> 1027
<212> PRT
<213> artificial sequence

<220>
<223> fusion between sequence signal - truncated core (1-148) -mutated Y07587 polymerase - sequence TM

<400> 11

Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe Pro Leu
1 5 10 15

Cys Phe Gly Lys Phe Pro Ile Asp Ile Asp Pro Tyr Lys Glu Phe Gly
20 25 30

Ala Thr Val Glu Leu Leu Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser
35 40 45

Val Arg Asp Leu Leu Asp Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu
50 55 60

Glu Ser Pro Glu His Cys Ser Pro His His Thr Ala Leu Arg Gln Ala
65 70 75 80

Ile Leu Cys Trp Gly Glu Leu Met Thr Leu Ala Thr Trp Val Gly Gly
85 90 95

Asn Leu Glu Asp Pro Ile Ser Arg Asp Leu Val Val Ser Tyr Val Asn
100 105 110

Thr Asn Met Gly Leu Lys Phe Arg Gln Leu Leu Trp Phe His Ile Ser
115 120 125

```
Cys Leu Thr Phe Gly Arg Glu Thr Val Ile Glu Tyr Leu Val Ser Phe
    130                 135                 140

Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro
145                 150                 155                 160

Ile Leu Ser Thr Leu Pro Glu Thr Thr Val Pro Leu Ser Tyr Gln His
                165                 170                 175

Phe Arg Arg Leu Leu Leu Leu Asp Asp Glu Ala Gly Pro Leu Glu Glu
            180                 185                 190

Glu Leu Pro Arg Leu Ala Asp Glu Gly Leu Asn Arg Arg Val Ala Glu
        195                 200                 205

Asp Leu Asn Leu Gly Asn Leu Asn Val Ser Ile Pro Trp Thr His Lys
    210                 215                 220

Val Gly Asn Phe Thr Gly Leu Tyr Ser Ser Thr Val Pro Val Phe Asn
225                 230                 235                 240

Pro His Trp Lys Thr Pro Ser Phe Pro Asn Ile His Leu His Gln Asp
                245                 250                 255

Ile Ile Lys Lys Cys Glu Gln Phe Val Gly Pro Leu Thr Val Asn Glu
            260                 265                 270

Lys Arg Arg Leu Gln Leu Ile Met Pro Ala Arg Phe Tyr Pro Asn Val
        275                 280                 285

Thr Lys Tyr Leu Pro Leu Asp Lys Gly Ile Lys Pro Tyr Tyr Pro Glu
    290                 295                 300

His Leu Val Asn His Tyr Phe Gln Thr Arg His Tyr Leu His Thr Leu
305                 310                 315                 320

Trp Lys Ala Gly Ile Leu Tyr Lys Arg Glu Thr Thr His Ser Ala Ser
                325                 330                 335

Phe Cys Gly Ser Pro Tyr Ser Trp Glu Gln Lys Leu Gln His Gly Ala
            340                 345                 350

Glu Ser Phe His Gln Gln Ser Ser Gly Ile Leu Ser Arg Pro Pro Val
        355                 360                 365

Gly Ser Ser Leu Gln Ser Lys His Arg Lys Ser Arg Leu Gly Leu Gln
    370                 375                 380

Ser Gln Gln Gly His Leu Ala Arg Arg Gln Gln Gly Arg Ser Trp Ser
385                 390                 395                 400
```

Ile Arg Ala Gly Ile His Pro Thr Ala Arg Arg Ser Phe Gly Val Glu
405 410 415

Pro Ser Gly Ser Gly His Ser Thr Asn Leu Ala Ser Lys Ser Ala Ser
420 425 430

Cys Leu Tyr Gln Ser Pro Val Arg Lys Ala Ala Tyr Pro Ala Val Ser
435 440 445

Thr Phe Glu Lys His Ser Ser Ser Gly His Ala Val Glu Leu His Asn
450 455 460

Leu Pro Pro Asn Ser Ala Arg Ser Gln Ser Glu Arg Pro Val Phe Pro
465 470 475 480

Cys Trp Trp Leu Gln Phe Arg Asn Ser Lys Pro Cys Ser Asp Tyr Cys
485 490 495

Leu Ser His Ile Val Asn Leu Leu Glu Asp Trp Gly Pro Cys Ala Glu
500 505 510

His Gly Glu His His Ile Arg Ile Pro Arg Thr Pro Ala Arg Val Thr
515 520 525

Gly Gly Val Phe Leu Val Asp Lys Asn Pro His Asn Thr Ala Glu Ser
530 535 540

Arg Leu Val Val Asp Phe Ser Gln Phe Ser Arg Gly Asn Tyr Arg Val
545 550 555 560

Ser Trp Pro Lys Phe Ala Val Pro Asn Leu Gln Ser Leu Thr Asn Leu
565 570 575

Leu Ser Ser Asn Leu Ser Trp Leu Ser Leu Asp Val Ser Ala Ala Phe
580 585 590

Tyr His Leu Pro Leu His Pro Ala Ala Met Pro His Leu Leu Val Gly
595 600 605

Ser Ser Gly Leu Ser Arg Tyr Val Ala Arg Leu Ser Ser Asn Ser Arg
610 615 620

Ile Phe Asn Tyr Gln His Gly Thr Met Gln Asn Leu His Asp Ser Cys
625 630 635 640

Ser Arg Asn Leu Tyr Val Ser Leu Leu Leu Leu Tyr Gln Thr Phe Gly
645 650 655

Arg Lys Leu His Leu Tyr Ser His Pro Ile Ile Leu Gly Phe Arg Lys
660 665 670

Ile Pro Met Gly Val Gly Leu Ser Pro Phe Leu Leu Ala Gln Phe Thr
675 680 685

Ser Ala Ile Cys Ser Val Val Arg Arg Ala Phe Pro His Cys Leu Ala
690 695 700

Phe Ser Gly Ala Lys Ser Val Gln His Leu Glu Ser Leu Phe Thr Ala
705 710 715 720

Val Thr Asn Phe Leu Leu Ser Leu Gly Ile His Leu Asn Pro Asn Lys
725 730 735

Thr Lys Arg Trp Gly Tyr Ser Leu His Phe Met Gly Tyr Val Ile Gly
740 745 750

Cys Tyr Gly Ser Leu Pro Gln Asp His Ile Ile Gln Lys Ile Lys Glu
755 760 765

Cys Phe Arg Lys Leu Pro Val Asn Arg Pro Ile Asp Trp Lys Val Cys
770 775 780

Gln Arg Ile Val Gly Leu Leu Gly Phe Ala Ala Pro Phe Thr Gln Cys
785 790 795 800

Gly Tyr Pro Ala Leu Met Pro Leu Tyr Ala Cys Ile Gln Ser Lys Gln
805 810 815

Ala Phe Thr Phe Ser Pro Thr Tyr Lys Ala Phe Leu Cys Lys Gln Tyr
820 825 830

Leu Asn Leu Tyr Pro Val Ala Arg Gln Arg Pro Gly Leu Cys Gln Val
835 840 845

Phe Ala His Ala Thr Pro Thr Gly Trp Gly Leu Val Met Gly His Gln
850 855 860

Arg Met Arg Gly Thr Phe Leu Ser Arg Lys Tyr Thr Ser Phe Pro Trp
865 870 875 880

Leu Leu Gly Cys Ala Ala Asn Trp Ile Leu Arg Gly Thr Ser Phe Val
885 890 895

Tyr Tyr Pro Ser Ala Leu Asn Pro Tyr His Asp Pro Ser Arg Gly Arg
900 905 910

Leu Gly Leu Ser Arg Pro Leu Leu Arg Leu Pro Phe Arg Pro Thr Thr
915 920 925

Gly Arg Thr Ser Leu Tyr Ala Asp Ser Pro Ser Val Pro Ser His Leu
930 935 940

```
Pro Asp Arg Val His Phe Ala Ser Pro Leu His Val Ala Trp Arg Pro
945                 950                 955                 960

Pro Tyr Val Leu Leu Ser Ala Gly Ala Leu Thr Ala Leu Met Leu Ile
                965                 970                 975

Ile Phe Leu Met Thr Cys Cys Arg Arg Val Asn Arg Ser Glu Pro Thr
            980                 985                 990

Gln His Asn Leu Arg Gly Thr Gly  Arg Glu Val Ser Val  Thr Pro Gln
        995                 1000                1005

Ser Gly  Lys Ile Ile Ser Ser  Trp Glu Ser His Lys  Ser Gly Gly
    1010                1015                1020

Glu Thr  Arg Leu
    1025
```

<210> 12
<211> 1095
<212> PRT
<213> artificial sequence

<220>
<223> fusion between signal sequence -core (1'148)- mutated Y07587 polymerase -env1-env2 and TM sequence

<400> 12

```
Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe Pro Leu
1               5                   10                  15

Cys Phe Gly Lys Phe Pro Ile Asp Ile Asp Pro Tyr Lys Glu Phe Gly
            20                  25                  30

Ala Thr Val Glu Leu Leu Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser
        35                  40                  45

Val Arg Asp Leu Leu Asp Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu
    50                  55                  60

Glu Ser Pro Glu His Cys Ser Pro His His Thr Ala Leu Arg Gln Ala
65                  70                  75                  80

Ile Leu Cys Trp Gly Glu Leu Met Thr Leu Ala Thr Trp Val Gly Gly
                85                  90                  95

Asn Leu Glu Asp Pro Ile Ser Arg Asp Leu Val Val Ser Tyr Val Asn
            100                 105                 110

Thr Asn Met Gly Leu Lys Phe Arg Gln Leu Leu Trp Phe His Ile Ser
        115                 120                 125
```

```
Cys Leu Thr Phe Gly Arg Glu Thr Val Ile Glu Tyr Leu Val Ser Phe
    130                 135                 140

Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro
145                 150                 155                 160

Ile Leu Ser Thr Leu Pro Glu Thr Thr Val Pro Leu Ser Tyr Gln His
                165                 170                 175

Phe Arg Arg Leu Leu Leu Leu Asp Asp Glu Ala Gly Pro Leu Glu Glu
            180                 185                 190

Glu Leu Pro Arg Leu Ala Asp Glu Gly Leu Asn Arg Arg Val Ala Glu
        195                 200                 205

Asp Leu Asn Leu Gly Asn Leu Asn Val Ser Ile Pro Trp Thr His Lys
    210                 215                 220

Val Gly Asn Phe Thr Gly Leu Tyr Ser Ser Thr Val Pro Val Phe Asn
225                 230                 235                 240

Pro His Trp Lys Thr Pro Ser Phe Pro Asn Ile His Leu His Gln Asp
                245                 250                 255

Ile Ile Lys Lys Cys Glu Gln Phe Val Gly Pro Leu Thr Val Asn Glu
            260                 265                 270

Lys Arg Arg Leu Gln Leu Ile Met Pro Ala Arg Phe Tyr Pro Asn Val
        275                 280                 285

Thr Lys Tyr Leu Pro Leu Asp Lys Gly Ile Lys Pro Tyr Tyr Pro Glu
    290                 295                 300

His Leu Val Asn His Tyr Phe Gln Thr Arg His Tyr Leu His Thr Leu
305                 310                 315                 320

Trp Lys Ala Gly Ile Leu Tyr Lys Arg Glu Thr Thr His Ser Ala Ser
                325                 330                 335

Phe Cys Gly Ser Pro Tyr Ser Trp Glu Gln Lys Leu Gln His Gly Ala
            340                 345                 350

Glu Ser Phe His Gln Gln Ser Ser Gly Ile Leu Ser Arg Pro Pro Val
        355                 360                 365

Gly Ser Ser Leu Gln Ser Lys His Arg Lys Ser Arg Leu Gly Leu Gln
    370                 375                 380

Ser Gln Gln Gly His Leu Ala Arg Arg Gln Gln Gly Arg Ser Trp Ser
385                 390                 395                 400
```

Ile Arg Ala Gly Ile His Pro Thr Ala Arg Arg Ser Phe Gly Val Glu
405 410 415

Pro Ser Gly Ser Gly His Ser Thr Asn Leu Ala Ser Lys Ser Ala Ser
420 425 430

Cys Leu Tyr Gln Ser Pro Val Arg Lys Ala Ala Tyr Pro Ala Val Ser
435 440 445

Thr Phe Glu Lys His Ser Ser Ser Gly His Ala Val Glu Leu His Asn
450 455 460

Leu Pro Pro Asn Ser Ala Arg Ser Gln Ser Glu Arg Pro Val Phe Pro
465 470 475 480

Cys Trp Trp Leu Gln Phe Arg Asn Ser Lys Pro Cys Ser Asp Tyr Cys
485 490 495

Leu Ser His Ile Val Asn Leu Leu Glu Asp Trp Gly Pro Cys Ala Glu
500 505 510

His Gly Glu His His Ile Arg Ile Pro Arg Thr Pro Ala Arg Val Thr
515 520 525

Gly Gly Val Phe Leu Val Asp Lys Asn Pro His Asn Thr Ala Glu Ser
530 535 540

Arg Leu Val Val Asp Phe Ser Gln Phe Ser Arg Gly Asn Tyr Arg Val
545 550 555 560

Ser Trp Pro Lys Phe Ala Val Pro Asn Leu Gln Ser Leu Thr Asn Leu
565 570 575

Leu Ser Ser Asn Leu Ser Trp Leu Ser Leu Asp Val Ser Ala Ala Phe
580 585 590

Tyr His Leu Pro Leu His Pro Ala Ala Met Pro His Leu Leu Val Gly
595 600 605

Ser Ser Gly Leu Ser Arg Tyr Val Ala Arg Leu Ser Ser Asn Ser Arg
610 615 620

Ile Phe Asn Tyr Gln His Gly Thr Met Gln Asn Leu His Asp Ser Cys
625 630 635 640

Ser Arg Asn Leu Tyr Val Ser Leu Leu Leu Leu Tyr Gln Thr Phe Gly
645 650 655

Arg Lys Leu His Leu Tyr Ser His Pro Ile Ile Leu Gly Phe Arg Lys
660 665 670

```
Ile Pro Met Gly Val Gly Leu Ser Pro Phe Leu Leu Ala Gln Phe Thr
        675                 680                 685

Ser Ala Ile Cys Ser Val Val Arg Arg Ala Phe Pro His Cys Leu Ala
    690                 695                 700

Phe Ser Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr
705                 710                 715                 720

Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly
                725                 730                 735

Gly Thr Thr Val Cys Leu Gly Gln Gly Ala Lys Ser Val Gln His Leu
            740                 745                 750

Glu Ser Leu Phe Thr Ala Val Thr Asn Phe Leu Leu Ser Leu Gly Ile
        755                 760                 765

His Leu Asn Pro Asn Lys Thr Lys Arg Trp Gly Tyr Ser Leu His Phe
    770                 775                 780

Met Gly Tyr Val Ile Gly Cys Tyr Gly Ser Leu Pro Gln Asp His Ile
785                 790                 795                 800

Ile Gln Lys Ile Lys Glu Cys Phe Arg Lys Leu Pro Val Asn Arg Pro
                805                 810                 815

Ile Asp Trp Lys Val Cys Gln Arg Ile Val Gly Leu Leu Gly Phe Ala
            820                 825                 830

Ala Pro Phe Thr Gln Cys Gly Tyr Pro Ala Leu Met Pro Leu Tyr Ala
        835                 840                 845

Cys Ile Gln Ser Lys Gln Ala Phe Thr Phe Ser Pro Thr Tyr Lys Ala
    850                 855                 860

Phe Leu Cys Lys Gln Tyr Leu Asn Leu Tyr Pro Val Ala Arg Gln Arg
865                 870                 875                 880

Pro Gly Leu Cys Gln Val Phe Ala His Ala Thr Pro Thr Gly Trp Gly
                885                 890                 895

Leu Val Met Gly His Gln Arg Met Arg Gly Thr Phe Leu Trp Ala Ser
            900                 905                 910

Ala Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe
        915                 920                 925

Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ser Arg Lys Tyr Thr
    930                 935                 940
```

```
Ser Phe Pro Trp Leu Leu Gly Cys Ala Ala Asn Trp Ile Leu Arg Gly
945                 950                 955                 960

Thr Ser Phe Val Tyr Tyr Pro Ser Ala Leu Asn Pro Tyr His Asp Pro
                965                 970                 975

Ser Arg Gly Arg Leu Gly Leu Ser Arg Pro Leu Leu Arg Leu Pro Phe
            980                 985                 990

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

Pro Ser  His Leu Pro Asp Arg  Val His Phe Ala Ser  Pro Leu His
    1010                1015                1020

Val Ala  Trp Arg Pro Pro Tyr  Val Leu Leu Ser Ala  Gly Ala Leu
    1025                1030                1035

Thr Ala  Leu Met Leu Ile Ile  Phe Leu Met Thr Cys  Cys Arg Arg
    1040                1045                1050

Val Asn  Arg Ser Glu Pro Thr  Gln His Asn Leu Arg  Gly Thr Gly
    1055                1060                1065

Arg Glu  Val Ser Val Thr Pro  Gln Ser Gly Lys Ile  Ile Ser Ser
    1070                1075                1080

Trp Glu  Ser His Lys Ser Gly  Gly Glu Thr Arg Leu
    1085                1090                1095
```

<210> 13
<211> 2379
<212> DNA
<213> artificial sequence

<220>
<223> nucleotide sequence encoding the mutated Y07587 polymerase

<400> 13

```
atgccactga gctaccagca ctttcgcagg ctgttactgc tggatgatga agctggaccg     60

ctggaggagg agctgccacg tctggctgat gagggactga accgtcgtgt ggctgaggac    120

ctgaacctgg gcaacctgaa cgtgagcatt ccttggactc ataaggtggg aaactttacg    180

ggactttatt cttctactgt acctgtcttt aaccctcatt ggaaaacacc ctcttttcct    240

aatatacatt tacaccaaga cattatcaag aaatgtgaac aatttgtagg accactcaca    300

gtcaatgaga aaagaagact gcaattgatt atgcctgcta ggttttatcc aaatgttacc    360

aaatatttgc cattggataa gggtattaaa ccttattatc cagaacatct agttaatcat    420

tacttccaaa ccagacatta tttacacact ctatggaagg caggtatatt atataagaga    480

gaaacaacac atagtgcctc attttgtggg tcaccatatt cttgggaaca aaagctacag    540
```

catggagcag aatctttcca ccagcaatcc tctgggattc tttcccgacc accagttgga 600

tccagccttc agagcaaaca ccgcaaatcc agattgggac ttcaatccca acaaggacac 660

ctggccagac gccaacaagg taggagctgg agcattcgag ctgggattca ccccaccgca 720

cggaggtctt ttggggtgga gccctcaggc tcagggcatt ctacaaacct tgccagcaaa 780

tcagcctcct gcctctacca atcgccagtc aggaaggcag cctaccctgc tgtctccacc 840

tttgagaaac actcatcctc aggccatgca gtggaactcc acaaccttcc accaaactct 900

gcaagatccc agagtgagag gcctgtattt ccctgctggt ggctccagtt caggaacagt 960

aaaccctgtt ccgactactg tctctcccat atcgtcaatc ttctcgagga ttggggaccc 1020

tgcgctgaac acggtgagca ccatattcgc atcccgagaa cgccagcacg cgtgaccggt 1080

ggcgtgttcc tggtggataa gaacccacat aacacggctg aaagccgtct ggttgttgac 1140

tttagccagt tcagccgtgg caattatcgc gttagctggc ctaagtttgc ggtgccgaat 1200

ctgcagagcc tgacgaatct gttaagcagc aatttaagct ggctgagctt agacgttagc 1260

gcagccttct accacctgcc actgcaccca gcagcgatgc cacacctgct ggtgggcagc 1320

agcggtctga gccgttacgt ggcacgcctg agcagcaaca gccgtatatt taattatcaa 1380

catggcacga tgcaaaattt acatgatagc tgtagccgta atctgtacgt gagcctgtta 1440

ctgttatatc agacgtttgg tcgcaagctg catttataca gccacccgat tattttaggg 1500

ttccgcaaga tcccgatggg tgttggtctg tctccattcc tgttagcgca attcaccagc 1560

gcaatctgca gcgttgtgcg cagagcgttt ccgcattgcc tggcgtttag cggtgcgaaa 1620

agcgtgcaac acctggaaag cctgttcacg gcagtgacga acttcctgct gagcctgggc 1680

attcacctga accctaacaa aacaaagaga tggggttact ctttacattt catgggctat 1740

gtcattggat gttatgggtc attgccacaa gatcacatca tacaaaagat caaagaatgt 1800

tttcgaaaac ttcctgttaa cagacctatt gattggaaag tctgtcaacg tattgtgggt 1860

cttttgggtt ttgctgctcc ttttacacaa tgtggttatc ctgctttaat gcctttgtat 1920

gcatgtattc agtcgaagca ggcttttact ttctcgccaa cttacaaggc ctttctgtgt 1980

aaacaatacc tgaaccttta ccctgttgct cggcaaagac caggtctgtg ccaagtgttt 2040

gctcacgcaa cccctactgg ctggggattg gtcatgggac atcagcgcat gcgtggaacc 2100

tttctgtcca gaaaatatac atcgtttcca tggctgctag gctgtgctgc caactggata 2160

ctgagaggca ccagcttcgt gtattatccc agcgctctca acccttacca tgatccttct 2220

cgaggtagac tgggcctgag cagacctctg ctgagactcc ccttccgacc cacaaccgga 2280

agaacaagcc tgtatgccga tagccctagc gtccccagcc acctccctga tagagtccat 2340

tttgccagcc cactccatgt ggcctggagg cctccctaa 2379

<210> 14
<211> 2820
<212> DNA
<213> artificial sequence

<220>
<223> nucleotide sequence encoding the fusion between truncated core (1-148) and mutated Y07587 polymerase

<400> 14

atggatatcg atccctacaa ggagttcggt gccaccgtcg aactgctgag cttcctgccc 60

agcgatttct tcccaagcgt acgtgacctt ctagatacag cctcagctct gtatcgggaa 120

gccttagagt ctcctgagca ttgttcacct caccatactg ctctcaggca agcaattctg 180

tgctggggag aactaatgac tctagctacc tgggtgggtg gtaatttgga agatccaata 240

tccagggacc tagtagtcag ttatgtcaac actaatatgg gactaaagtt ccgacaacta 300

ttgtggtttc acatttcttg tctcactttt ggaagagaaa cagttataga atatttggtg 360

tctttcggag tgtggattcg cactcctcca gcttatagac caccaaacgc accgatactg 420

agcaccctgc cagaaaccac cgtgccactg agctaccagc actttcgcag gctgttactg 480

ctggatgatg aagctggacc gctggaggag gagctgccac gtctggctga tgagggactg 540

aaccgtcgtg tggctgagga cctgaacctg ggcaacctga acgtgagcat tccttggact 600

cataaggtgg gaaactttac gggactttat tcttctactg tacctgtctt taaccctcat 660

tggaaaacac cctcttttcc taatatacat ttacaccaag acattatcaa gaaatgtgaa 720

caatttgtag gaccactcac agtcaatgag aaaagaagac tgcaattgat tatgcctgct 780

aggttttatc caaatgttac caaatatttg ccattggata agggtattaa accttattat 840

ccagaacatc tagttaatca ttacttccaa accagacatt atttacacac tctatggaag 900

gcaggtatat tatataagag agaaacaaca catagtgcct cattttgtgg gtcaccatat 960

tcttgggaac aaaagctaca gcatggagca gaatctttcc accagcaatc ctctgggatt 1020

ctttcccgac caccagttgg atccagcctt cagagcaaac accgcaaatc cagattggga 1080

cttcaatccc aacaaggaca cctggccaga cgccaacaag gtaggagctg gagcattcga 1140

gctgggattc accccaccgc acggaggtct tttggggtgg agccctcagg ctcagggcat 1200

tctacaaacc ttgccagcaa atcagcctcc tgcctctacc aatcgccagt caggaaggca 1260

gcctaccctg ctgtctccac ctttgagaaa cactcatcct caggccatgc agtggaactc 1320

cacaaccttc caccaaactc tgcaagatcc cagagtgaga ggcctgtatt tccctgctgg 1380

tggctccagt tcaggaacag taaaccctgt tccgactact gtctctccca tatcgtcaat 1440

cttctcgagg attggggacc ctgcgctgaa cacggtgagc accatattcg catcccgaga 1500

acgccagcac gcgtgaccgg tggcgtgttc ctggtggata agaacccaca taacacggct 1560

gaaagccgtc tggttgttga ctttagccag ttcagccgtg gcaattatcg cgttagctgg 1620

cctaagtttg cggtgccgaa tctgcagagc ctgacgaatc tgttaagcag caatttaagc 1680

tggctgagct tagacgttag cgcagccttc taccacctgc cactgcaccc agcagcgatg 1740

ccacacctgc tggtgggcag cagcggtctg agccgttacg tggcacgcct gagcagcaac 1800

agccgtatat ttaattatca acatggcacg atgcaaaatt tacatgatag ctgtagccgt 1860

aatctgtacg tgagcctgtt actgttatat cagacgtttg gtcgcaagct gcatttatac 1920

agccacccga ttattttagg gttccgcaag atcccgatgg gtgttggtct gtctccattc 1980

ctgttagcgc aattcaccag cgcaatctgc agcgttgtgc gcagagcgtt tccgcattgc 2040

ctggcgttta gcggtgcgaa aagcgtgcaa cacctggaaa gcctgttcac ggcagtgacg 2100

aacttcctgc tgagcctggg cattcacctg aaccctaaca aaacaaagag atggggttac 2160

tctttacatt tcatgggcta tgtcattgga tgttatgggt cattgccaca agatcacatc 2220

atacaaaaga tcaaagaatg ttttcgaaaa cttcctgtta acagacctat tgattggaaa 2280

gtctgtcaac gtattgtggg tcttttgggt tttgctgctc cttttacaca atgtggttat 2340

cctgctttaa tgcctttgta tgcatgtatt cagtcgaagc aggcttttac tttctcgcca 2400

acttacaagg cctttctgtg taaacaatac ctgaaccttt accctgttgc tcggcaaaga 2460

ccaggtctgt gccaagtgtt tgctcacgca acccctactg gctggggatt ggtcatggga 2520

catcagcgca tgcgtggaac ctttctgtcc agaaaatata catcgtttcc atggctgcta 2580

ggctgtgctg ccaactggat actgagaggc accagcttcg tgtattatcc cagcgctctc 2640

aacccttacc atgatccttc tcgaggtaga ctgggcctga gcagacctct gctgagactc 2700

cccttccgac ccacaaccgg aagaacaagc ctgtatgccg atagccctag cgtccccagc 2760

cacctccctg atagagtcca ttttgccagc ccactccatg tggcctggag gcctccctaa 2820

<210> 15
<211> 3024
<212> DNA
<213> artificial sequence

<220>
<223> nucleotide sequence encoding the fusion between truncated core (1-148)-mutated Y07587 polymerase-env1 and env2

<400> 15
atggatatcg atccctacaa ggagttcggt gccaccgtcg aactgctgag cttcctgccc 60

agcgatttct tcccaagcgt acgtgacctt ctagatacag cctcagctct gtatcgggaa 120

gccttagagt ctcctgagca ttgttcacct caccatactg ctctcaggca agcaattctg 180

tgctggggag aactaatgac tctagctacc tgggtgggtg gtaatttgga agatccaata 240

tccagggacc tagtagtcag ttatgtcaac actaatatgg gactaaagtt ccgacaacta 300

ttgtggtttc acatttcttg tctcactttt ggaagagaaa cagttataga atatttggtg 360

tctttcggag tgtggattcg cactcctcca gcttatagac caccaaacgc accgatactg 420

agcaccctgc cagaaaccac cgtgccactg agctaccagc actttcgcag gctgttactg 480

ctggatgatg aagctggacc gctggaggag gagctgccac gtctggctga tgagggactg 540

aaccgtcgtg tggctgagga cctgaacctg ggcaacctga acgtgagcat tccttggact 600

cataaggtgg gaaactttac gggactttat tcttctactg tacctgtctt taaccctcat 660

tggaaaacac cctcttttcc taatatacat ttacaccaag acattatcaa gaaatgtgaa 720

caatttgtag gaccactcac agtcaatgag aaaagaagac tgcaattgat tatgcctgct 780

aggttttatc caaatgttac caaatatttg ccattggata agggtattaa accttattat 840
ccagaacatc tagttaatca ttacttccaa accagacatt atttacacac tctatggaag 900
gcaggtatat tatataagag agaaacaaca catagtgcct cattttgtgg gtcaccatat 960
tcttgggaac aaaagctaca gcatggagca gaatctttcc accagcaatc ctctgggatt 1020
ctttcccgac caccagttgg atccagcctt cagagcaaac accgcaaatc cagattggga 1080
cttcaatccc aacaaggaca cctggccaga cgccaacaag gtaggagctg gagcattcga 1140
gctgggattc accccaccgc acggaggtct tttggggtgg agccctcagg ctcagggcat 1200
tctacaaacc ttgccagcaa atcagcctcc tgcctctacc aatcgccagt caggaaggca 1260
gcctaccctg ctgtctccac ctttgagaaa cactcatcct caggccatgc agtggaactc 1320
cacaaccttc caccaaactc tgcaagatcc cagagtgaga ggcctgtatt tccctgctgg 1380
tggctccagt tcaggaacag taaaccctgt tccgactact gtctctccca tatcgtcaat 1440
cttctcgagg attggggacc ctgcgctgaa cacggtgagc accatattcg catcccgaga 1500
acgccagcac gcgtgaccgg tggcgtgttc ctggtggata agaacccaca taacacggct 1560
gaaagccgtc tggttgttga ctttagccag ttcagccgtg gcaattatcg cgttagctgg 1620
cctaagtttg cggtgccgaa tctgcagagc ctgacgaatc tgttaagcag caatttaagc 1680
tggctgagct tagacgttag cgcagccttc taccacctgc cactgcaccc agcagcgatg 1740
ccacacctgc tggtgggcag cagcggtctg agccgttacg tggcacgcct gagcagcaac 1800
agccgtatat ttaattatca acatggcacg atgcaaaatt tacatgatag ctgtagccgt 1860
aatctgtacg tgagcctgtt actgttatat cagacgtttg gtcgcaagct gcatttatac 1920
agccacccga ttattttagg gttccgcaag atcccgatgg gtgttggtct gtctccattc 1980
ctgttagcgc aattcaccag cgcaatctgc agcgttgtgc gcagagcgtt tccgcattgc 2040
ctggcgttta gcgtcctgca agcaggcttc ttcctgctga cccgtattct gaccattcca 2100
caaagcctgg atagctggtg gaccagcctg aacttcctgg gtggcaccac ggtttgcctg 2160
ggtcagggtg cgaaaagcgt gcaacacctg gaaagcctgt tcacggcagt gacgaacttc 2220
ctgctgagcc tgggcattca cctgaaccct aacaaaacaa agagatgggg ttactcttta 2280
catttcatgg gctatgtcat tggatgttat gggtcattgc cacaagatca catcatacaa 2340
aagatcaaag aatgttttcg aaaacttcct gttaacagac ctattgattg gaaagtctgt 2400
caacgtattg tgggtctttt gggttttgct gctcctttta cacaatgtgg ttatcctgct 2460
ttaatgcctt tgtatgcatg tattcagtcg aagcaggctt ttactttctc gccaacttac 2520
aaggcctttc tgtgtaaaca atacctgaac ctttaccctg ttgctcggca aagaccaggt 2580
ctgtgccaag tgtttgctca cgcaacccct actggctggg gattggtcat gggacatcag 2640
cgcatgcgtg gaacctttct gtgggcaagc gcacgcttta gctggctgag cctgctggtt 2700
ccgttcgtgc aatggtttgt gggtctgagc ccaaccgtgt ggctgagcgt gtccagaaaa 2760
tatacatcgt ttccatggct gctaggctgt gctgccaact ggatactgag aggcaccagc 2820

ttcgtgtatt atcccagcgc tctcaaccct taccatgatc cttctcgagg tagactgggc 2880

ctgagcagac ctctgctgag actccccttc cgacccacaa ccggaagaac aagcctgtat 2940

gccgatagcc ctagcgtccc cagccacctc cctgatagag tccattttgc cagcccactc 3000

catgtggcct ggaggcctcc ctaa 3024

<210> 16
<211> 3723
<212> DNA
<213> artificial sequence

<220>
<223> nucleotide sequence encoding core (1-183) IRES and fusion between mutated Y07587 polymerase-env1-env2

<400> 16
atggatatcg atccctacaa ggagttcggt gccaccgtcg aactgctgag cttcctgccc 60

agcgatttct tcccaagcgt acgtgacctt ctagatacag cctcagctct gtatcgggaa 120

gccttagagt ctcctgagca ttgttcacct caccatactg ctctcaggca agcaattctg 180

tgctggggag aactaatgac tctagctacc tgggtgggtg gtaatttgga agatccaata 240

tccagggacc tagtagtcag ttatgtcaac actaatatgg gactaaagtt ccgacaacta 300

ttgtggtttc acatttcttg tctcactttt ggaagagaaa cagttataga atatttggtg 360

tctttcggag tgtggattcg cactcctcca gcttatagac caccaaacgc accgatactg 420

agcaccctgc cagaaaccac cgtggtgcgt cgtcgtggtc gcagcccacg caggcgtacc 480

ccaagcccac gtcgtcgcag aagccagagc ccacgacgtc gcaggagcca gagccgtgag 540

agccagtgct aaaagcttga tatcgaattc acgcgtcccc cccctaacgt tactggccga 600

agccgcttgg aataaggccg gtgtgcgttt gtctatatgt tattttccac catattgccg 660

tcttttggca atgtgagggc ccggaaacct ggccctgtct tcttgacgag cattcctagg 720

ggtctttccc ctctcgccaa aggaatgcaa ggtctgttga atgtcgtgaa ggaagcagtt 780

cctctggaag cttcttgaag acaaacaacg tctgtagcga ccctttgcag gcagcggaac 840

ccccacctg gcgacaggtg cctctgcggc caaaagccac gtgtataaga tacacctgca 900

aaggcggcac aaccccagtg ccacgttgtg agttggatag ttgtggaaag agtcaaatgg 960

ctctcctcaa gcgtattcaa caaggggctg aaggatgccc agaaggtacc ccattgtatg 1020

ggatctgatc tggggcctcg gtgcacatgc tttacatgtg tttagtcgag gttaaaaaac 1080

gtctaggccc cccgaaccac ggggacgtgg ttttcctttg aaaaacacga tgataatacc 1140

atgccactga gctaccagca ctttcgcagg ctgttactgc tggatgatga agctggaccg 1200

ctggaggagg agctgccacg tctggctgat gagggactga accgtcgtgt ggctgaggac 1260

ctgaacctgg gcaacctgaa cgtgagcatt ccttggactc ataaggtggg aaactttacg 1320

ggactttatt cttctactgt acctgtcttt aaccctcatt ggaaaacacc ctcttttcct 1380

aatatacatt tacaccaaga cattatcaag aaatgtgaac aatttgtagg accactcaca 1440

gtcaatgaga aaagaagact gcaattgatt atgcctgcta ggttttatcc aaatgttacc 1500

aaatatttgc cattggataa gggtattaaa ccttattatc cagaacatct agttaatcat 1560
tacttccaaa ccagacatta tttacacact ctatggaagg caggtatatt atataagaga 1620
gaaacaacac atagtgcctc attttgtggg tcaccatatt cttgggaaca aaagctacag 1680
catggagcag aatctttcca ccagcaatcc tctgggattc tttcccgacc accagttgga 1740
tccagccttc agagcaaaca ccgcaaatcc agattgggac ttcaatccca acaaggacac 1800
ctggccagac gccaacaagg taggagctgg agcattcgag ctgggattca ccccaccgca 1860
cggaggtctt ttggggtgga gccctcaggc tcagggcatt ctacaaacct tgccagcaaa 1920
tcagcctcct gcctctacca atcgccagtc aggaaggcag cctaccctgc tgtctccacc 1980
tttgagaaac actcatcctc aggccatgca gtggaactcc acaaccttcc accaaactct 2040
gcaagatccc agagtgagag gcctgtattt ccctgctggt ggctccagtt caggaacagt 2100
aaaccctgtt ccgactactg tctctcccat atcgtcaatc ttctcgagga ttggggaccc 2160
tgcgctgaac acggtgagca ccatattcgc atcccgagaa cgccagcacg cgtgaccggt 2220
ggcgtgttcc tggtggataa gaacccacat aacacggctg aaagccgtct ggttgttgac 2280
tttagccagt tcagccgtgg caattatcgc gttagctggc ctaagtttgc ggtgccgaat 2340
ctgcagagcc tgacgaatct gttaagcagc aatttaagct ggctgagctt agacgttagc 2400
gcagccttct accacctgcc actgcaccca gcagcgatgc cacacctgct ggtgggcagc 2460
agcggtctga gccgttacgt ggcacgcctg agcagcaaca gccgtatatt taattatcaa 2520
catggcacga tgcaaaattt acatgatagc tgtagccgta atctgtacgt gagcctgtta 2580
ctgttatatc agacgtttgg tcgcaagctg catttataca gccacccgat tattttaggg 2640
ttccgcaaga tcccgatggg tgttggtctg tctccattcc tgttagcgca attcaccagc 2700
gcaatctgca gcgttgtgcg cagagcgttt ccgcattgcc tggcgtttag cgtcctgcaa 2760
gcaggcttct tcctgctgac ccgtattctg accattccac aaagcctgga tagctggtgg 2820
accagcctga acttcctggg tggcaccacg gtttgcctgg gtcagggtgc gaaaagcgtg 2880
caacacctgg aaagcctgtt cacggcagtg acgaacttcc tgctgagcct gggcattcac 2940
ctgaacccta acaaaacaaa gagatggggt tactctttac atttcatggg ctatgtcatt 3000
ggatgttatg ggtcattgcc acaagatcac atcatacaaa agatcaaaga atgttttcga 3060
aaacttcctg ttaacagacc tattgattgg aaagtctgtc aacgtattgt gggtcttttg 3120
ggttttgctg ctccttttac acaatgtggt tatcctgctt taatgccttt gtatgcatgt 3180
attcagtcga agcaggcttt tactttctcg ccaacttaca aggcctttct gtgtaaacaa 3240
tacctgaacc tttaccctgt tgctcggcaa agaccaggtc tgtgccaagt gtttgctcac 3300
gcaacccCta ctggctgggg attggtcatg ggacatcagc gcatgcgtgg aacctttctg 3360
tgggcaagcg cacgctttag ctggctgagc ctgctggttc cgttcgtgca atggtttgtg 3420
ggtctgagcc caaccgtgtg gctgagcgtg tccagaaaat atacatcgtt tccatggctg 3480
ctaggctgtg ctgccaactg gatactgaga ggcaccagct tcgtgtatta tcccagcgct 3540

ctcaaccctt accatgatcc ttctcgaggt agactgggcc tgagcagacc tctgctgaga 3600

ctccccttcc gacccacaac cggaagaaca agcctgtatg ccgatagccc tagcgtcccc 3660

agccacctcc ctgatagagt ccattttgcc agcccactcc atgtggcctg gaggcctccc 3720

taa 3723

<210> 17
<211> 3723
<212> DNA
<213> artificial sequence

<220>
<223> nucleotide sequence encoding fusion mutated Y07587 polymerase-env1-env2 IRES core (1-183)

<400> 17
atgccactga gctaccagca ctttcgcagg ctgttactgc tggatgatga agctggaccg 60

ctggaggagg agctgccacg tctggctgat gagggactga accgtcgtgt ggctgaggac 120

ctgaacctgg gcaacctgaa cgtgagcatt ccttggactc ataaggtggg aaactttacg 180

ggactttatt cttctactgt acctgtcttt aaccctcatt ggaaaacacc ctcttttcct 240

aatatacatt tacaccaaga cattatcaag aaatgtgaac aatttgtagg accactcaca 300

gtcaatgaga aaagaagact gcaattgatt atgcctgcta ggttttatcc aaatgttacc 360

aaatatttgc cattggataa gggtattaaa ccttattatc cagaacatct agttaatcat 420

tacttccaaa ccagacatta tttacacact ctatggaagg caggtatatt atataagaga 480

gaaacaacac atagtgcctc attttgtggg tcaccatatt cttgggaaca aaagctacag 540

catggagcag aatctttcca ccagcaatcc tctgggattc tttcccgacc accagttgga 600

tccagccttc agagcaaaca ccgcaaatcc agattgggac ttcaatccca acaaggacac 660

ctggccagac gccaacaagg taggagctgg agcattcgag ctgggattca ccccaccgca 720

cggaggtctt ttggggtgga gccctcaggc tcagggcatt ctacaaacct tgccagcaaa 780

tcagcctcct gcctctacca atcgccagtc aggaaggcag cctaccctgc tgtctccacc 840

tttgagaaac actcatcctc aggccatgca gtggaactcc acaaccttcc accaaactct 900

gcaagatccc agagtgagag gcctgtattt ccctgctggt ggctccagtt caggaacagt 960

aaaccctgtt ccgactactg tctctcccat atcgtcaatc ttctcgagga ttggggaccc 1020

tgcgctgaac acggtgagca ccatattcgc atcccgagaa cgccagcacg cgtgaccggt 1080

ggcgtgttcc tggtggataa gaacccacat aacacggctg aaagccgtct ggttgttgac 1140

tttagccagt tcagccgtgg caattatcgc gttagctggc ctaagtttgc ggtgccgaat 1200

ctgcagagcc tgacgaatct gttaagcagc aatttaagct ggctgagctt agacgttagc 1260

gcagccttct accacctgcc actgcaccca gcagcgatgc cacacctgct ggtgggcagc 1320

agcggtctga gccgttacgt ggcacgcctg agcagcaaca gccgtatatt taattatcaa 1380

catggcacga tgcaaaattt acatgatagc tgtagccgta atctgtacgt gagcctgtta 1440

ctgttatatc agacgtttgg tcgcaagctg catttataca gccacccgat tattttaggg 1500
ttccgcaaga tcccgatggg tgttggtctg tctccattcc tgttagcgca attcaccagc 1560
gcaatctgca gcgttgtgcg cagagcgttt ccgcattgcc tggcgtttag cgtcctgcaa 1620
gcaggcttct tcctgctgac ccgtattctg accattccac aaagcctgga tagctggtgg 1680
accagcctga acttcctggg tggcaccacg gtttgcctgg gtcagggtgc gaaaagcgtg 1740
caacacctgg aaagcctgtt cacggcagtg acgaacttcc tgctgagcct gggcattcac 1800
ctgaacccta acaaaacaaa gagatggggt tactctttac atttcatggg ctatgtcatt 1860
ggatgttatg ggtcattgcc acaagatcac atcatacaaa agatcaaaga atgttttcga 1920
aaacttcctg ttaacagacc tattgattgg aaagtctgtc aacgtattgt gggtcttttg 1980
ggttttgctg ctccttttac acaatgtggt tatcctgctt taatgccttt gtatgcatgt 2040
attcagtcga agcaggcttt tactttctcg ccaacttaca aggcctttct gtgtaaacaa 2100
tacctgaacc tttaccctgt tgctcggcaa agaccaggtc tgtgccaagt gtttgctcac 2160
gcaacccctа ctggctgggg attggtcatg ggacatcagc gcatgcgtgg aacctttctg 2220
tgggcaagcg cacgctttag ctggctgagc ctgctggttc cgttcgtgca atggtttgtg 2280
ggtctgagcc caaccgtgtg gctgagcgtg tccagaaaat atacatcgtt tccatggctg 2340
ctaggctgtg ctgccaactg gatactgaga ggcaccagct tcgtgtatta tcccagcgct 2400
ctcaaccctt accatgatcc ttctcgaggt agactgggcc tgagcagacc tctgctgaga 2460
ctccccttcc gacccacaac cggaagaaca agcctgtatg ccgatagccc tagcgtcccc 2520
agccacctcc ctgatagagt ccattttgcc agcccactcc atgtggcctg gaggcctccc 2580
taaaagcttg atatcgaatt cacgcgtccc ccccctaacg ttactggccg aagccgcttg 2640
gaataaggcc ggtgtgcgtt tgtctatatg ttattttcca ccatattgcc gtcttttggc 2700
aatgtgaggg cccggaaacc tggccctgtc ttcttgacga gcattcctag gggtctttcc 2760
cctctcgcca aaggaatgca aggtctgttg aatgtcgtga aggaagcagt tcctctggaa 2820
gcttcttgaa gacaaacaac gtctgtagcg acccttttgca ggcagcggaa ccccccacct 2880
ggcgacaggt gcctctgcgg ccaaaagcca cgtgtataag atacacctgc aaaggcggca 2940
caaccccagt gccacgttgt gagttggata gttgtggaaa gagtcaaatg gctctcctca 3000
agcgtattca acaaggggct gaaggatgcc cagaaggtac cccattgtat gggatctgat 3060
ctggggcctc ggtgcacatg ctttacatgt gtttagtcga ggttaaaaaa cgtctaggcc 3120
ccccgaacca cggggacgtg gttttccttt gaaaaacacg atgataatac catggatatc 3180
gatccctaca aggagttcgg tgccaccgtc gaactgctga gcttcctgcc cagcgatttc 3240
ttcccaagcg tacgtgacct tctagataca gcctcagctc tgtatcggga agccttagag 3300
tctcctgagc attgttcacc tcaccatact gctctcaggc aagcaattct gtgctgggga 3360
gaactaatga ctctagctac ctgggtgggt ggtaatttgg aagatccaat atccagggac 3420
ctagtagtca gttatgtcaa cactaatatg ggactaaagt tccgacaact attgtggttt 3480

cacatttctt gtctcacttt tggaagagaa acagttatag aatatttggt gtctttcgga 3540

gtgtggattc gcactcctcc agcttataga ccaccaaacg caccgatact gagcaccctg 3600

ccagaaacca ccgtggtgcg tcgtcgtggt cgcagcccac gcaggcgtac cccaagccca 3660

cgtcgtcgca gaagccagag cccacgacgt cgcaggagcc agagccgtga gagccagtgc 3720

taa 3723

<210> 18
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> FLP peptide (core 18-27)

<400> 18

Phe Leu Pro Ser Asp Phe Phe Pro Ser Val
1 5 10

<210> 19
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> ILC peptide (core 99-108)

<400> 19

Ile Leu Cys Trp Gly Glu Leu Met Thr
1 5

<210> 20
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> VLQ peptide (env1)

<400> 20

Val Leu Gln Ala Gly Phe Phe Leu Leu
1 5

<210> 21
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> FLG peptide (env1 41-49)

<400> 21

Phe Leu Gly Gly Thr Thr Val Cys Leu
1 5

<210> 22

<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> GLS peptide (env2)

<400> 22

Gly Leu Ser Pro Thr Val Trp Leu Ser Val
1 5 10

<210> 23
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> SLY peptide (polymerase 816-824)

<400> 23

Ser Leu Tyr Ala Asp Ser Pro Ser Val
1 5

<210> 24
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> VSA peptide (polymerase)

<400> 24

Val Ser Ala Ala Phe Tyr His Leu Pro Leu
1 5 10

<210> 25
<211> 15
<212> PRT
<213> artificial sequence

<220>
<223> N13F peptide (polymerase)

<400> 25

Asn Leu Asn Val Ser Ile Pro Trp Thr His Lys Val Gly Asn Phe
1 5 10 15

<210> 26
<211> 15
<212> PRT
<213> artificial sequence

<220>
<223> F13L peptide (env)

<400> 26

Phe Leu Trp Glu Trp Ala Ser Ala Arg Phe Ser Trp Leu Ser Leu
1 5 10 15