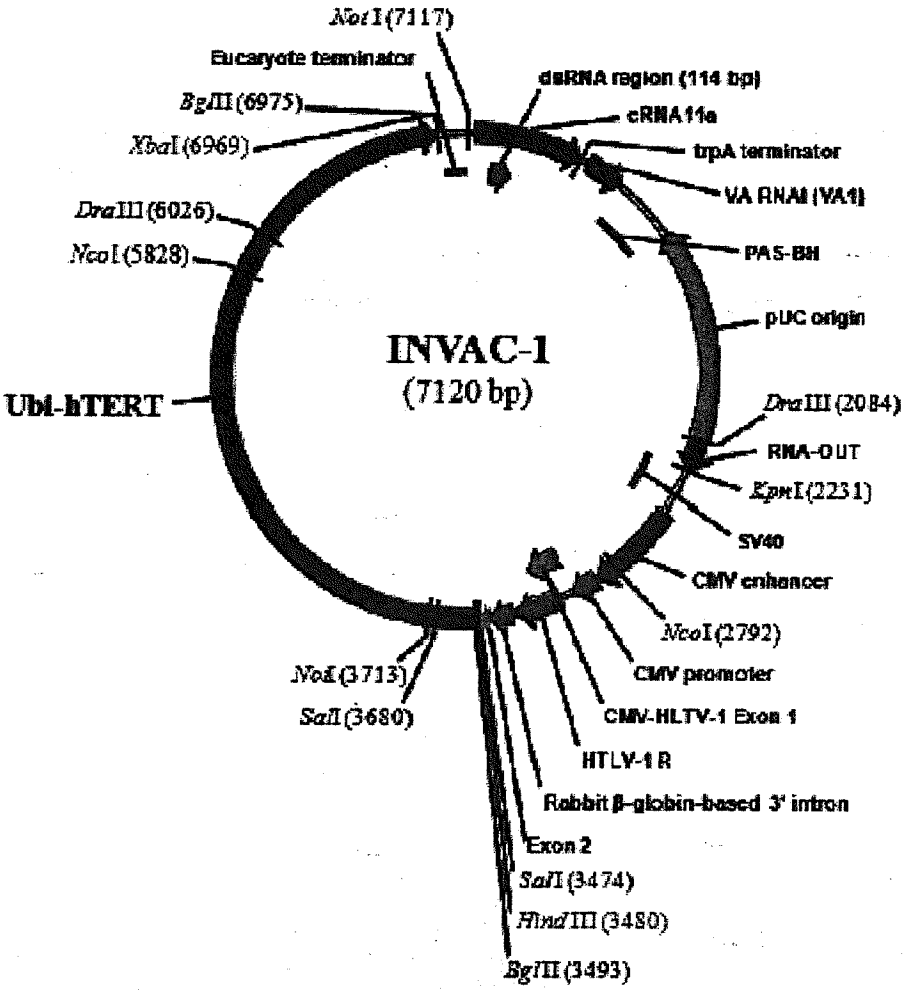


FIGURE 1A

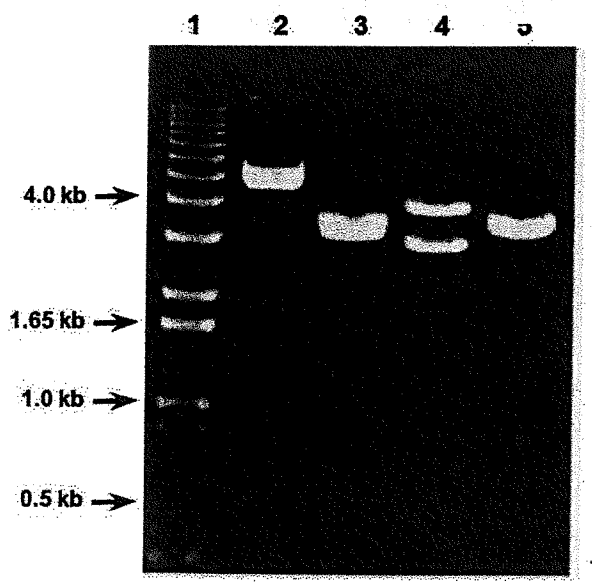


FIGURE 1B

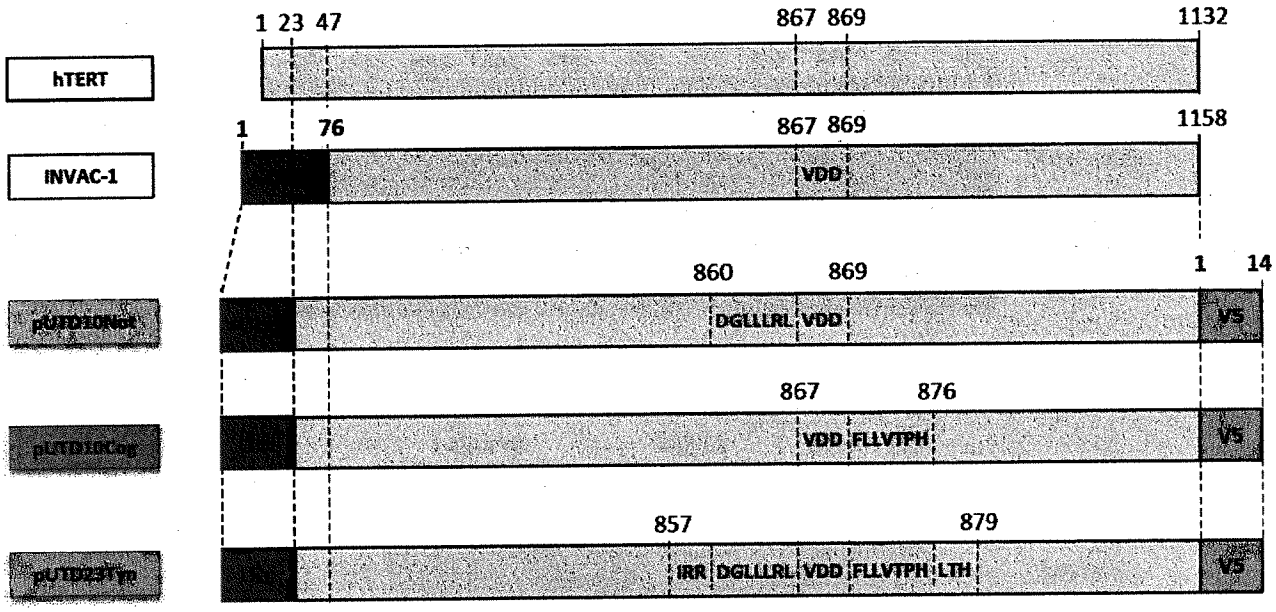


FIGURE 2A

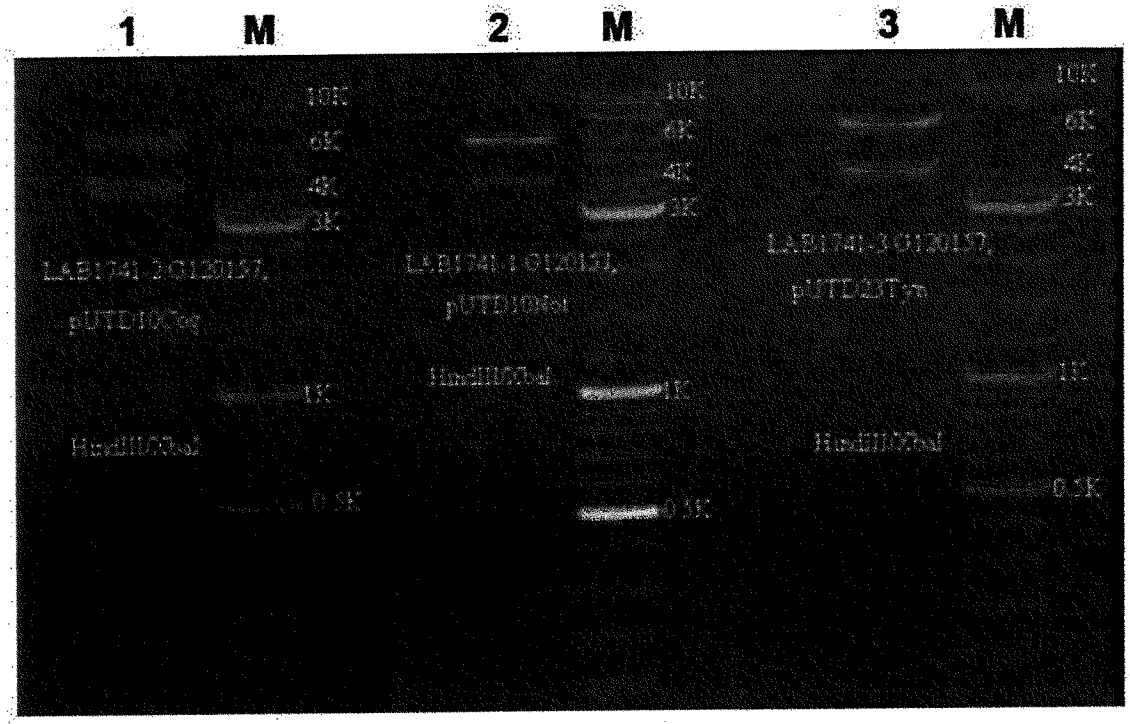


FIGURE 2B

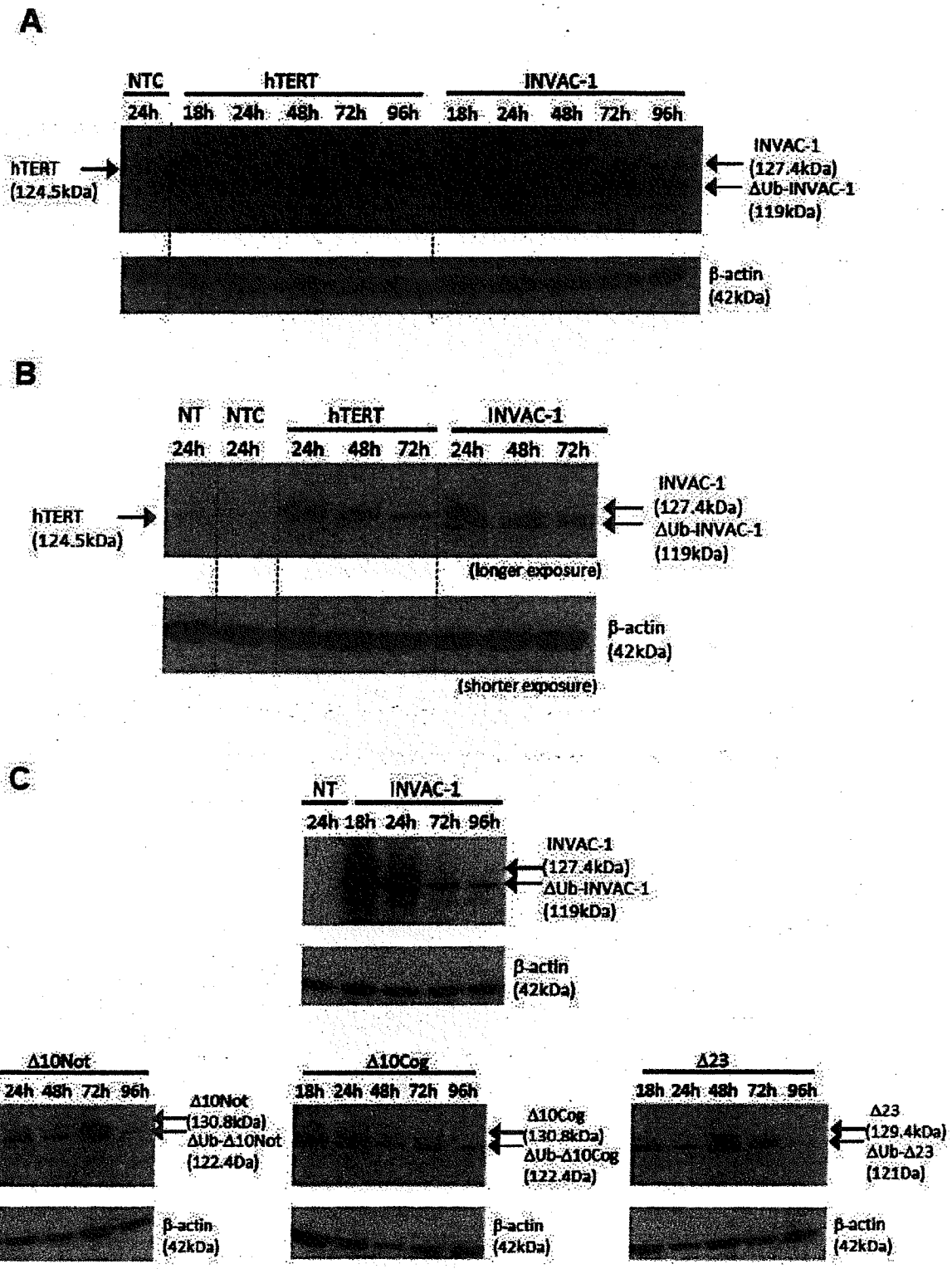

A
NTC
hTERT
INVAC-1
24h
18h 24h 48h 72h 96h
18h 24h 48h 72h 96h
hTERT
(124.5kDa)
INVAC-1
(127.4kDa)
ΔUb-INVAC-1
(119kDa)
β-actin
(42kDa)
B
NT NTC
hTERT
INVAC-1
24h 24h
24h 48h 72h
24h 48h 72h
hTERT
(124.5kDa)
INVAC-1
(127.4kDa)
ΔUb-INVAC-1
(119kDa)
(longer exposure)
β-actin
(42kDa)
(shorter exposure)
C
NT
INVAC-1
24h 18h 24h 72h 96h
INVAC-1
(127.4kDa)
ΔUb-INVAC-1
(119kDa)
β-actin
(42kDa)
NT
Δ10Not
24h 18h 24h 48h 72h 96h
Δ10Not
(130.8kDa)
ΔUb-Δ10Not
(122.4Da)
β-actin
(42kDa)
Δ10Cog
18h 24h 48h 72h 96h
Δ10Cog
(130.8kDa)
ΔUb-Δ10Cog
(122.4Da)
β-actin
(42kDa)
Δ23
18h 24h 48h 72h 96h
Δ23
(129.4kDa)
ΔUb-Δ23
(121Da)
β-actin
(42kDa)

FIGURE 3

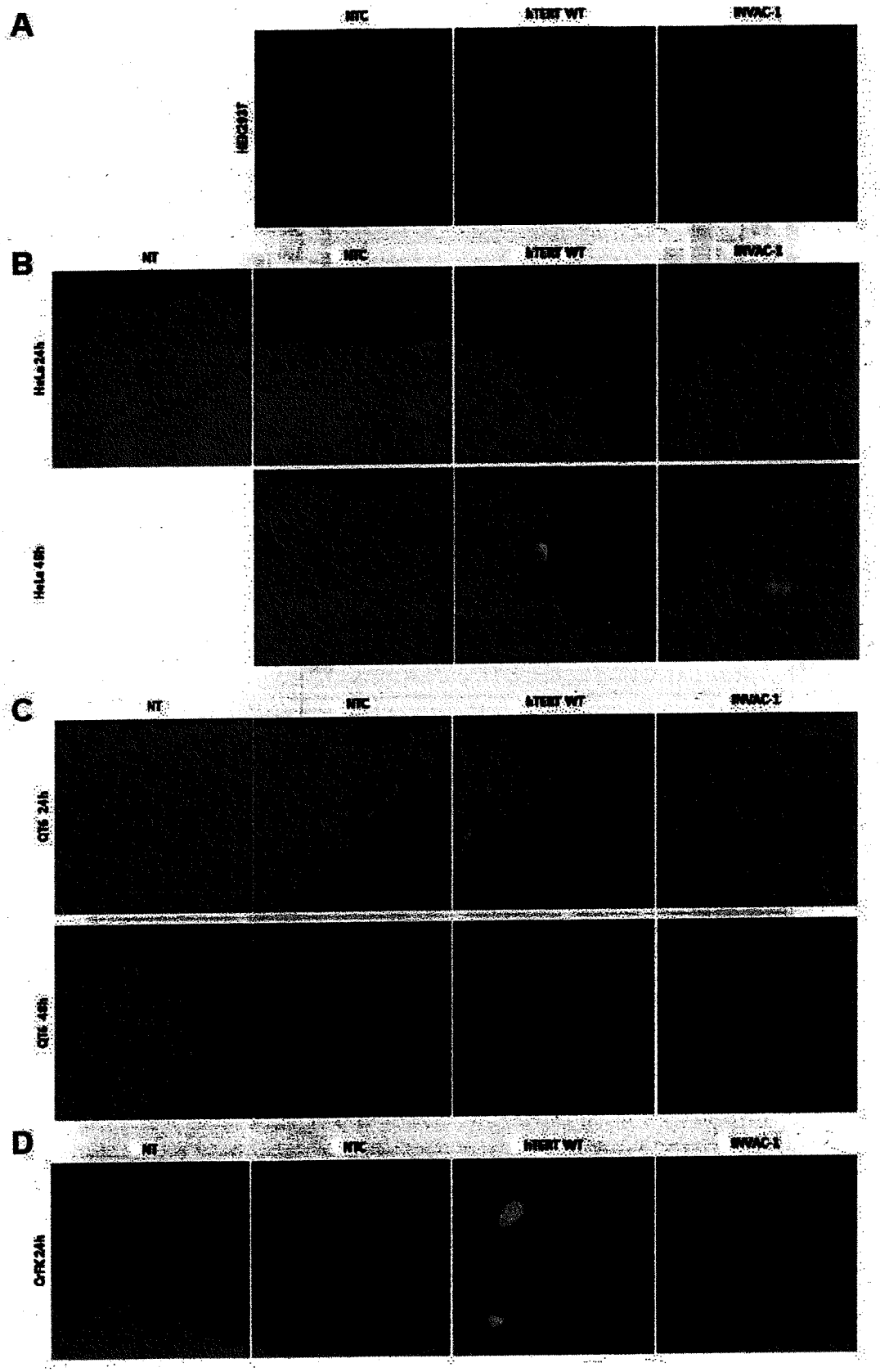

A
NTC
ATERT WT
SHVAC-1
HEK293T
B
NT
NTC
ATERT WT
SHVAC-1
Hela 24h
Hela 48h
C
NT
NTC
ATERT WT
SHVAC-1
OTS 24h
OTS 48h
D
NT
NTC
ATERT WT
SHVAC-1
CRK 24h

FIGURE 4

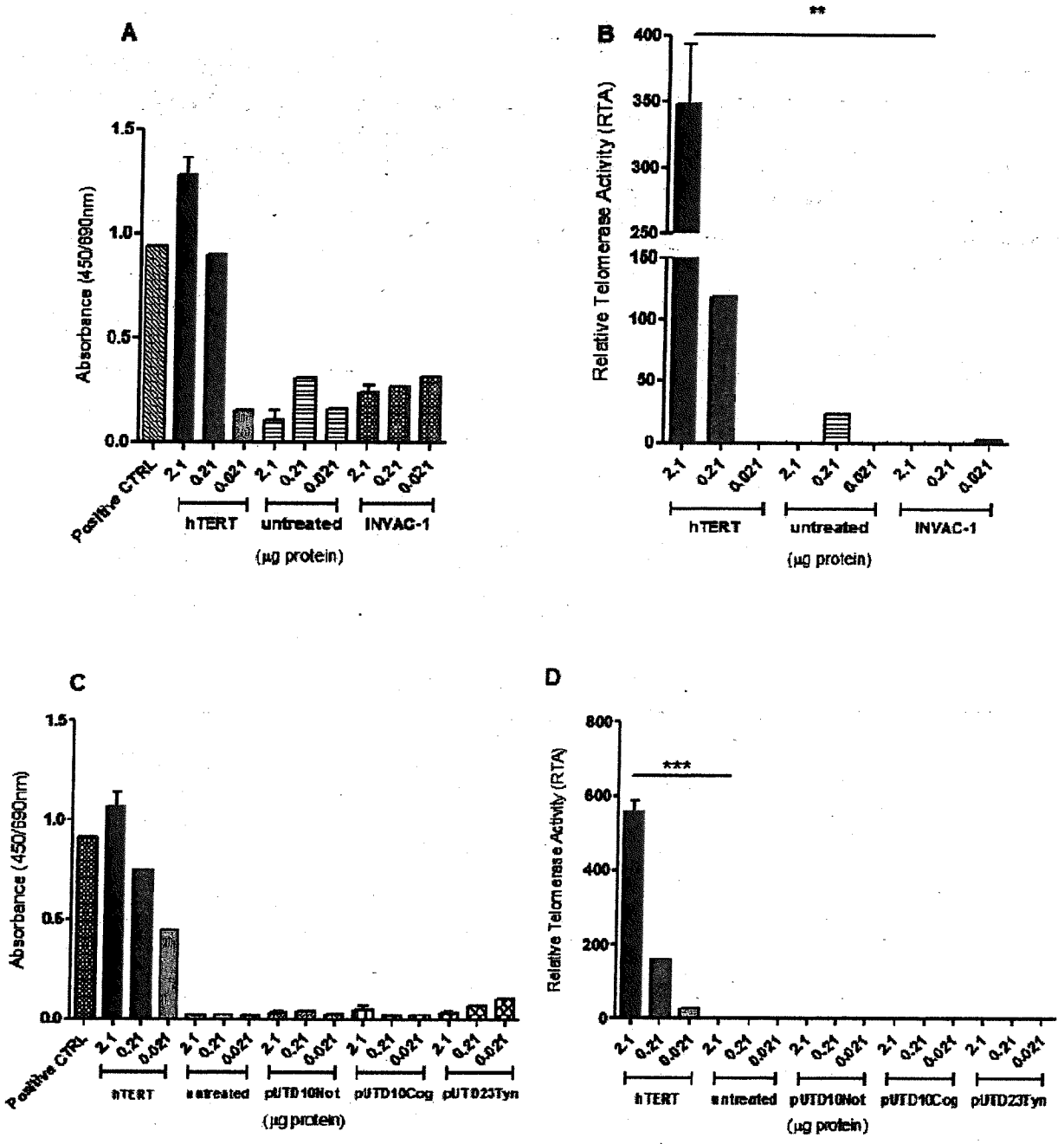

A
Absorbance (450/690nm)
1.5
1.0
0.5
0.0
Positive CTRL
2.1
0.21
0.021
hTERT
untreated
INVAC-1
(µg protein)
B
**
Relative Telomerase Activity (RTA)
400
350
300
250
150
100
50
0
hTERT
untreated
INVAC-1
(µg protein)
C
Absorbance (450/690nm)
1.5
1.0
0.5
0.0
Positive CTRL
hTERT
untreated
pUTD10Not
pUTD10Cog
pUTD23Tyn
(µg protein)
D
***
Relative Telomerase Activity (RTA)
800
600
400
200
0
hTERT
untreated
pUTD10Not
pUTD10Cog
pUTD23Tyn
(µg protein)

FIGURE 5

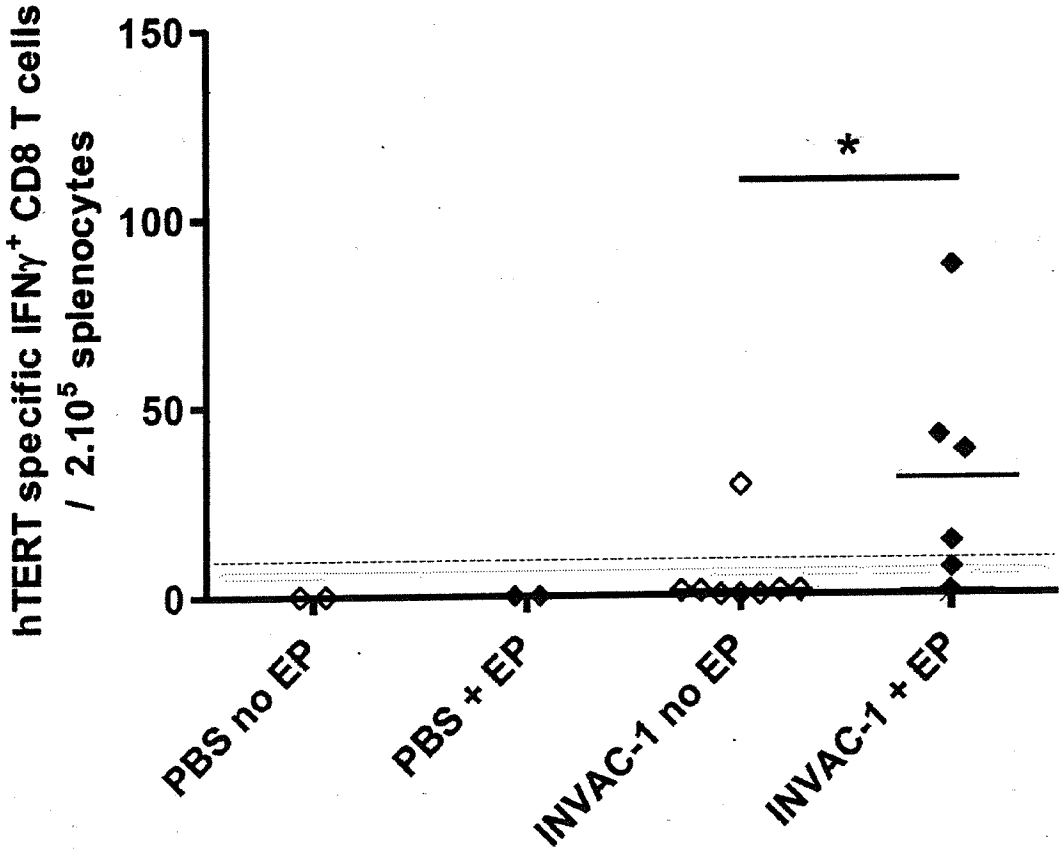

hTERT specific IFNγ+ CD8 T cells / 2.10^5 splenocytes
150
100
50
0
*
PBS no EP
PBS + EP
INVAC-1 no EP
INVAC-1 + EP

FIGURE 6

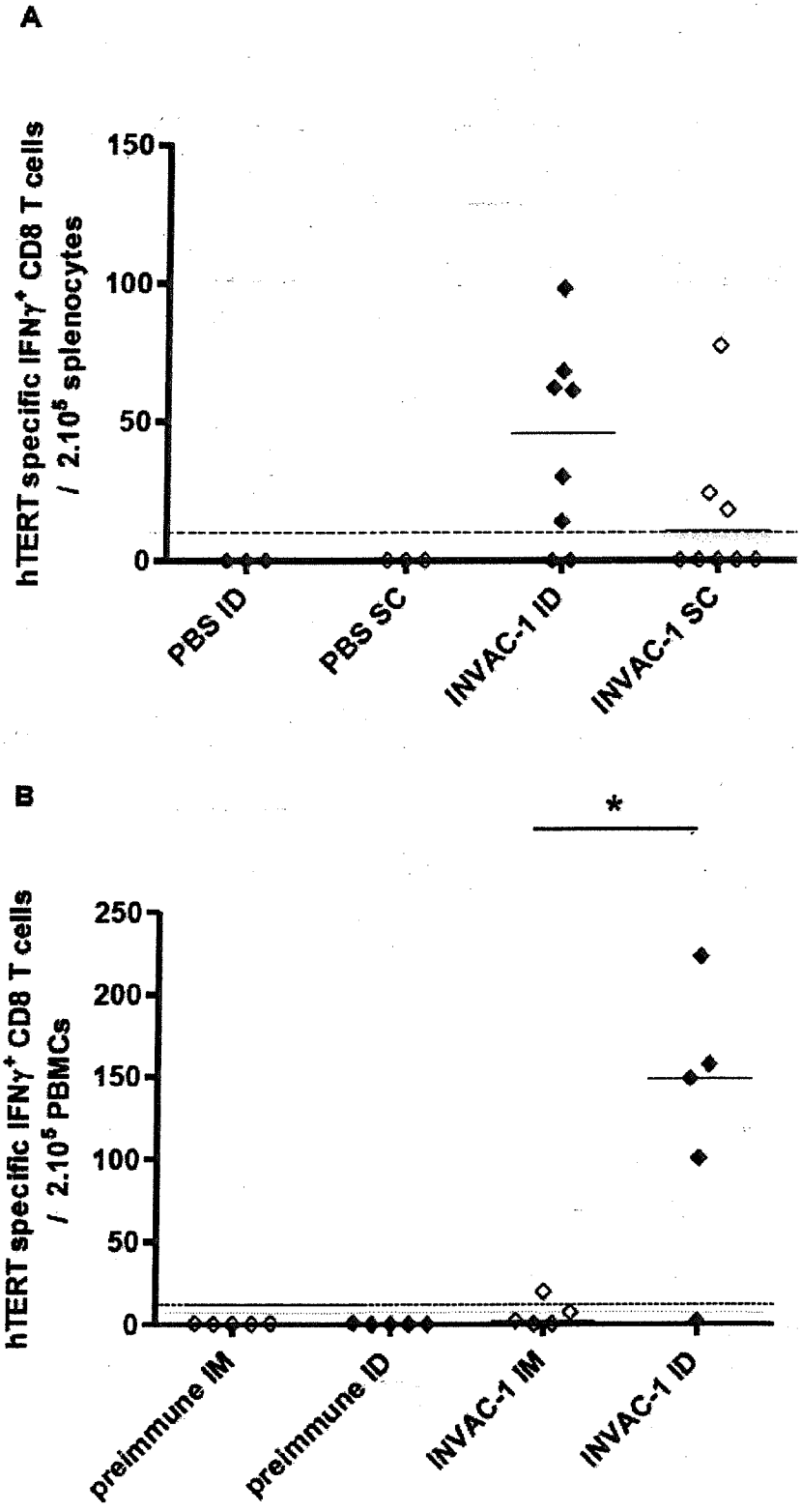

A
hTERT specific IFNγ+ CD8 T cells / 2.10^5 splenocytes
150
100
50
0
PBS ID
PBS SC
INVAC-1 ID
INVAC-1 SC
B
*
hTERT specific IFNγ+ CD8 T cells / 2.10^5 PBMCs
250
200
150
100
50
0
preimmune IM
preimmune ID
INVAC-1 IM
INVAC-1 ID

FIGURE 7

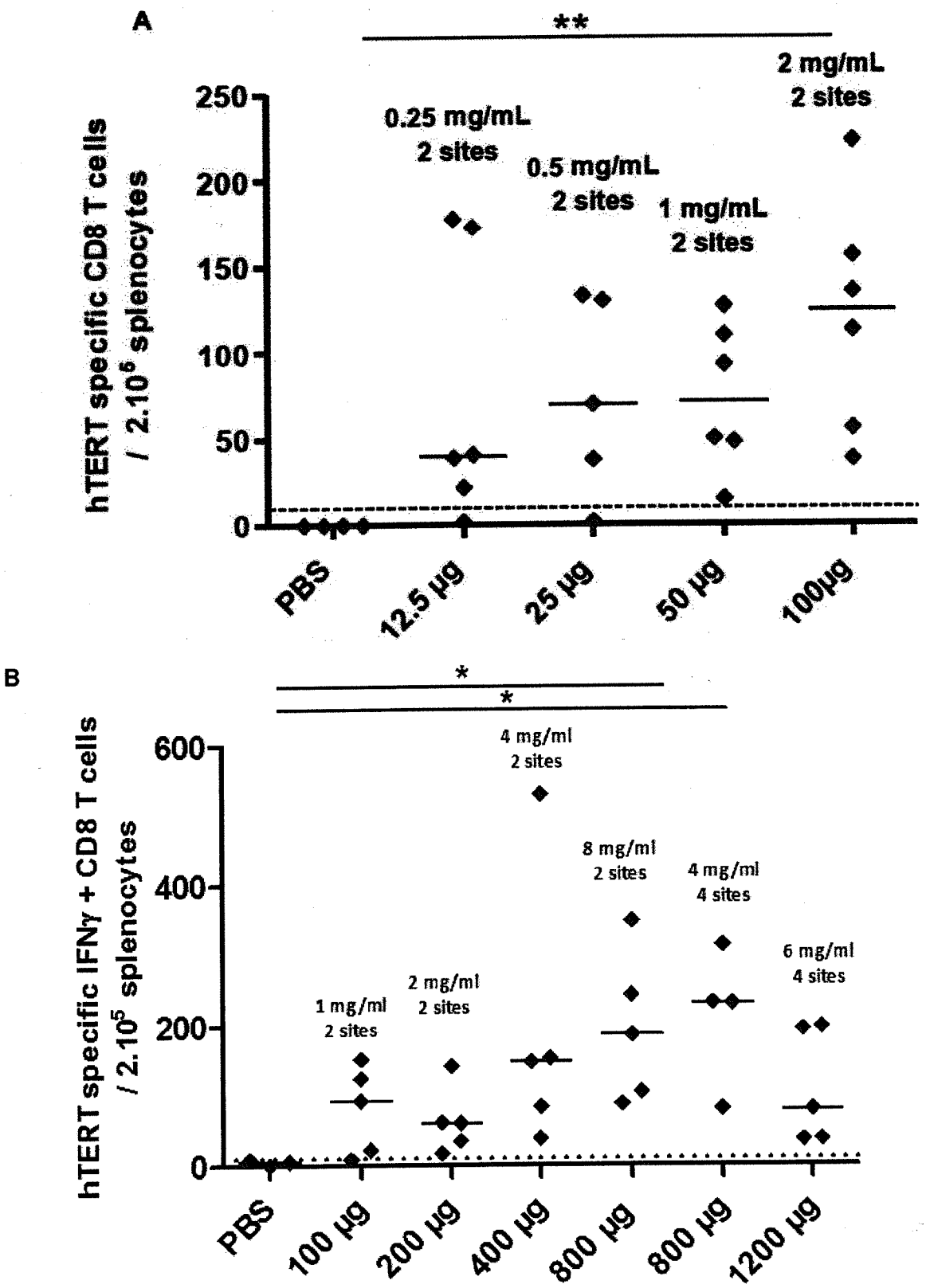

A
**
hTERT specific CD8 T cells / 2.10⁶ splenocytes
250
200
150
100
50
0
0.25 mg/mL 2 sites
0.5 mg/mL 2 sites
1 mg/mL 2 sites
2 mg/mL 2 sites
PBS
12.5 µg
25 µg
50 µg
100µg
B
*
*
hTERT specific IFNγ + CD8 T cells / 2.10⁵ splenocytes
600
400
200
0
1 mg/ml 2 sites
2 mg/ml 2 sites
4 mg/ml 2 sites
8 mg/ml 2 sites
4 mg/ml 4 sites
6 mg/ml 4 sites
PBS
100 µg
200 µg
400 µg
800 µg
800 µg
1200 µg

FIGURE 8

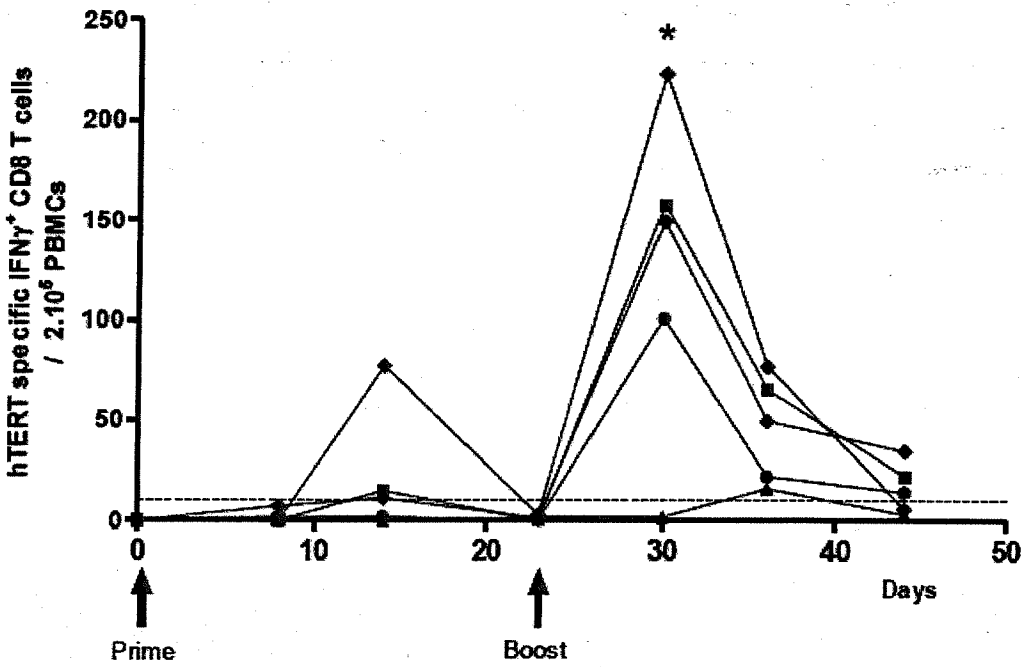

hTERT specific IFNγ+ CD8 T cells / 2.10^6 PBMCs
250
200
150
100
50
0
*
0
10
20
30
40
50
Days
Prime
Boost

FIGURE 9

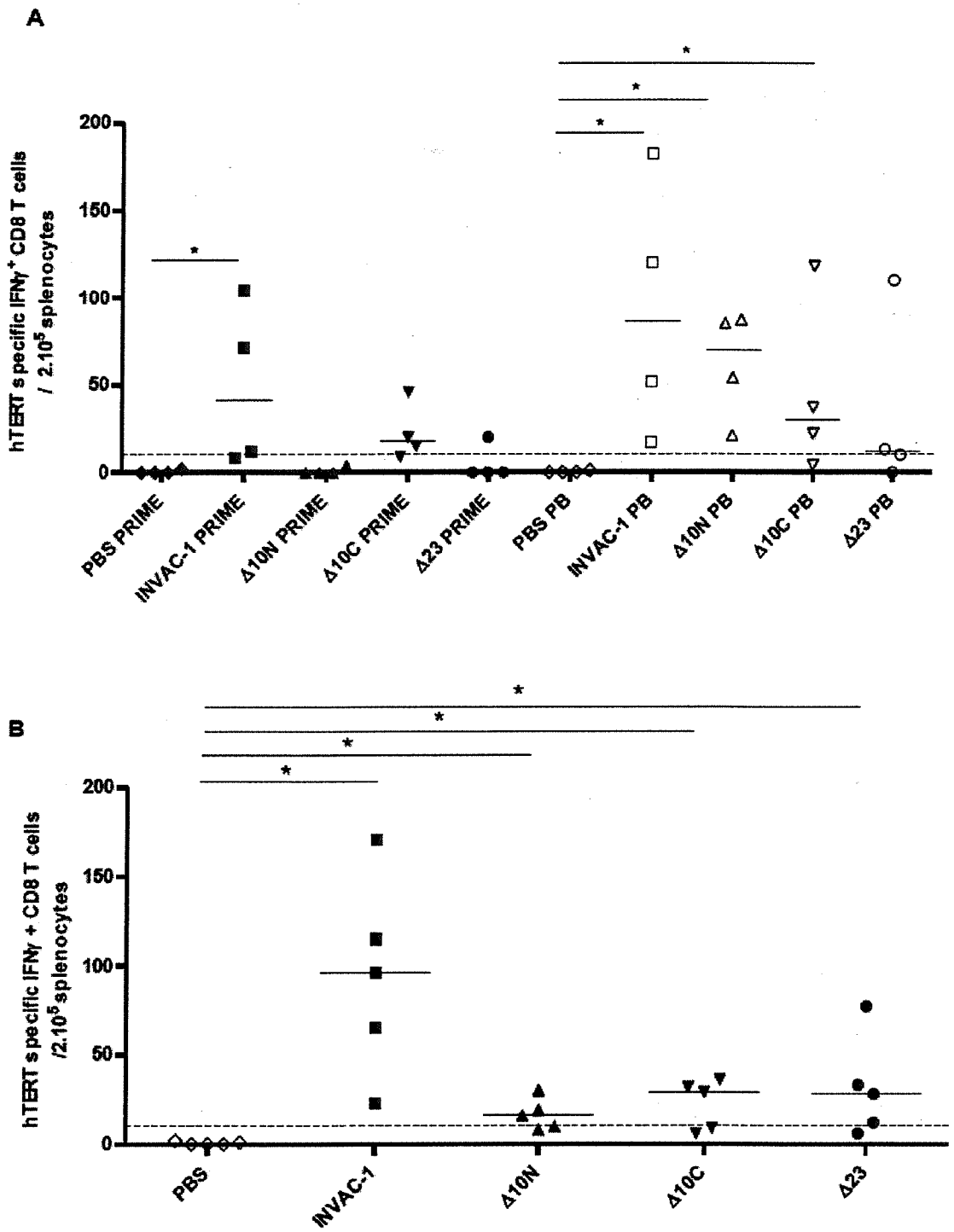

A
hTERT specific IFNγ+ CD8 T cells / 2.10^5 splenocytes
200
150
100
50
0
PBS PRIME
INVAC-1 PRIME
Δ10N PRIME
Δ10C PRIME
Δ23 PRIME
PBS PB
INVAC-1 PB
Δ10N PB
Δ10C PB
Δ23 PB
B
hTERT specific IFNγ + CD8 T cells /2.10^5 splenocytes
200
150
100
50
0
PBS
INVAC-1
Δ10N
Δ10C
Δ23

FIGURE 10

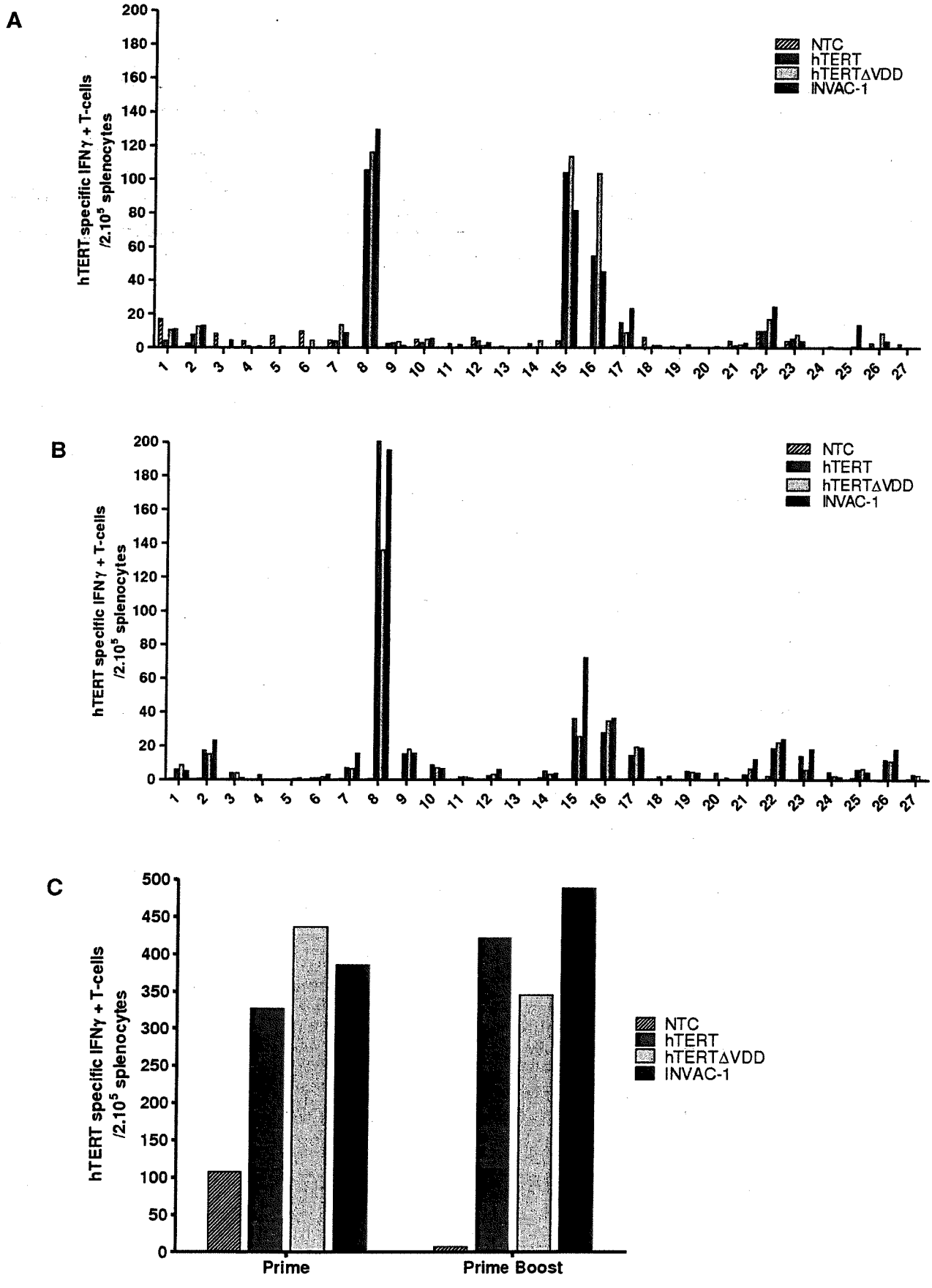

A
hTERT specific IFNγ + T-cells /2.10^5 splenocytes
NTC
hTERT
hTERTΔVDD
INVAC-1
B
hTERT specific IFNγ + T-cells /2.10^5 splenocytes
NTC
hTERT
hTERTΔVDD
INVAC-1
C
hTERT specific IFNγ + T-cells /2.10^5 splenocytes
NTC
hTERT
hTERTΔVDD
INVAC-1
Prime
Prime Boost

FIGURE 11

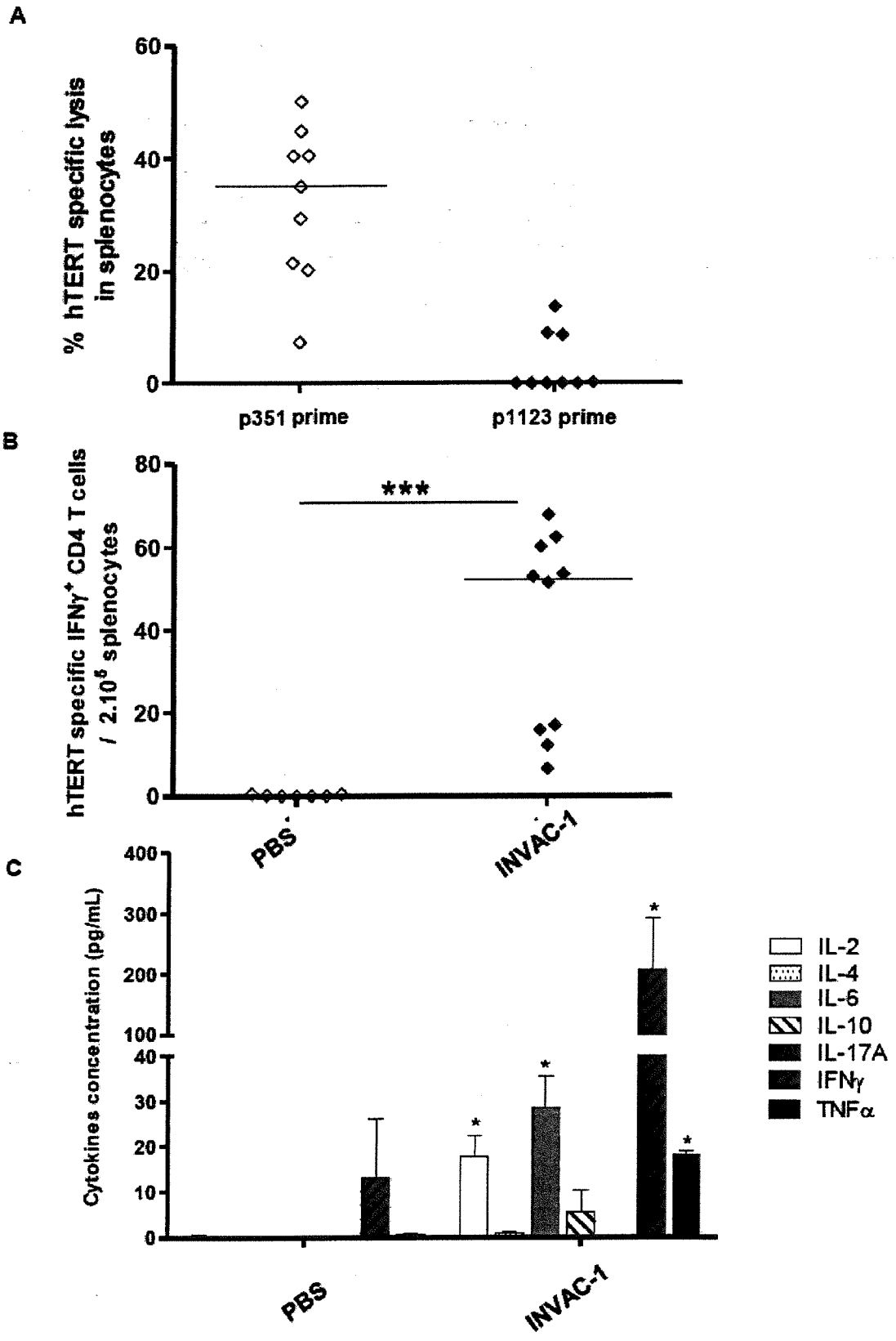
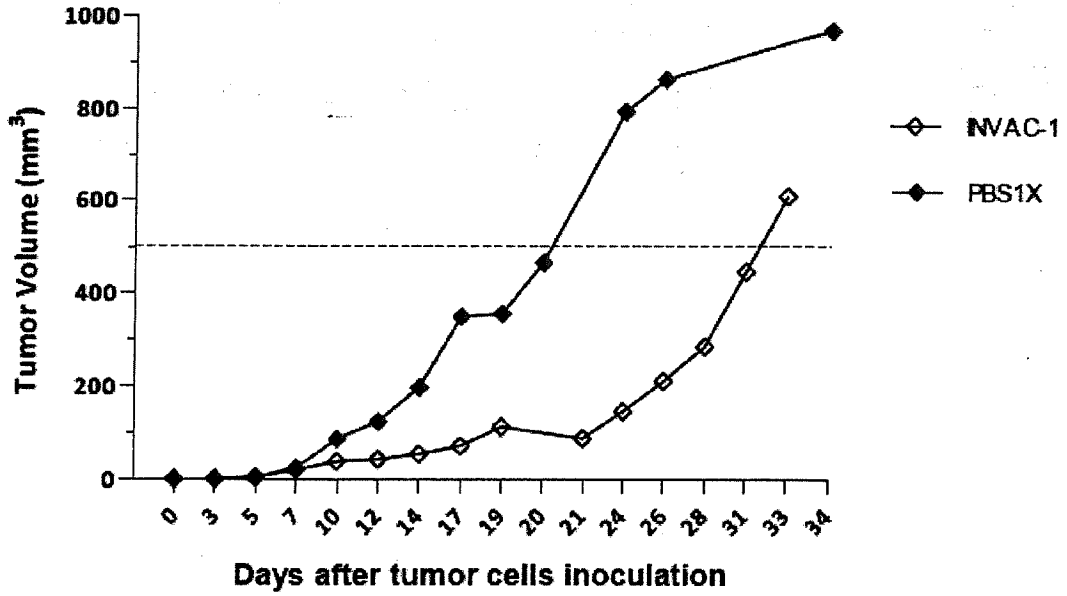

A
% hTERT specific lysis in splenocytes
60
40
20
0
p351 prime
p1123 prime
B
hTERT specific IFNγ+ CD4 T cells / 2.10^5 splenocytes
80
60
40
20
0
***
PBS
INVAC-1
C
Cytokines concentration (pg/mL)
400
300
200
100
40
30
20
10
0
*
PBS
INVAC-1
IL-2
IL-4
IL-6
IL-10
IL-17A
IFNγ
TNFα

FIGURE 12

A


1000
800
600
400
200
0
Tumor Volume (mm3)
0 3 5 7 10 12 14 17 19 20 21 24 26 28 31 33 34
Days after tumor cells inoculation
INVAC-1
PBS1X

B

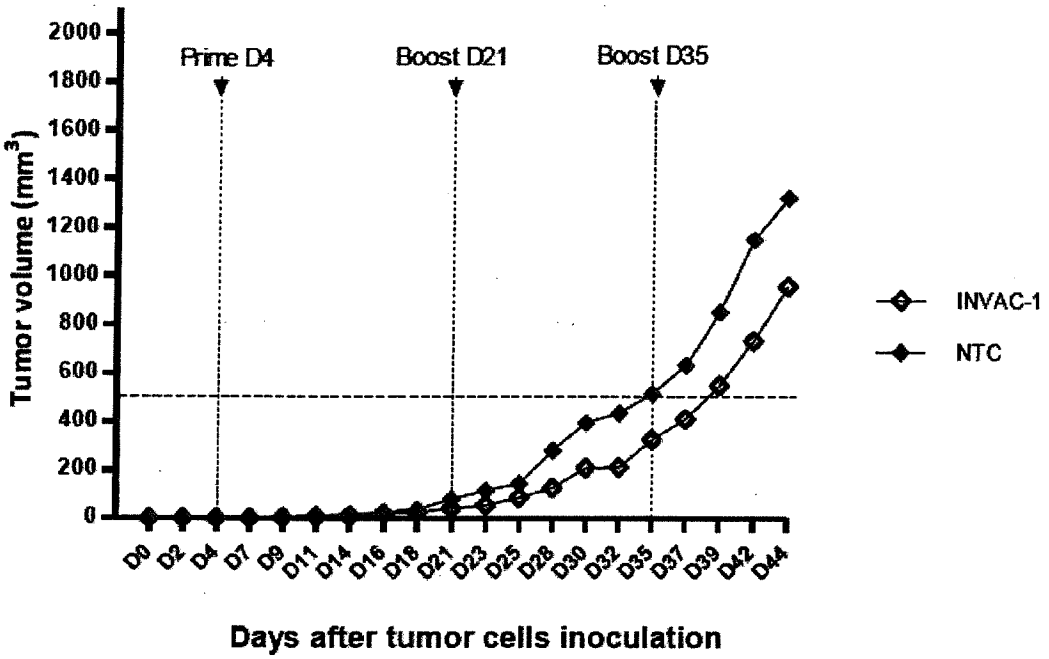

2000
1800
1600
1400
1200
1000
800
600
400
200
0
Tumor volume (mm3)
Prime D4
Boost D21
Boost D35
D0 D2 D4 D7 D9 D11 D14 D16 D18 D21 D23 D25 D28 D30 D32 D35 D37 D39 D42 D44
Days after tumor cells inoculation
INVAC-1
NTC

FIGURE 13

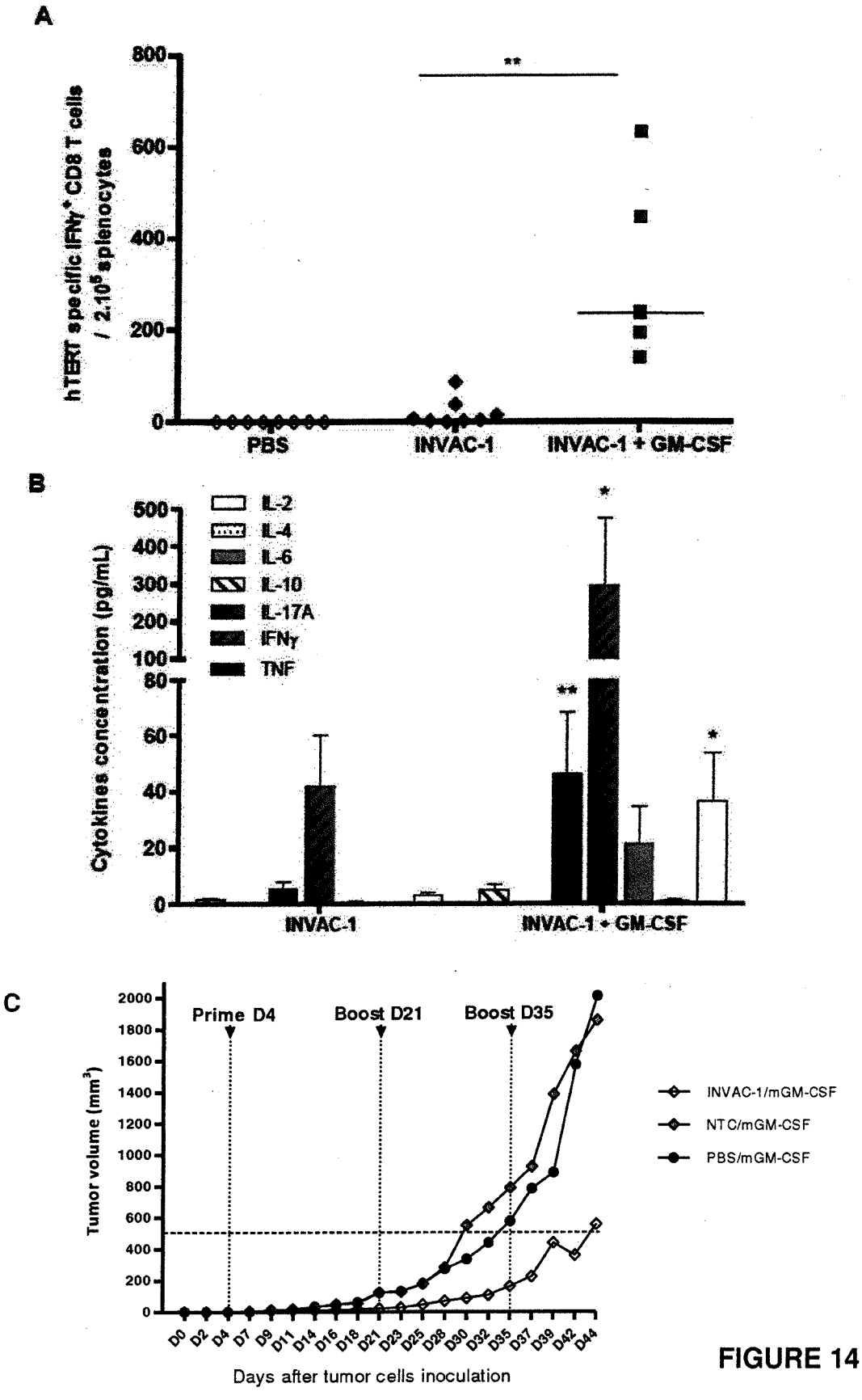

A
hTERT specific IFNγ+ CD8 T cells / 2.10^5 splenocytes
800
600
400
200
0
**
PBS
INVAC-1
INVAC-1 + GM-CSF
B
Cytokines concentration (pg/mL)
500
400
300
200
100
80
60
40
20
0
IL-2
IL-4
IL-6
IL-10
IL-17A
IFNγ
TNF
*
**
*
INVAC-1
INVAC-1 + GM-CSF
C
Tumor volume (mm3)
2000
1800
1600
1400
1200
1000
800
600
400
200
0
Prime D4
Boost D21
Boost D35
D0 D2 D4 D7 D9 D11 D14 D16 D18 D21 D23 D25 D28 D30 D32 D35 D37 D39 D42 D44
Days after tumor cells inoculation
INVAC-1/mGM-CSF
NTC/mGM-CSF
PBS/mGM-CSF

FIGURE 14

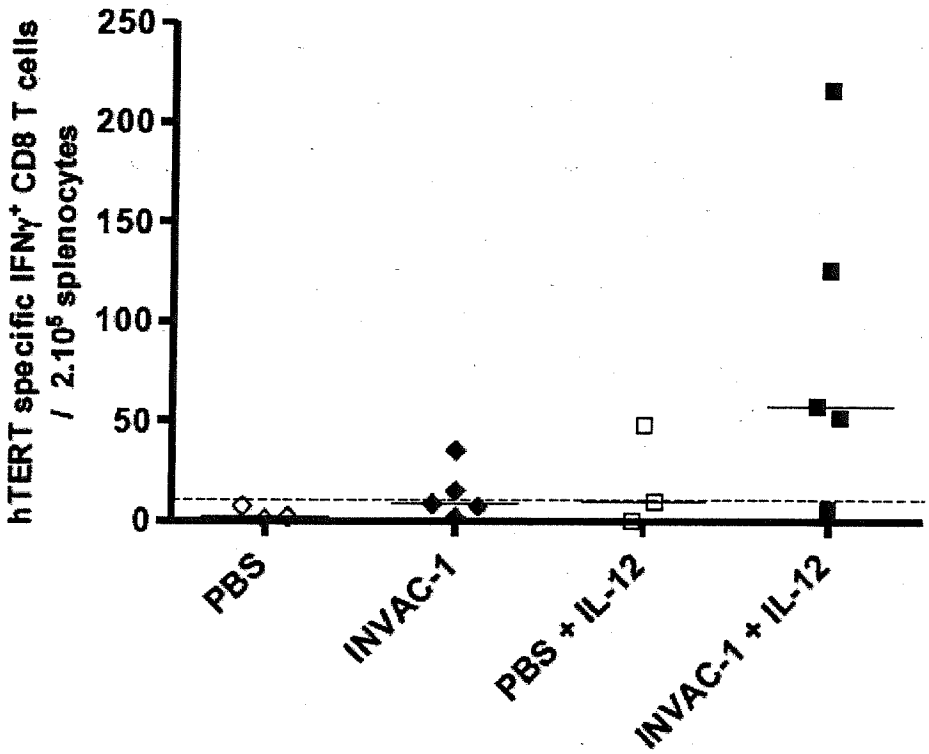

hTERT specific IFNγ+ CD8 T cells / 2.10^5 splenocytes
250
200
150
100
50
0
PBS
INVAC-1
PBS + IL-12
INVAC-1 + IL-12

FIGURE 15

NotI < eRNA11a RIGI agonist
1 gctagcaccgttggtttccgtagtgtagtggttatcacgttcgcctaacacgcgaaaggt 60

< dsRNA region
61 ccccggttcgaaaccgggcactacaaaccaacaacgttaaaaaacaggtcctccccatac 120

121 tctttcattgtacacaccgcaagctcgacaatcatcggattgaagcattgtcgcacacat 180

dsRNA region >
181 cttccacacaggatcagtacctgctttcgcttttaaccaaggcttttctccaagggatat 240

241 ttatagtctcaaaacacacaattactttacagttagggtgagtttccttttgtgctgttt 300

301 tttaaaataataatttagtatttgtatctcttatagaaatccaagcctatcatgtaaaat 360

361 gtagctagtattaaaaagaacagattatctgtcttttatcgcacattaagcctctatagt 420

421 tactaggaaatattatatgcaaattaaccggggcaggggagtagccgagcttctcccaca 480

eRNA11a RIGI agonist > <trpA
481 agtctgtgcgaggggccggcgcgggcctagagatggcggcgtcggatcggccagcccgc 540

Prokaryotic terminator > < Adenovirus 5 VA RNAI
541 ctaatgagcgggctttttttttcttagggtgcaaaaggagagcctgtaagcgggcactctt 600

601 ccgtggtctggtggataaattcgcaagggtatcatggcggacgaccggggttcgagcccc 660

661 gtatccggccgtccgccgtgatccatgcggttaccgcccgcgtgtcgaacccaggtgtgc 720

VA RNAI > < PAS-BH
721 gacgtcagacaacgggggagtgctccttttggcttccttccccctaccggtctgcctcgcg 780

Primosomal assembly site (PAS-BH) extended origin
781 cgtttcggtgatgacggtgaaaacctctgacacatgcagctcccggagacggtcacagct 840

841 tgtctgtaagcggatgccgggagcagacaagcccgtcagggcgcgtcagcgggtgttggc 900

901 gggtgtcggggcgcagccatgacccagtcacgtagcgatagcggagtgtatactggctta 960

961 actatgcggcatcagagcagattgtactgagagtgcaccatatgcggtgtgaaataccgc 1020

PAS-BH >< pUC replication origin
1021 acagatgcgtaaggagaaaataccgcatcaggcgctcttccgcttcctcgctcactgact 1080

1081 cgctgcgctcggtcgttcggctgcggcgagcggtatcagctcactcaaaggcggtaatac 1140

1141 ggttatccacagaatcaggggataacgcaggaaagaacatgtgagcaaaaggccagcaaa 1200

1201 aggccaggaaccgtaaaaaggccgcgttgctggcgtttttccataggctccgccccctg 1260

1261 acgagcatcacaaaaatcgacgctcaagtcagaggtggcgaaacccgacaggactataaa 1320

1321 gataccaggcgtttcccccctggaagctccctcgtgcgctctcctgttccgaccctgccgc 1380

1381 ttaccggatacctgtccgcctttctcccttcgggaagcgtggcgctttctcatagctcac 1440

1441 gctgtaggtatctcagttcggtgtaggtcgttcgctccaagctgggctgtgtgcacgaac 1500

1501 ccccgttcagcccgaccgctgcgccttatccggtaactatcgtcttgagtccaacccgg 1560

1561 taagacacgacttatcgccactggcagcagccactggtaacaggattagcagagcgaggt 1620

1621 atgtaggcggtgctacagagttcttgaagtggtggcctaactacggctacactagaagaa 1680

1681 cagtatttggtatctgcgctctgctgaagccagttaccttcggaaaaagagttggtagct 1740

1741 cttgatccggcaaacaaaccaccgctggtagcggtggtttttttgtttgcaagcagcaga 1800

1801 ttacgcgcagaaaaaaaggatctcaagaagatcctttgatcttttctacggggtctgacg 1860

FIGURE 16

```
1861 ctcagtggaacgaaaactcacgttaagggattttggtcatgagattatcaaaaaggatct 1920

1921 tcacctagatccttttaaattaaaaatgaagttttaaatcaatctaaagtatatatgagt 1980

1981 aaacttggtctgacagttaccaatgcttaatcagtgaggcacctatctcagcgatctgtc 2040

          pUC replication origin >       DraIII    <  RNA-OUT
2041 tatttcgttcatccatagttgcctgactcctgcaaaccacgttgtggtagaattggtaaa 2100

2101 gagagtcgtgtaaaatatcgagttcgcacatcttgttgtctgattattgatttttggcga 2160

2161 aaccatttgatcatatgacaagatgtgtatctaccttaacttaatgattttgataaaaat 2220

     RNA-OUT  >< SV40 enhancer block
2221 cattaggtaccccctgatcaactgtggaatgtgtgtcagttagggtgtggaaagtccccagg 2280
           KpnI     BclI

2281 ctccccagcaggcagaagtatgcaaagcatgcatctcaattagtcagcaaccaggtgtgg 2340

2341 aaagtccccaggctccccagcaggcagaagtatgcaaagcatgcatctcaattagtcagc 2400

                                    SV40 enhancer block  ><
2401 aaccatagtcccgcccctaactccgcccatcccgcccctaactccgcccagttacggggt 2460

     Human CMV-IE enhancer promoter block
2461 cattagttcatagcccatatatggagttccgcgttacataacttacggtaaatggcccgc 2520

2521 ctggctgaccgcccaacgacccccgcccattgacgtcaataatgacgtatgttcccatag 2580

2581 taacgccaatagggactttccattgacgtcaatgggtggagtatttacggtaaactgccc 2640

2641 acttggcagtacatcaagtgtatcatatgccaagtacgccccctattgacgtcaatgacg 2700

2701 gtaaatggcccgcctggcattatgcccagtacatgaccttatgggactttcctacttggc 2760

                                   NcoI
2761 agtacatctacgtattagtcatcgctattaccatggtgatgcggttttggcagtacatca 2820

2821 atgggcgtggatagcggtttgactcacggggatttccaagtctccaccccattgacgtca 2880


                     ><      CMV promoter
2881 atgggagtttgttttggcaccaaaatcaacgggactttccaaaatgtcgtaacaactccg 2940

2941 ccccattgacgcaaatgggcggtaggcgtgtacggtgggaggtctatataagcagagctc 3000

                     >< untranslated leader (exon 1)
3001 gtttagtgaaccgtcagatcgcctggagacgccatccacgctgttttgacctccatagaa 3060

                                  < HTLV-1 R region of LTR
3061 gacaccgggaccgatccagcctccgcggctcgcatctctccttcacgcgcccgccgccct 3120

3121 acctgaggccgccatccacgccggttgagtcgcgttctgccgcctcccgcctgtggtgcc 3180

       untranslated leader >
3181 tcctgaactgcgtccgccgtctaggtaagtttaaagctcaggtcgagaccgggcctttgt 3240

3241 ccggcgctcccttggagcctacctagactcagccggctctccacgctttgcctgaccctg 3300

      HTLV-1 R   >         < 3' Rabbit beta-globin-based intron
3301 cttgctcaactctagttctctcgttaacttaatgagacagatagaaactggtcttgtaga 3360

3361 aacagagtagtcgcctgcttttctgccaggtgctgacttctctcccctgggctttttttct 3420

           >< Exon 2 (SR-protein binding sites)          SalI>
3421 ttttctcaggttgaaaagaagaagacgaagaagacgaagaagacaaaccgtcgtcgacaa 3480

  HindIII       BglII
3481 gcttaccatgcagatcttcgtgaagaccctgaccggcaagaccatcactctcgaggtgga 3540
          M  Q  I  F  V  K  T  L  T  G  K  T  I  T  L  E  V  E
```

FIGURE 16 cont.

< Human ubiquitin

```
3541 gcccagtgacaccatcgaaaatgtgaaggccaagatccaagataaagaaggcatcccacc 3600
      P  S  D  T  I  E  N  V  K  A  K  I  Q  D  K  E  G  I  P  P

3601 cgaccagcagaggctcatctttgctggcaagcagctggaagatggccgcactctgtctga 3660
      D  Q  Q  R  L  I  F  A  G  K  Q  L  E  D  G  R  T  L  S  D

                          SalI                                NotI
3661 ctacaacatccagaaagagtcgaccctgcacctggtcctgcgtctgagaggcggccgcgc 3720
      Y  N  I  Q  K  E  S  T  L  H  L  V  L  R  L  R  G  G  R  A
                                        Human ubiquitin   >< hTERT

3721 tctggtggcccagtgcctggtgtgcgtgccctgggacgcacggccacccccctgccgcacc 3780
      L  V  A  Q  C  L  V  C  V  P  W  D  A  R  P  P  P  A  A  P
      Human telomerase reverse transcriptase coding sequence (hTERT)

3781 ctcattccgccaagtgtcctgcctgaaggagctggtggcccgagtgctgcagaggctgtg 3840
      S  F  R  Q  V  S  C  L  K  E  L  V  A  R  V  L  Q  R  L  C

3841 cgagcgcggcgcgaagaacgtgctggccttcggcttcgcgctgctggacggggctcgcgg 3900
      E  R  G  A  K  N  V  L  A  F  G  F  A  L  L  D  G  A  R  G

3901 aggcccacccgaggccttcaccaccagcgtgcgcagctacctgcccaacacggtgaccga 3960
      G  P  P  E  A  F  T  T  S  V  R  S  Y  L  P  N  T  V  T  D

3961 cgcactgcgggggagcgggggcgtgggggctgctgttgcgccgcgtgggcgacgacgtgct 4020
      A  L  R  G  S  G  A  W  G  L  L  L  R  R  V  G  D  D  V  L

4021 ggttcacctgctggcacgctgcgcgctctttgtgctggtggctcccagctgcgcctacca 4080
      V  H  L  L  A  R  C  A  L  F  V  L  V  A  P  S  C  A  Y  Q

4081 ggtgtgcgggccgccgctgtaccagctcggcgctgccactcaggcacggcctccacctca 4140
      V  C  G  P  P  L  Y  Q  L  G  A  A  T  Q  A  R  P  P  P  H

4141 cgctagtggaccccgaaggcgtctgggatgcgaacgggcctggaaccatagcgtcaggga 4200
      A  S  G  P  R  R  R  L  G  C  E  R  A  W  N  H  S  V  R  E

4201 ggccggggtccccctgggcctgccagccccgggtgcgaggaggcgcgggggcagtgccag 4260
      A  G  V  P  L  G  L  P  A  P  G  A  R  R  R  G  G  S  A  S

4261 ccgaagtctgccgttgcccaagaggcccaggcgtggcgctgcccctgagccggagcggac 4320
      R  S  L  P  L  P  K  R  P  R  R  G  A  A  P  E  P  E  R  T

4321 gcccgttgggcaggggtcctgggcccacccgggcaggacgcgtggaccgagtgaccgtgg 4380
      P  V  G  Q  G  S  W  A  H  P  G  R  T  R  G  P  S  D  R  G

4381 tttctgtgtggtgtcacctgccagacccgccgaagaagccacctctttggagggtgcgct 4440
      F  C  V  V  S  P  A  R  P  A  E  E  A  T  S  L  E  G  A  L

4441 ctctggcacgcgccactcccacccatccgtgggccgccagcaccacgcgggcccccccatc 4500
      S  G  T  R  H  S  H  P  S  V  G  R  Q  H  H  A  G  P  P  S

4501 cacatcgcggccaccacgtccctgggacacgccttgtcccccggtgtacgccgagaccaa 4560
      T  S  R  P  P  R  P  W  D  T  P  C  P  P  V  Y  A  E  T  K

4561 gcacttcctctactcctcaggcgacaaggagcagctgcggccatccttcctgctgagctc 4620
      H  F  L  Y  S  S  G  D  K  E  Q  L  R  P  S  F  L  L  S  S

4621 tctgaggcccagcctgactggcgctcggaggctcgtggagaccatctttctgggttccag 4680
      L  R  P  S  L  T  G  A  R  R  L  V  E  T  I  F  L  G  S  R

4681 gccctggatgccagggactccccgcaggttgccccgcctgccccagcgctactggcaaat 4740
      P  W  M  P  G  T  P  R  R  L  P  R  L  P  Q  R  Y  W  Q  M

4741 gcggcccctgtttctggagctgcttgggaaccacgcgcagtgcccctacggggtgctcct 4800
      R  P  L  F  L  E  L  L  G  N  H  A  Q  C  P  Y  G  V  L  L
```

FIGURE 16 cont.

```
4801 caagacgcactgcccgctgcgagctgcggtcaccccagcagccggtgtctgtgcccggga 4860
      K  T  H  C  P  L  R  A  A  V  T  P  A  A  G  V  C  A  R  E

4861 gaagccccagggctctgtggcggcccccgaggaggaggacacagacccccgtcgcctggt 4920
      K  P  Q  G  S  V  A  A  P  E  E  E  D  T  D  P  R  R  L  V

4921 gcagctgctccgccagcacagcagcccctggcaggtgtacggcttcgtgcgggcctgcct 4980
      Q  L  L  R  Q  H  S  S  P  W  Q  V  Y  G  F  V  R  A  C  L

4981 gcgccggctggtgcccccaggcctctggggctccaggcacaacgaacgccgcttcctcag 5040
      R  R  L  V  P  P  G  L  W  G  S  R  H  N  E  R  R  F  L  R

5041 gaacaccaagaagttcatctccctggggaagcatgccaagctctcgctgcaggagctgac 5100
      N  T  K  K  F  I  S  L  G  K  H  A  K  L  S  L  Q  E  L  T

5101 gtggaagatgagcgtgcggggctgcgcttggctgcgcaggagcccaggggttggctgtgt 5160
      W  K  M  S  V  R  G  C  A  W  L  R  R  S  P  G  V  G  C  V

5161 tccggccgcagagcaccgtctgcgtgaggagatcctggccaagttcctgcactggctgat 5220
      P  A  A  E  H  R  L  R  E  E  I  L  A  K  F  L  H  W  L  M

5221 gagtgtgtacgtcgtcgagctgctcaggtcattcttttacgtgacggagaccacgtttca 5280
      S  V  Y  V  V  E  L  L  R  S  F  F  Y  V  T  E  T  T  F  Q

5281 aaagaacaggctgtttttctaccggaagagtgtctggagcaagttgcaaagcattggaat 5340
      K  N  R  L  F  F  Y  R  K  S  V  W  S  K  L  Q  S  I  G  I

5341 cagacagcacttgaagagggtgcagctgcgggagctgtcggaagcagaggtcaggcagca 5400
      R  Q  H  L  K  R  V  Q  L  R  E  L  S  E  A  E  V  R  Q  H

5401 tcgggaagccaggcccgccctgctgacgtccagactccgcttcatccccaagcctgacgg 5460
      R  E  A  R  P  A  L  L  T  S  R  L  R  F  I  P  K  P  D  G

5461 gctgcggccgattgtgaacatggactacgtcgtgggagccagaacgttccgcagagaaaa 5520
      L  R  P  I  V  N  M  D  Y  V  V  G  A  R  T  F  R  R  E  K

5521 gagggccgagcgtctcacctcacgggtgaaggcactgttcagcgtgctcaactacgagcg 5580
      R  A  E  R  L  T  S  R  V  K  A  L  F  S  V  L  N  Y  E  R

5581 ggctcggcgccctggcctcctgggcgcctctgtgctgggcctggacgatatccacagggc 5640
      A  R  R  P  G  L  L  G  A  S  V  L  G  L  D  D  I  H  R  A

5641 ctggcgcaccttcgtgctgcgtgtgcgggcccaggacccgccgcctgagctgtactttgt 5700
      W  R  T  F  V  L  R  V  R  A  Q  D  P  P  P  E  L  Y  F  V

5701 caaggtggatgtgacgggcgcgtacgacaccatcccccaggacaggctcacggaggtcat 5760
      K  V  D  V  T  G  A  Y  D  T  I  P  Q  D  R  L  T  E  V  I

5761 cgccagcatcatcaaaccccagaacacgtactgcgtgcgtcggtatgccgtggtccagaa 5820
      A  S  I  I  K  P  Q  N  T  Y  C  V  R  R  Y  A  V  V  Q  K

            NcoI
5821 ggccgcccatgggcacgtccgcaaggccttcaagagccacgtctctaccttgacagacct 5880
      A  A  H  G  H  V  R  K  A  F  K  S  H  V  S  T  L  T  D  L

5881 ccagccgtacatgcgacagttcgtggctcacctgcaggagaccagcccgctgagggatgc 5940
      Q  P  Y  M  R  Q  F  V  A  H  L  Q  E  T  S  P  L  R  D  A

5941 cgtcgtcatcgagcagagctcctccctgaatgaggccagcagtggcctcttcgacgtctt 6000
      V  V  I  E  Q  S  S  S  L  N  E  A  S  S  G  L  F  D  V  F

                        DraIII
6001 cctacgcttcatgtgccaccacgccgtgcgcatcaggggcaagtcctacgtccagtgcca 6060
      L  R  F  M  C  H  H  A  V  R  I  R  G  K  S  Y  V  Q  C  Q

6061 gggcatcccgcagggctccatcctctccacgctgctctgcagcctgtgctacggcgacat 6120
      G  I  P  Q  G  S  I  L  S  T  L  L  C  S  L  C  Y  G  D  M
```

FIGURE 16 cont.

```
6121 ggagaacaagctgtttgcggggattcggcgggacgggctgctcctgcgtttgttcttgtt 6180
      E  N  K  L  F  A  G  I  R  R  D  G  L  L  L  R  L  F  L  L
                                                      *

6181 ggtgacacctcacctcacccacgcgaaaaccttcctcaggaccctggtccgaggtgtccc 6240
      V  T  P  H  L  T  H  A  K  T  F  L  R  T  L  V  R  G  V  P

6241 tgagtatggctgcgtggtgaacttgcggaagacagtggtgaacttccctgtagaagacga 6300
      E  Y  G  C  V  V  N  L  R  K  T  V  V  N  F  P  V  E  D  E

6301 ggccctgggtggcacggcttttgttcagatgccggcccacggcctattcccctggtgcgg 6360
      A  L  G  G  T  A  F  V  Q  M  P  A  H  G  L  F  P  W  C  G

6361 cctgctgctggatacccggaccctggaggtgcagagcgactactccagctatgcccggac 6420
      L  L  L  D  T  R  T  L  E  V  Q  S  D  Y  S  S  Y  A  R  T

6421 ctccatcagagccagtctcaccttcaaccgcggcttcaaggctgggaggaacatgcgtcg 6480
      S  I  R  A  S  L  T  F  N  R  G  F  K  A  G  R  N  M  R  R

6481 caaactctttggggtcttgcggctgaagtgtcacagcctgtttctggatttgcaggtgaa 6540
      K  L  F  G  V  L  R  L  K  C  H  S  L  F  L  D  L  Q  V  N

6541 cagcctccagacggtgtgcaccaacatctacaagatcctcctgctgcaggcgtacaggtt 6600
      S  L  Q  T  V  C  T  N  I  Y  K  I  L  L  L  Q  A  Y  R  F

6601 tcacgcatgtgtgctgcagctcccatttcatcagcaagtttggaagaaccccacattttt 6660
      H  A  C  V  L  Q  L  P  F  H  Q  Q  V  W  K  N  P  T  F  F

6661 cctgcgcgtcatctctgacacggcctccctctgctactccatcctgaaagccaagaacgc 6720
      L  R  V  I  S  D  T  A  S  L  C  Y  S  I  L  K  A  K  N  A

6721 agggatgtcgctgggggccaagggcgccgccggccctctgccctccgaggccgtgcagtg 6780
      G  M  S  L  G  A  K  G  A  A  G  P  L  P  S  E  A  V  Q  W


6781 gctgtgccaccaagcattcctgctcaagctgactcgacaccgtgtcacctacgtgccact 6840
      L  C  H  Q  A  F  L  L  K  L  T  R  H  R  V  T  Y  V  P  L

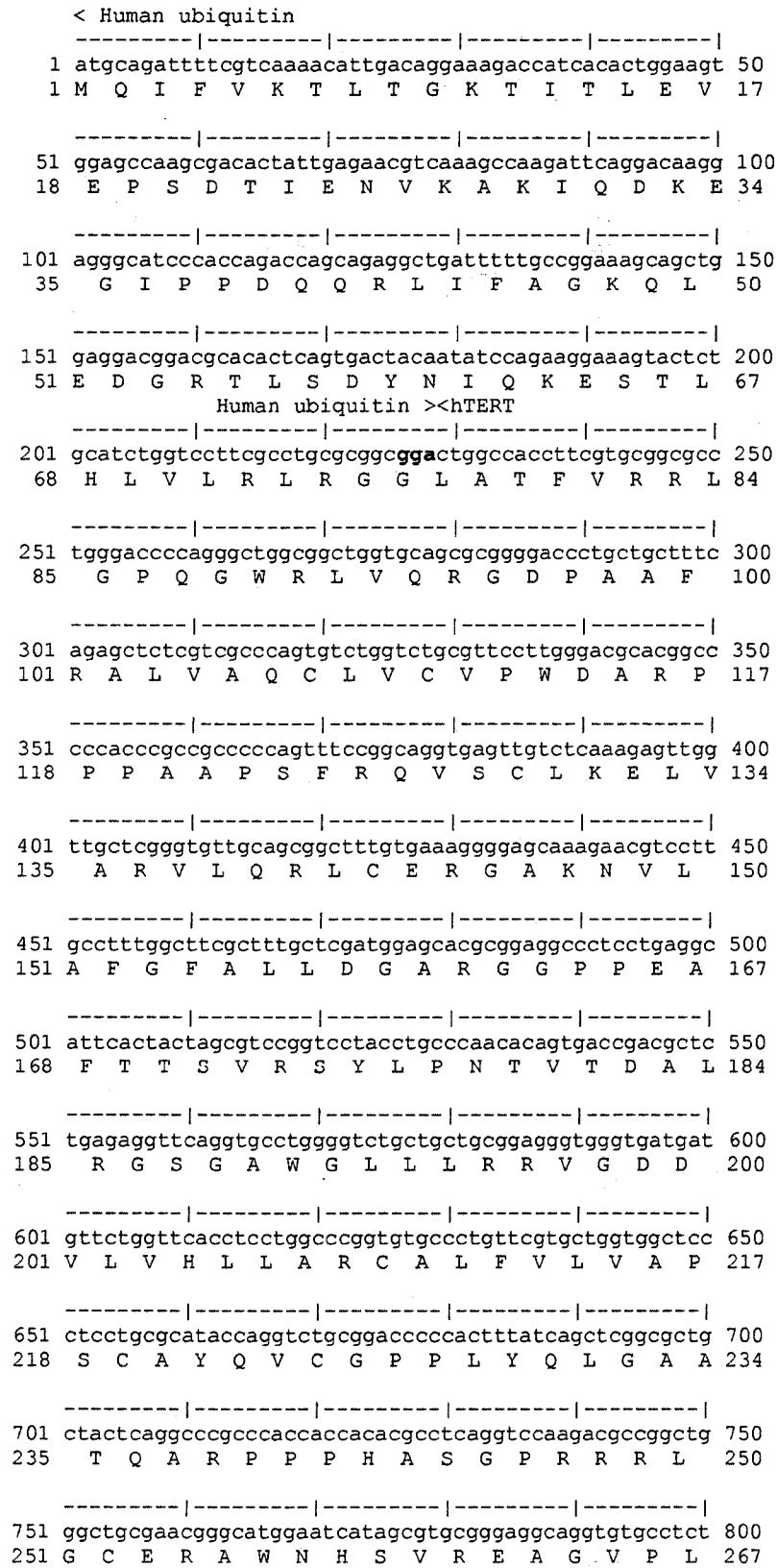
6841 cctggggtcactcaggacagcccagacgcagctgagtcggaagctcccggggacgacgct 6900
      L  G  S  L  R  T  A  Q  T  Q  L  S  R  K  L  P  G  T  T  L

                                                  human TERT orf end
6901 gactgccctggaggccgcagccaacccggcactgccctcagacttcaagaccatcctgga 6960
      T  A  L  E  A  A  A  N  P  A  L  P  S  D  F  K  T  I  L  D

     >       >XbaI BglII < Eukaryotic terminator
6961 ctaataatctagaagatctttttccctctgccaaaaattatggggacatcatgaagcccc 7020
      □  □
                polyA signal sequence
7021 ttgagcatctgacttctggctaataaaggaaatttattttcattgcaatagtgtgttgga 7080

                 Eukaryotic terminator > NotI
7081 atttttttgtgtctctcactcggaaggacataagggcggccc 7120
```

FIGURE 16 cont.




```
    < Human ubiquitin
    ---------|---------|---------|---------|---------|
  1 atgcagattttcgtcaaaacattgacaggaaagaccatcacactggaagt 50
  1 M  Q  I  F  V  K  T  L  T  G  K  T  I  T  L  E  V 17

    ---------|---------|---------|---------|---------|
 51 ggagccaagcgacactattgagaacgtcaaagccaagattcaggacaagg 100
 18  E  P  S  D  T  I  E  N  V  K  A  K  I  Q  D  K  E 34

    ---------|---------|---------|---------|---------|
101 agggcatcccaccagaccagcagaggctgatttttgccggaaagcagctg 150
 35   G  I  P  P  D  Q  Q  R  L  I  F  A  G  K  Q  L  50

    ---------|---------|---------|---------|---------|
151 gaggacggacgcacactcagtgactacaatatccagaaggaaagtactct 200
 51 E  D  G  R  T  L  S  D  Y  N  I  Q  K  E  S  T  L 67
              Human ubiquitin ><hTERT
    ---------|---------|---------|---------|---------|
201 gcatctggtccttcgcctgcgcggcggactggccaccttcgtgcggcgcc 250
 68  H  L  V  L  R  L  R  G  G  L  A  T  F  V  R  R  L 84

    ---------|---------|---------|---------|---------|
251 tgggaccccagggctggcggctggtgcagcgcggggaccctgctgctttc 300
 85   G  P  Q  G  W  R  L  V  Q  R  G  D  P  A  A  F  100

    ---------|---------|---------|---------|---------|
301 agagctctcgtcgcccagtgtctggtctgcgttccttgggacgcacggcc 350
101 R  A  L  V  A  Q  C  L  V  C  V  P  W  D  A  R  P 117

    ---------|---------|---------|---------|---------|
351 cccacccgccgcccccagtttccggcaggtgagttgtctcaaagagttgg 400
118  P  P  A  A  P  S  F  R  Q  V  S  C  L  K  E  L  V 134

    ---------|---------|---------|---------|---------|
401 ttgctcgggtgttgcagcggctttgtgaaaggggagcaaagaacgtcctt 450
135   A  R  V  L  Q  R  L  C  E  R  G  A  K  N  V  L  150

    ---------|---------|---------|---------|---------|
451 gcctttggcttcgctttgctcgatggagcacgcggaggccctcctgaggc 500
151 A  F  G  F  A  L  L  D  G  A  R  G  G  P  P  E  A 167

    ---------|---------|---------|---------|---------|
501 attcactactagcgtccggtcctacctgcccaacacagtgaccgacgctc 550
168  F  T  T  S  V  R  S  Y  L  P  N  T  V  T  D  A  L 184

    ---------|---------|---------|---------|---------|
551 tgagaggttcaggtgcctggggtctgctgctgcggagggtgggtgatgat 600
185   R  G  S  G  A  W  G  L  L  L  R  R  V  G  D  D   200

    ---------|---------|---------|---------|---------|
601 gttctggttcacctcctggcccggtgtgccctgttcgtgctggtggctcc 650
201 V  L  V  H  L  L  A  R  C  A  L  F  V  L  V  A  P 217

    ---------|---------|---------|---------|---------|
651 ctcctgcgcataccaggtctgcggacccccactttatcagctcggcgctg 700
218  S  C  A  Y  Q  V  C  G  P  P  L  Y  Q  L  G  A  A 234

    ---------|---------|---------|---------|---------|
701 ctactcaggcccgcccaccaccacacgcctcaggtccaagacgccggctg 750
235   T  Q  A  R  P  P  P  H  A  S  G  P  R  R  R  L   250

    ---------|---------|---------|---------|---------|
751 ggctgcgaacgggcatggaatcatagcgtgcgggaggcaggtgtgcctct 800
251 G  C  E  R  A  W  N  H  S  V  R  E  A  G  V  P  L 267
```

FIGURE 17

```
    ---------|---------|---------|---------|---------|
 801 cggcctgccagcccccggagcaaggagacgcggtggatccgccagtcgct 850
 268  G  L  P  A  P  G  A  R  R  R  G  G  S  A  S  R  S 284

    ---------|---------|---------|---------|---------|
 851 cactccccttgcctaagaggccaagaagaggagccgcccctgaacccgag 900
 285   L  P  L  P  K  R  P  R  R  G  A  A  P  E  P  E   300

    ---------|---------|---------|---------|---------|
 901 agaacacctgtcggccagggctcctgggctcaccccggaaggaccagggg 950
 301 R  T  P  V  G  Q  G  S  W  A  H  P  G  R  T  R  G  317

    ---------|---------|---------|---------|---------|
 951 cccaagcgataggggcttctgtgttgtgtcaccagccaggcctgccgaag 1000
 318  P  S  D  R  G  F  C  V  V  S  P  A  R  P  A  E  E 334

    ---------|---------|---------|---------|---------|
1001 aggctacctccttggaaggagccctcagtggcaccaggcattctcatcca 1050
 335   A  T  S  L  E  G  A  L  S  G  T  R  H  S  H  P   350

    ---------|---------|---------|---------|---------|
1051 tctgtgggtaggcagcatcatgccggcccccctctacaagcagacctcc 1100
 351 S  V  G  R  Q  H  H  A  G  P  P  S  T  S  R  P  P  367

    ---------|---------|---------|---------|---------|
1101 cagaccttgggacacaccctgcccaccagtgtatgccgagaccaagcact 1150
 368  R  P  W  D  T  P  C  P  P  V  Y  A  E  T  K  H  F 384

    ---------|---------|---------|---------|---------|
1151 ttttgtattccagtggcgataaagagcagctccggccctcttttctgctc 1200
 385   L  Y  S  S  G  D  K  E  Q  L  R  P  S  F  L  L   400

    ---------|---------|---------|---------|---------|
1201 tcaagcctccgcccctctctgaccggagctcgcaggctggtggagaccat 1250
 401 S  S  L  R  P  S  L  T  G  A  R  R  L  V  E  T  I  417

    ---------|---------|---------|---------|---------|
1251 ctttctgggctcaagaccatggatgccaggcacccccgcagactgccca 1300
 418  F  L  G  S  R  P  W  M  P  G  T  P  R  R  L  P  R 434

    ---------|---------|---------|---------|---------|
1301 ggctcccccagcggtactggcagatgcgccctctctttctggaacttctg 1350
 435   L  P  Q  R  Y  W  Q  M  R  P  L  F  L  E  L  L   450

    ---------|---------|---------|---------|---------|
1351 ggtaaccacgcccagtgcccatatggcgtcctgctgaagacccactgtcc 1400
 451 G  N  H  A  Q  C  P  Y  G  V  L  L  K  T  H  C  P  467

    ---------|---------|---------|---------|---------|
1401 tctgagggccgccgtgaccccagccgccggtgtgtgtgctagagaaaaac 1450
 468  L  R  A  A  V  T  P  A  A  G  V  C  A  R  E  K  P 484

    ---------|---------|---------|---------|---------|
1451 cccagggctcagtggctgcacctgaagaggaggacactgaccctcgccgc 1500
 485   Q  G  S  V  A  A  P  E  E  E  D  T  D  P  R  R   500

    ---------|---------|---------|---------|---------|
1501 cttgtccagttgctcaggcagcattcatcaccatggcaggtgtacggctt 1550
 501 L  V  Q  L  L  R  Q  H  S  S  P  W  Q  V  Y  G  F  517

    ---------|---------|---------|---------|---------|
1551 cgtgagggcttgcctgcggagactggtccccccccggattgtggggatctc 1600
 518  V  R  A  C  L  R  R  L  V  P  P  G  L  W  G  S  R 534

    ---------|---------|---------|---------|---------|
1601 ggcacaacgaacggcgctttctgaggaatacaaagaagtttatctccctg 1650
 535   H  N  E  R  R  F  L  R  N  T  K  K  F  I  S  L   550
```

FIGURE 17 cont.

```
     ---------|---------|---------|---------|---------|
1651 ggcaagcatgcaaagctcagcttgcaggagctgacatggaagatgagcgt 1700
 551 G  K  H  A  K  L  S  L  Q  E  L  T  W  K  M  S  V  567

     ---------|---------|---------|---------|---------|
1701 tagaggatgcgcatggctcaggcggtcacctggagttggatgcgttccag 1750
 568  R  G  C  A  W  L  R  R  S  P  G  V  G  C  V  P  A 584

     ---------|---------|---------|---------|---------|
1751 cagcagagcacaggctgcgcgaagagattctcgcaaagttcctgcactgg 1800
 585   A  E  H  R  L  R  E  E  I  L  A  K  F  L  H  W   600

     ---------|---------|---------|---------|---------|
1801 cttatgagcgtctacgtggtcgaactgctgcggtctttcttctacgtgac 1850
 601 L  M  S  V  Y  V  V  E  L  L  R  S  F  F  Y  V  T  617

     ---------|---------|---------|---------|---------|
1851 agagaccacttttcagaagaacagactgttcttctacaggaagtccgtct 1900
 618  E  T  T  F  Q  K  N  R  L  F  F  Y  R  K  S  V  W 634

     ---------|---------|---------|---------|---------|
1901 ggagcaagctccagagtattggtattagacagcaccttaagagagttcag 1950
 635   S  K  L  Q  S  I  G  I  R  Q  H  L  K  R  V  Q   650

     ---------|---------|---------|---------|---------|
1951 cttagagagctgtccgaagctgaagtccgccagcaccgcgaagctcgccc 2000
 651 L  R  E  L  S  E  A  E  V  R  Q  H  R  E  A  R  P  667

     ---------|---------|---------|---------|---------|
2001 cgccctcctgacctctcggctgcggtttattcccaaacccgatggcctta 2050
 668  A  L  L  T  S  R  L  R  F  I  P  K  P  D  G  L  R 684

     ---------|---------|---------|---------|---------|
2051 gacctatcgtgaatatggattacgtcgtgggtgcccgcactttcagaagg 2100
 685   P  I  V  N  M  D  Y  V  V  G  A  R  T  F  R  R   700

     ---------|---------|---------|---------|---------|
2101 gagaagcgcgccgagagactgacatctcgcgtgaaggcacttttttctgt 2150
 701 E  K  R  A  E  R  L  T  S  R  V  K  A  L  F  S  V  717

     ---------|---------|---------|---------|---------|
2151 gcttaattatgaaagagcccgcagacctggtcttctcggagccagcgtgc 2200
 718  L  N  Y  E  R  A  R  R  P  G  L  L  G  A  S  V  L 734

     ---------|---------|---------|---------|---------|
2201 tcggcctggatgatatccatcgggcttggcgcacctttgtgcttcgggtg 2250
 735   G  L  D  D  I  H  R  A  W  R  T  F  V  L  R  V   750

     ---------|---------|---------|---------|---------|
2251 agggcacaggatcctcctcctgagctttattttgtgaaagttgatgttac 2300
 751 R  A  Q  D  P  P  P  E  L  Y  F  V  K  V  D  V  T  767

     ---------|---------|---------|---------|---------|
2301 tggtgcttacgatacaatccctcaggaccggctcaccgaggtgatcgcct 2350
 768  G  A  Y  D  T  I  P  Q  D  R  L  T  E  V  I  A  S 784

     ---------|---------|---------|---------|---------|
2351 ctattatcaaaccccagaacacctactgcgtgagaaggtacgccgtcgtt 2400
 785   I  I  K  P  Q  N  T  Y  C  V  R  R  Y  A  V  V   800

     ---------|---------|---------|---------|---------|
2401 cagaaagccgcacacggacacgtgcgcaaagctttcaaatcccacgtgtc 2450
 801 Q  K  A  A  H  G  H  V  R  K  A  F  K  S  H  V  S  817

     ---------|---------|---------|---------|---------|
2451 taccttgacagacctccagccttatatgcggcagtttgtcgcacacctgc 2500
 818  T  L  T  D  L  Q  P  Y  M  R  Q  F  V  A  H  L  Q 834
```

FIGURE 17 cont.

```
     ---------|---------|---------|---------|---------|
2501 aggagactagccccttgagggacgctgtggtcatcgaacagtccagctct 2550
 835   E  T  S  P  L  R  D  A  V  V  I  E  Q  S  S  S   850

     ---------|---------|---------|---------|---------|
2551 ctcaatgaggcatcctcaggcctgtttgatgtgttcctgcgctttatgtg 2600
 851 L  N  E  A  S  S  G  L  F  D  V  F  L  R  F  M  C  867

     ---------|---------|---------|---------|---------|
2601 ccaccacgccgtgcggattaggggcaagtcttacgtgcagtgccagggca 2650
 868  H  H  A  V  R  I  R  G  K  S  Y  V  Q  C  Q  G  I 884

     ---------|---------|---------|---------|---------|
2651 tcccacagggtagcatcctgagcacactgctgtgtagcctgtgctatggc 2700
 885   P  Q  G  S  I  L  S  T  L  L  C  S  L  C  Y  G   900

     ---------|---------|---------|---------|---------|
2701 gatatggagaataaattgttcgccggtatcagaagattcctgctggttac 2750
 901 D  M  E  N  K  L  F  A  G  I  R  R  F  L  L  V  T  917
                                     *

     ---------|---------|---------|---------|---------|
2751 cccccatctgactcatgccaaaacatttttgcggactctggttaggggcg 2800
 918  P  H  L  T  H  A  K  T  F  L  R  T  L  V  R  G  V 934

     ---------|---------|---------|---------|---------|
2801 tgccagagtatggctgtgttgtgaatttgcggaaaactgtggttaatttc 2850
 935   P  E  Y  G  C  V  V  N  L  R  K  T  V  V  N  F   950

     ---------|---------|---------|---------|---------|
2851 ccagtggaggacgaagctctcggaggcacagcttttgttcagatgcctgc 2900
 951 P  V  E  D  E  A  L  G  G  T  A  F  V  Q  M  P  A  967

     ---------|---------|---------|---------|---------|
2901 ccacggcctgttcccatggtgcggactgctgctcgatacccggaccctcg 2950
 968  H  G  L  F  P  W  C  G  L  L  L  D  T  R  T  L  E 984

     ---------|---------|---------|---------|---------|
2951 aggtgcagtccgattatagttcctatgcaagaacatcaattcgggctagc 3000
 985   V  Q  S  D  Y  S  S  Y  A  R  T  S  I  R  A  S   1000

     ---------|---------|---------|---------|---------|
3001 ctgactttcaacaggggcttcaaggccggccggaatatgagaaggaaact 3050
1001 L  T  F  N  R  G  F  K  A  G  R  N  M  R  R  K  L  1017

     ---------|---------|---------|---------|---------|
3051 gttcggagtgttgagacttaagtgtcatagtctttttttggacttgcagg 3100
1018  F  G  V  L  R  L  K  C  H  S  L  F  L  D  L  Q  V 1034

     ---------|---------|---------|---------|---------|
3101 tcaattctctccagacagtgtgtaccaacatttataaaatcctcttgctg 3150
1035   N  S  L  Q  T  V  C  T  N  I  Y  K  I  L  L  L   1050

     ---------|---------|---------|---------|---------|
3151 caggcttacagattccatgcctgcgtcctgcagctgcctttccaccagca 3200
1051 Q  A  Y  R  F  H  A  C  V  L  Q  L  P  F  H  Q  Q  1067

     ---------|---------|---------|---------|---------|
3201 ggtgtggaaaaaccctaccttcttcctgcgggtgattagcgacaccgcca 3250
1068  V  W  K  N  P  T  F  F  L  R  V  I  S  D  T  A  S 1084

     ---------|---------|---------|---------|---------|
3251 gtctttgctactccatcttgaaagcaaaaaacgctggcatgagcttggga 3300
1085   L  C  Y  S  I  L  K  A  K  N  A  G  M  S  L  G   1100

     ---------|---------|---------|---------|---------|
3301 gctaagggcgccgctggacctctgcccagtgaagcagtccagtggctgtg 3350
1101 A  K  G  A  A  G  P  L  P  S  E  A  V  Q  W  L  C  1117
```

FIGURE 17 cont.

```
     ---------|---------|---------|---------|---------|
3351 tcatcaggctttcctccttaaactgacacgccaccgcgtgacttacgtcc 3400
1118  H  Q  A  F  L  L  K  L  T  R  H  R  V  T  Y  V  P 1134

     ---------|---------|---------|---------|---------|
3401 cactcctgggctccctgagaactgctcagacccagctttcccggaagctt 3450
1135   L  L  G  S  L  R  T  A  Q  T  Q  L  S  R  K  L   1150

     ---------|---------|---------|---------|---------|
3451 ccaggcactacccttaccgcactcgaagcagccgccaaccctgccctgcc 3500
1151 P  G  T  T  L  T  A  L  E  A  A  A  N  P  A  L  P  1167
                          hTERT>< tag V5
     ---------|---------|---------|---------|---------|
3501 ctccgactttaagactatcctggacggcaagccaattcctaatccattgc 3550
1168  S  D  F  K  T  I  L  D  G  K  P  I  P  N  P  L  L 1184
                       >STOP
     ---------|---------|
3551 tgggcctggactcaacttga 3570
1185   G  L  D  S  T  □   1189
```

FIGURE 17 cont.

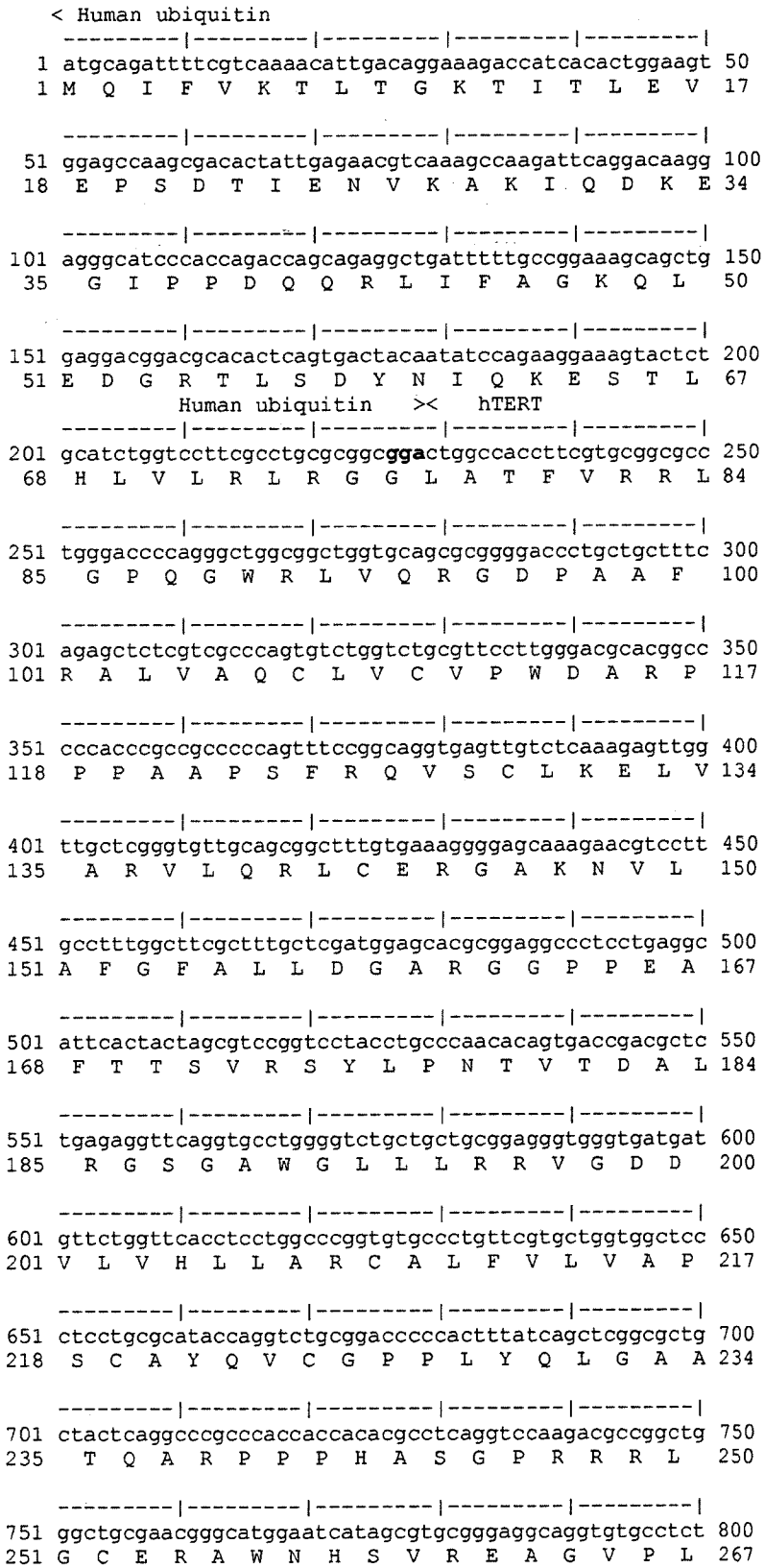


FIGURE 18

```
    ---------|---------|---------|---------|---------|
 801 cggcctgccagcccccggagcaaggagacgcggtggatccgccagtcgct 850
 268  G  L  P  A  P  G  A  R  R  R  G  G  S  A  S  R  S 284

    ---------|---------|---------|---------|---------|
 851 cactccccttgcctaagaggccaagaagaggagccgcccctgaacccgag 900
 285   L  P  L  P  K  R  P  R  R  G  A  A  P  E  P  E   300

    ---------|---------|---------|---------|---------|
 901 agaacacctgtcggccagggctcctgggctcaccccggaaggaccagggg 950
 301 R  T  P  V  G  Q  G  S  W  A  H  P  G  R  T  R  G 317

    ---------|---------|---------|---------|---------|
 951 cccaagcgatagggggcttctgtgttgtgtcaccagccaggcctgccgaag 1000
 318  P  S  D  R  G  F  C  V  V  S  P  A  R  P  A  E  E 334

    ---------|---------|---------|---------|---------|
1001 aggctacctccttggaaggagccctcagtggcaccaggcattctcatcca 1050
 335   A  T  S  L  E  G  A  L  S  G  T  R  H  S  H  P   350

    ---------|---------|---------|---------|---------|
1051 tctgtgggtaggcagcatcatgccggcccccccctctacaagcagacctcc 1100
 351 S  V  G  R  Q  H  H  A  G  P  P  S  T  S  R  P  P  367

    ---------|---------|---------|---------|---------|
1101 cagaccttgggacacaccctgcccaccagtgtatgccgagaccaagcact 1150
 368  R  P  W  D  T  P  C  P  P  V  Y  A  E  T  K  H  F 384

    ---------|---------|---------|---------|---------|
1151 ttttgtattccagtggcgataaagagcagctccggccctcttttctgctc 1200
 385   L  Y  S  S  G  D  K  E  Q  L  R  P  S  F  L  L   400

    ---------|---------|---------|---------|---------|
1201 tcaagcctccgcccctctctgaccggagctcgcaggctggtggagaccat 1250
 401 S  S  L  R  P  S  L  T  G  A  R  R  L  V  E  T  I  417

    ---------|---------|---------|---------|---------|
1251 ctttctgggctcaagaccatggatgccaggcacccccgcagactgccca 1300
 418  F  L  G  S  R  P  W  M  P  G  T  P  R  R  L  P  R 434

    ---------|---------|---------|---------|---------|
1301 ggctcccccagcggtactggcagatgcgccctctctttctggaacttctg 1350
 435   L  P  Q  R  Y  W  Q  M  R  P  L  F  L  E  L  L   450

    ---------|---------|---------|---------|---------|
1351 ggtaaccacgcccagtgcccatatggcgtcctgctgaagacccactgtcc 1400
 451 G  N  H  A  Q  C  P  Y  G  V  L  L  K  T  H  C  P  467

    ---------|---------|---------|---------|---------|
1401 tctgagggccgccgtgaccccagccgccggtgtgtgtgctagagaaaaac 1450
 468  L  R  A  A  V  T  P  A  A  G  V  C  A  R  E  K  P 484

    ---------|---------|---------|---------|---------|
1451 cccagggctcagtggctgcacctgaagaggaggacactgaccctcgccgc 1500
 485   Q  G  S  V  A  A  P  E  E  E  D  T  D  P  R  R   500

    ---------|---------|---------|---------|---------|
1501 cttgtccagttgctcaggcagcattcatcaccatggcaggtgtacggctt 1550
 501 L  V  Q  L  L  R  Q  H  S  S  P  W  Q  V  Y  G  F  517

    ---------|---------|---------|---------|---------|
1551 cgtgagggcttgcctgcggagactggtccccccggattgtggggatctc 1600
 518  V  R  A  C  L  R  R  L  V  P  P  G  L  W  G  S  R 534

    ---------|---------|---------|---------|---------|
1601 ggcacaacgaacggcgctttctgaggaatacaaagaagtttatctccctg 1650
 535   H  N  E  R  R  F  L  R  N  T  K  K  F  I  S  L   550
```

FIGURE 18 cont.

```
     ---------|---------|---------|---------|---------|
1651 ggcaagcatgcaaagctcagcttgcaggagctgacatggaagatgagcgt 1700
 551 G  K  H  A  K  L  S  L  Q  E  L  T  W  K  M  S  V  567

     ---------|---------|---------|---------|---------|
1701 tagaggatgcgcatggctcaggcggtcacctggagttggatgcgttccag 1750
 568  R  G  C  A  W  L  R  R  S  P  G  V  G  C  V  P  A 584

     ---------|---------|---------|---------|---------|
1751 cagcagagcacaggctgcgcgaagagattctcgcaaagttcctgcactgg 1800
 585   A  E  H  R  L  R  E  E  I  L  A  K  F  L  H  W   600

     ---------|---------|---------|---------|---------|
1801 cttatgagcgtctacgtggtcgaactgctgcggtctttcttctacgtgac 1850
 601 L  M  S  V  Y  V  V  E  L  L  R  S  F  F  Y  V  T  617

     ---------|---------|---------|---------|---------|
1851 agagaccacttttcagaagaacagactgttcttctacaggaagtccgtct 1900
 618  E  T  T  F  Q  K  N  R  L  F  F  Y  R  K  S  V  W 634

     ---------|---------|---------|---------|---------|
1901 ggagcaagctccagagtattggtattagacagcaccttaagagagttcag 1950
 635   S  K  L  Q  S  I  G  I  R  Q  H  L  K  R  V  Q   650

     ---------|---------|---------|---------|---------|
1951 cttagagagctgtccgaagctgaagtccgccagcaccgcgaagctcgccc 2000
 651 L  R  E  L  S  E  A  E  V  R  Q  H  R  E  A  R  P  667

     ---------|---------|---------|---------|---------|
2001 cgccctcctgacctctcggctgcggtttattcccaaacccgatggcctta 2050
 668  A  L  L  T  S  R  L  R  F  I  P  K  P  D  G  L  R 684

     ---------|---------|---------|---------|---------|
2051 gacctatcgtgaatatggattacgtcgtgggtgcccgcactttcagaagg 2100
 685   P  I  V  N  M  D  Y  V  V  G  A  R  T  F  R  R   700

     ---------|---------|---------|---------|---------|
2101 gagaagcgcgccgagagactgacatctcgcgtgaaggcacttttttctgt 2150
 701 E  K  R  A  E  R  L  T  S  R  V  K  A  L  F  S  V  717

     ---------|---------|---------|---------|---------|
2151 gcttaattatgaaagagcccgcagacctggtcttctcggagccagcgtgc 2200
 718  L  N  Y  E  R  A  R  R  P  G  L  L  G  A  S  V  L 734

     ---------|---------|---------|---------|---------|
2201 tcggcctggatgatatccatcgggcttggcgcacctttgtgcttcgggtg 2250
 735   G  L  D  D  I  H  R  A  W  R  T  F  V  L  R  V   750

     ---------|---------|---------|---------|---------|
2251 agggcacaggatcctcctcctgagctttatttttgtgaaagttgatgttac 2300
 751 R  A  Q  D  P  P  P  E  L  Y  F  V  K  V  D  V  T  767

     ---------|---------|---------|---------|---------|
2301 tggtgcttacgatacaatccctcaggaccggctcaccgaggtgatcgcct 2350
 768  G  A  Y  D  T  I  P  Q  D  R  L  T  E  V  I  A  S 784

     ---------|---------|---------|---------|---------|
2351 ctattatcaaaccccagaacacctactgcgtgagaaggtacgccgtcgtt 2400
 785   I  I  K  P  Q  N  T  Y  C  V  R  R  Y  A  V  V   800

     ---------|---------|---------|---------|---------|
2401 cagaaagccgcacacggacacgtgcgcaaagctttcaaatcccacgtgtc 2450
 801 Q  K  A  A  H  G  H  V  R  K  A  F  K  S  H  V  S  817

     ---------|---------|---------|---------|---------|
2451 taccttgacagacctccagccttatatgcggcagtttgtcgcacacctgc 2500
 818  T  L  T  D  L  Q  P  Y  M  R  Q  F  V  A  H  L  Q 834
```

FIGURE 18 cont.

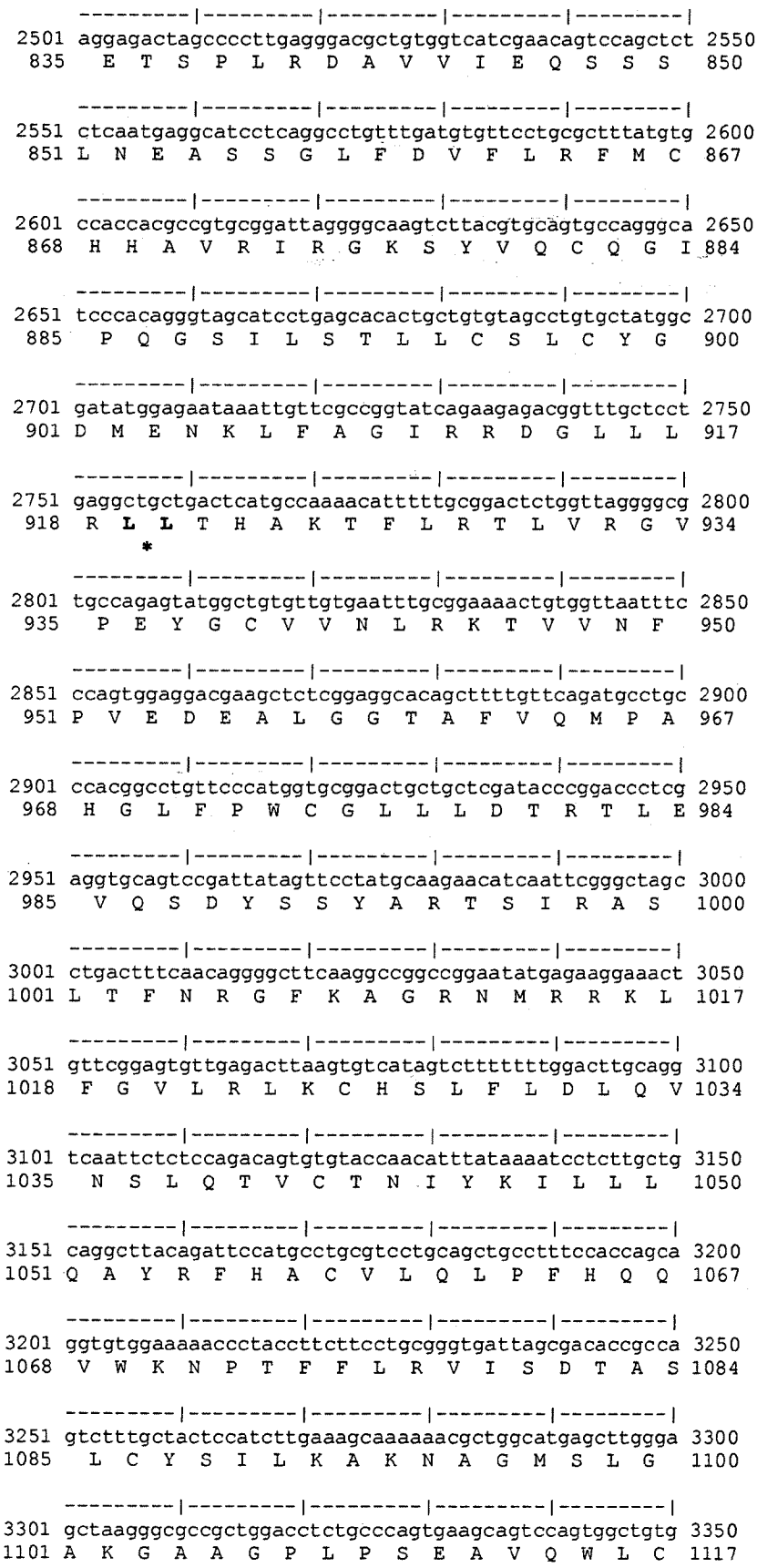


FIGURE 18 cont.

```
     ---------|---------|---------|---------|---------|
3351 tcatcaggctttcctccttaaactgacacgccaccgcgtgacttacgtcc 3400
1118  H  Q  A  F  L  L  K  L  T  R  H  R  V  T  Y  V  P 1134

     ---------|---------|---------|---------|---------|
3401 cactcctgggctccctgagaactgctcagacccagctttcccggaagctt 3450
1135   L  L  G  S  L  R  T  A  Q  T  Q  L  S  R  K  L  1150

     ---------|---------|---------|---------|---------|
3451 ccaggcactaccttaccgcactcgaagcagccgccaaccctgccctgcc 3500
1151 P  G  T  T  L  T  A  L  E  A  A  A  N  P  A  L  P 1167
                        hTERT>< tag V5
     ---------|---------|---------|---------|---------|
3501 ctccgactttaagactatcctggacggcaagccaattcctaatccattgc 3550
1168  S  D  F  K  T  I  L  D  G  K  P  I  P  N  P  L  L 1184
                       >STOP
     ---------|---------|
3551 tgggcctggactcaacttga 3570
1185   G  L  D  S  T   □  1189
```

FIGURE 18 cont.

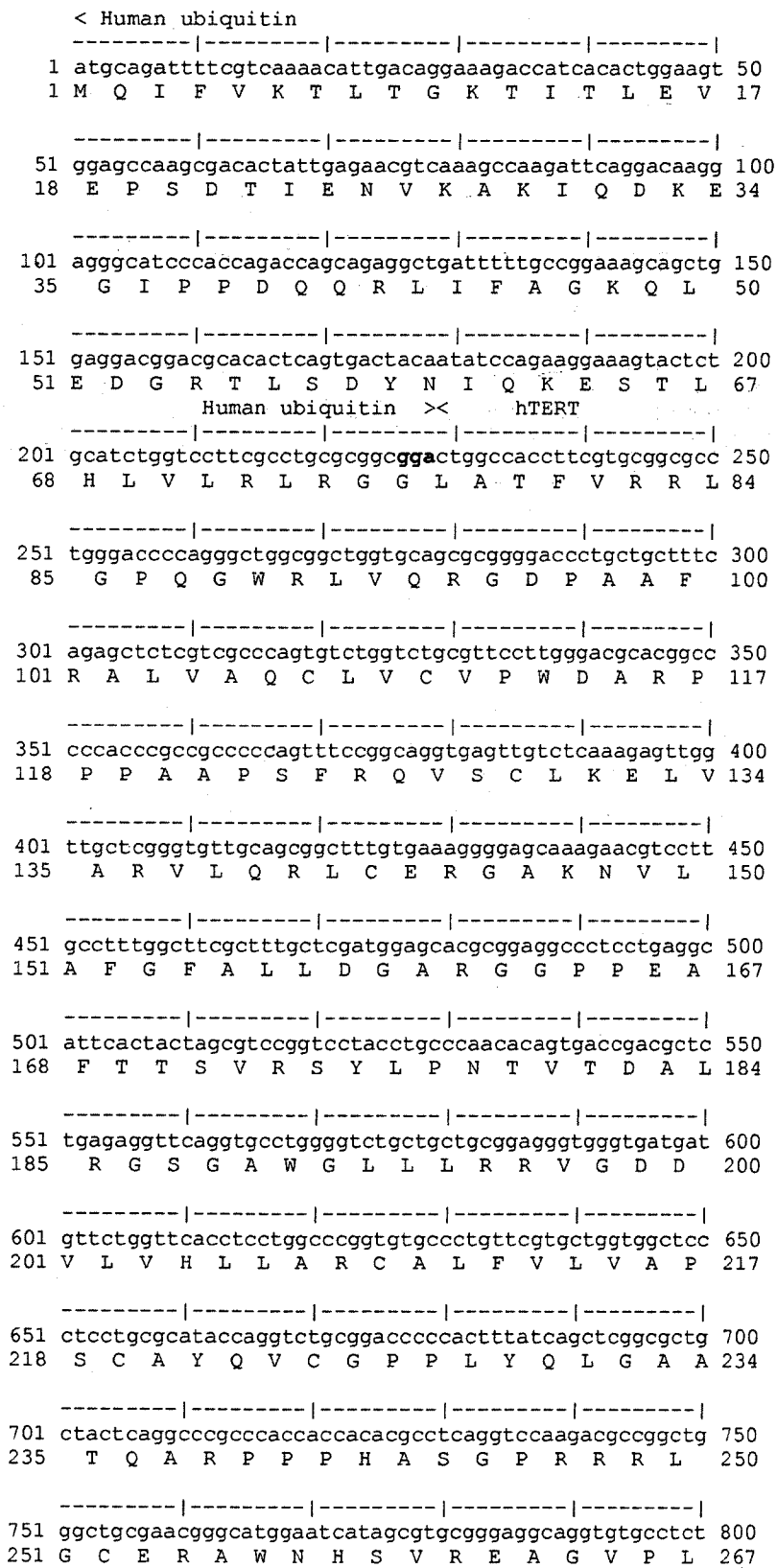

< Human ubiquitin
1 atgcagattttcgtcaaaacattgacaggaaagaccatcacactggaagt 50
1 M Q I F V K T L T G K T I T L E V 17
51 ggagccaagcgacactattgagaacgtcaaagccaagattcaggacaagg 100
18 E P S D T I E N V K A K I Q D K E 34
101 agggcatcccaccagaccagcagaggctgatttttgccggaaagcagctg 150
35 G I P P D Q Q R L I F A G K Q L 50
151 gaggacggacgcacactcagtgactacaatatccagaaggaaagtactct 200
51 E D G R T L S D Y N I Q K E S T L 67
Human ubiquitin >< hTERT
201 gcatctggtccttcgcctgcgcggcggactggccaccttcgtgcggcgcc 250
68 H L V L R L R G G L A T F V R R L 84
251 tgggaccccagggctggcggctggtgcagcgcggggaccctgctgctttc 300
85 G P Q G W R L V Q R G D P A A F 100
301 agagctctcgtcgcccagtgtctggtctgcgttccttgggacgcacggcc 350
101 R A L V A Q C L V C V P W D A R P 117
351 cccacccgccgcccccagtttccggcaggtgagttgtctcaaagagttgg 400
118 P P A A P S F R Q V S C L K E L V 134
401 ttgctcgggtgttgcagcggctttgtgaaaggggagcaaagaacgtcctt 450
135 A R V L Q R L C E R G A K N V L 150
451 gcctttggcttcgctttgctcgatggagcacgcggaggccctcctgaggc 500
151 A F G F A L L D G A R G G P P E A 167
501 attcactactagcgtccggtcctacctgcccaacacagtgaccgacgctc 550
168 F T T S V R S Y L P N T V T D A L 184
551 tgagaggttcaggtgcctggggtctgctgctgcggagggtgggtgatgat 600
185 R G S G A W G L L L R R V G D D 200
601 gttctggttcacctcctggcccggtgtgccctgttcgtgctggtggctcc 650
201 V L V H L L A R C A L F V L V A P 217
651 ctcctgcgcataccaggtctgcggacccccactttatcagctcggcgctg 700
218 S C A Y Q V C G P P L Y Q L G A A 234
701 ctactcaggcccgcccaccaccacacgcctcaggtccaagacgccggctg 750
235 T Q A R P P P H A S G P R R R L 250
751 ggctgcgaacgggcatggaatcatagcgtgcgggaggcaggtgtgcctct 800
251 G C E R A W N H S V R E A G V P L 267

FIGURE 19

```
     ---------|---------|---------|---------|---------|
 801 cggcctgccagcccccggagcaaggagacgcggtggatccgccagtcgct 850
 268  G  L  P  A  P  G  A  R  R  R  G  G  S  A  S  R  S 284

     ---------|---------|---------|---------|---------|
 851 cactccccttgcctaagaggccaagaagaggagccgcccctgaacccgag 900
 285   L  P  L  P  K  R  P  R  R  G  A  A  P  E  P  E   300

     ---------|---------|---------|---------|---------|
 901 agaacacctgtcggccagggctcctgggctcacccccggaaggaccagggg 950
 301 R  T  P  V  G  Q  G  S  W  A  H  P  G  R  T  R  G  317

     ---------|---------|---------|---------|---------|
 951 cccaagcgataggggcttctgtgttgtgtcaccagccaggcctgccgaag 1000
 318  P  S  D  R  G  F  C  V  V  S  P  A  R  P  A  E  E 334

     ---------|---------|---------|---------|---------|
1001 aggctacctccttggaaggagccctcagtggcaccaggcattctcatcca 1050
 335   A  T  S  L  E  G  A  L  S  G  T  R  H  S  H  P   350

     ---------|---------|---------|---------|---------|
1051 tctgtgggtaggcagcatcatgccggccccccctctacaagcagacctcc 1100
 351 S  V  G  R  Q  H  H  A  G  P  P  S  T  S  R  P  P  367

     ---------|---------|---------|---------|---------|
1101 cagaccttgggacacaccctgcccaccagtgtatgccgagaccaagcact 1150
 368  R  P  W  D  T  P  C  P  P  V  Y  A  E  T  K  H  F 384

     ---------|---------|---------|---------|---------|
1151 ttttgtattccagtggcgataaagagcagctccggccctcttttctgctc 1200
 385   L  Y  S  S  G  D  K  E  Q  L  R  P  S  F  L  L   400

     ---------|---------|---------|---------|---------|
1201 tcaagcctccgcccctctctgaccggagctcgcaggctggtggagaccat 1250
 401 S  S  L  R  P  S  L  T  G  A  R  R  L  V  E  T  I  417

     ---------|---------|---------|---------|---------|
1251 ctttctgggctcaagaccatggatgccaggcacccccgcagactgccca 1300
 418  F  L  G  S  R  P  W  M  P  G  T  P  R  R  L  P  R 434

     ---------|---------|---------|---------|---------|
1301 ggctcccccagcggtactggcagatgcgccctctctttctggaacttctg 1350
 435   L  P  Q  R  Y  W  Q  M  R  P  L  F  L  E  L  L   450

     ---------|---------|---------|---------|---------|
1351 ggtaaccacgcccagtgcccatatggcgtcctgctgaagacccactgtcc 1400
 451 G  N  H  A  Q  C  P  Y  G  V  L  L  K  T  H  C  P  467

     ---------|---------|---------|---------|---------|
1401 tctgagggccgccgtgaccccagccgccggtgtgtgtgctagagaaaaac 1450
 468  L  R  A  A  V  T  P  A  A  G  V  C  A  R  E  K  P 484

     ---------|---------|---------|---------|---------|
1451 cccagggctcagtggctgcacctgaagaggaggacactgaccctcgccgc 1500
 485   Q  G  S  V  A  A  P  E  E  E  D  T  D  P  R  R   500

     ---------|---------|---------|---------|---------|
1501 cttgtccagttgctcaggcagcattcatcaccatggcaggtgtacggctt 1550
 501 L  V  Q  L  L  R  Q  H  S  S  P  W  Q  V  Y  G  F  517

     ---------|---------|---------|---------|---------|
1551 cgtgagggcttgcctgcggagactggtccccccggattgtggggatctc 1600
 518  V  R  A  C  L  R  R  L  V  P  P  G  L  W  G  S  R 534

     ---------|---------|---------|---------|---------|
1601 ggcacaacgaacggcgctttctgaggaatacaaagaagtttatctccctg 1650
 535   H  N  E  R  R  F  L  R  N  T  K  K  F  I  S  L   550
```

FIGURE 19 cont.

```
     ---------|---------|---------|---------|---------|
1651 ggcaagcatgcaaagctcagcttgcaggagctgacatggaagatgagcgt 1700
 551 G  K  H  A  K  L  S  L  Q  E  L  T  W  K  M  S  V  567

     ---------|---------|---------|---------|---------|
1701 tagaggatgcgcatggctcaggcggtcacctggagttggatgcgttccag 1750
 568  R  G  C  A  W  L  R  R  S  P  G  V  G  C  V  P  A 584

     ---------|---------|---------|---------|---------|
1751 cagcagagcacaggctgcgcgaagagattctcgcaaagttcctgcactgg 1800
 585   A  E  H  R  L  R  E  E  I  L  A  K  F  L  H  W   600

     ---------|---------|---------|---------|---------|
1801 cttatgagcgtctacgtggtcgaactgctgcggtctttcttctacgtgac 1850
 601 L  M  S  V  Y  V  V  E  L  L  R  S  F  F  Y  V  T  617

     ---------|---------|---------|---------|---------|
1851 agagaccacttttcagaagaacagactgttcttctacaggaagtccgtct 1900
 618  E  T  T  F  Q  K  N  R  L  F  F  Y  R  K  S  V  W 634

     ---------|---------|---------|---------|---------|
1901 ggagcaagctccagagtattggtattagacagcaccttaagagagttcag 1950
 635   S  K  L  Q  S  I  G  I  R  Q  H  L  K  R  V  Q   650

     ---------|---------|---------|---------|---------|
1951 cttagagagctgtccgaagctgaagtccgccagcaccgcgaagctcgccc 2000
 651 L  R  E  L  S  E  A  E  V  R  Q  H  R  E  A  R  P  667

     ---------|---------|---------|---------|---------|
2001 cgccctcctgacctctcggctgcggtttattcccaaacccgatggcctta 2050
 668  A  L  L  T  S  R  L  R  F  I  P  K  P  D  G  L  R 684

     ---------|---------|---------|---------|---------|
2051 gacctatcgtgaatatggattacgtcgtgggtgcccgcactttcagaagg 2100
 685   P  I  V  N  M  D  Y  V  V  G  A  R  T  F  R  R   700

     ---------|---------|---------|---------|---------|
2101 gagaagcgcgccgagagactgacatctcgcgtgaaggcacttttttctgt 2150
 701 E  K  R  A  E  R  L  T  S  R  V  K  A  L  F  S  V  717

     ---------|---------|---------|---------|---------|
2151 gcttaattatgaaagagcccgcagacctggtcttctcggagccagcgtgc 2200
 718  L  N  Y  E  R  A  R  R  P  G  L  L  G  A  S  V  L 734

     ---------|---------|---------|---------|---------|
2201 tcggcctggatgatatccatcgggcttggcgcacctttgtgcttcgggtg 2250
 735   G  L  D  D  I  H  R  A  W  R  T  F  V  L  R  V   750

     ---------|---------|---------|---------|---------|
2251 agggcacaggatcctcctcctgagctttatttgtgaaagttgatgttac 2300
 751 R  A  Q  D  P  P  P  E  L  Y  F  V  K  V  D  V  T  767

     ---------|---------|---------|---------|---------|
2301 tggtgcttacgatacaatccctcaggaccggctcaccgaggtgatcgcct 2350
 768  G  A  Y  D  T  I  P  Q  D  R  L  T  E  V  I  A  S 784

     ---------|---------|---------|---------|---------|
2351 ctattatcaaaccccagaacacctactgcgtgagaaggtacgccgtcgtt 2400
 785   I  I  K  P  Q  N  T  Y  C  V  R  R  Y  A  V  V   800

     ---------|---------|---------|---------|---------|
2401 cagaaagccgcacacggacacgtgcgcaaagctttcaaatcccacgtgtc 2450
 801 Q  K  A  A  H  G  H  V  R  K  A  F  K  S  H  V  S  817

     ---------|---------|---------|---------|---------|
2451 taccttgacagacctccagccttatatgcggcagtttgtcgcacacctgc 2500
 818  T  L  T  D  L  Q  P  Y  M  R  Q  F  V  A  H  L  Q 834
```

FIGURE 19 cont.

```
         ---------|---------|---------|---------|---------|
2501 aggagactagccccttgagggacgctgtggtcatcgaacagtccagctct 2550
 835   E  T  S  P  L  R  D  A  V  V  I  E  Q  S  S  S   850

         ---------|---------|---------|---------|---------|
2551 ctcaatgaggcatcctcaggcctgtttgatgtgttcctgcgctttatgtg 2600
 851 L  N  E  A  S  S  G  L  F  D  V  F  L  R  F  M  C  867

         ---------|---------|---------|---------|---------|
2601 ccaccacgccgtgcggattaggggcaagtcttacgtgcagtgccagggca 2650
 868  H  H  A  V  R  I  R  G  K  S  Y  V  Q  C  Q  G  I 884

         ---------|---------|---------|---------|---------|
2651 tcccacagggtagcatcctgagcacactgctgtgtagcctgtgctatggc 2700
 885   P  Q  G  S  I  L  S  T  L  L  C  S  L  C  Y  G   900

         ---------|---------|---------|---------|---------|
2701 gatatggagaataaattgttcgccggtgccaaaacatttttgcggactct 2750
 901 D  M  E  N  K  L  F  A  G  A  K  T  F  L  R  T  L  917
                            *
         ---------|---------|---------|---------|---------|
2751 ggttaggggcgtgccagagtatggctgtgttgtgaatttgcggaaaactg 2800
 918  V  R  G  V  P  E  Y  G  C  V  V  N  L  R  K  T  V 934

         ---------|---------|---------|---------|---------|
2801 tggttaatttcccagtggaggacgaagctctcggaggcacagcttttgtt 2850
 935   V  N  F  P  V  E  D  E  A  L  G  G  T  A  F  V   950

         ---------|---------|---------|---------|---------|
2851 cagatgcctgcccacggcctgttcccatggtgcggactgctgctcgatac 2900
 951 Q  M  P  A  H  G  L  F  P  W  C  G  L  L  L  D  T  967

         ---------|---------|---------|---------|---------|
2901 ccggaccctcgaggtgcagtccgattatagttcctatgcaagaacatcaa 2950
 968  R  T  L  E  V  Q  S  D  Y  S  S  Y  A  R  T  S  I 984

         ---------|---------|---------|---------|---------|
2951 ttcgggctagcctgactttcaacaggggcttcaaggccggccggaatatg 3000
 985   R  A  S  L  T  F  N  R  G  F  K  A  G  R  N  M   1000

         ---------|---------|---------|---------|---------|
3001 agaaggaaactgttcggagtgttgagacttaagtgtcatagtctttttt 3050
1001 R  R  K  L  F  G  V  L  R  L  K  C  H  S  L  F  L  1017

         ---------|---------|---------|---------|---------|
3051 ggacttgcaggtcaattctctccagacagtgtgtaccaacatttataaaa 3100
1018  D  L  Q  V  N  S  L  Q  T  V  C  T  N  I  Y  K  I 1034

         ---------|---------|---------|---------|---------|
3101 tcctcttgctgcaggcttacagattccatgcctgcgtcctgcagctgcct 3150
1035   L  L  L  Q  A  Y  R  F  H  A  C  V  L  Q  L  P   1050

         ---------|---------|---------|---------|---------|
3151 ttccaccagcaggtgtggaaaaaccctaccttcttcctgcgggtgattag 3200
1051 F  H  Q  Q  V  W  K  N  P  T  F  F  L  R  V  I  S  1067

         ---------|---------|---------|---------|---------|
3201 cgacaccgccagtctttgctactccatcttgaaagcaaaaaacgctggca 3250
1068  D  T  A  S  L  C  Y  S  I  L  K  A  K  N  A  G  M 1084

         ---------|---------|---------|---------|---------|
3251 tgagcttgggagctaagggcgccgctggacctctgcccagtgaagcagtc 3300
1085   S  L  G  A  K  G  A  A  G  P  L  P  S  E  A  V   1100

         ---------|---------|---------|---------|---------|
3301 cagtggctgtgtcatcaggctttcctccttaaactgacacgccaccgcgt 3350
1101 Q  W  L  C  H  Q  A  F  L  L  K  L  T  R  H  R  V  1117
```

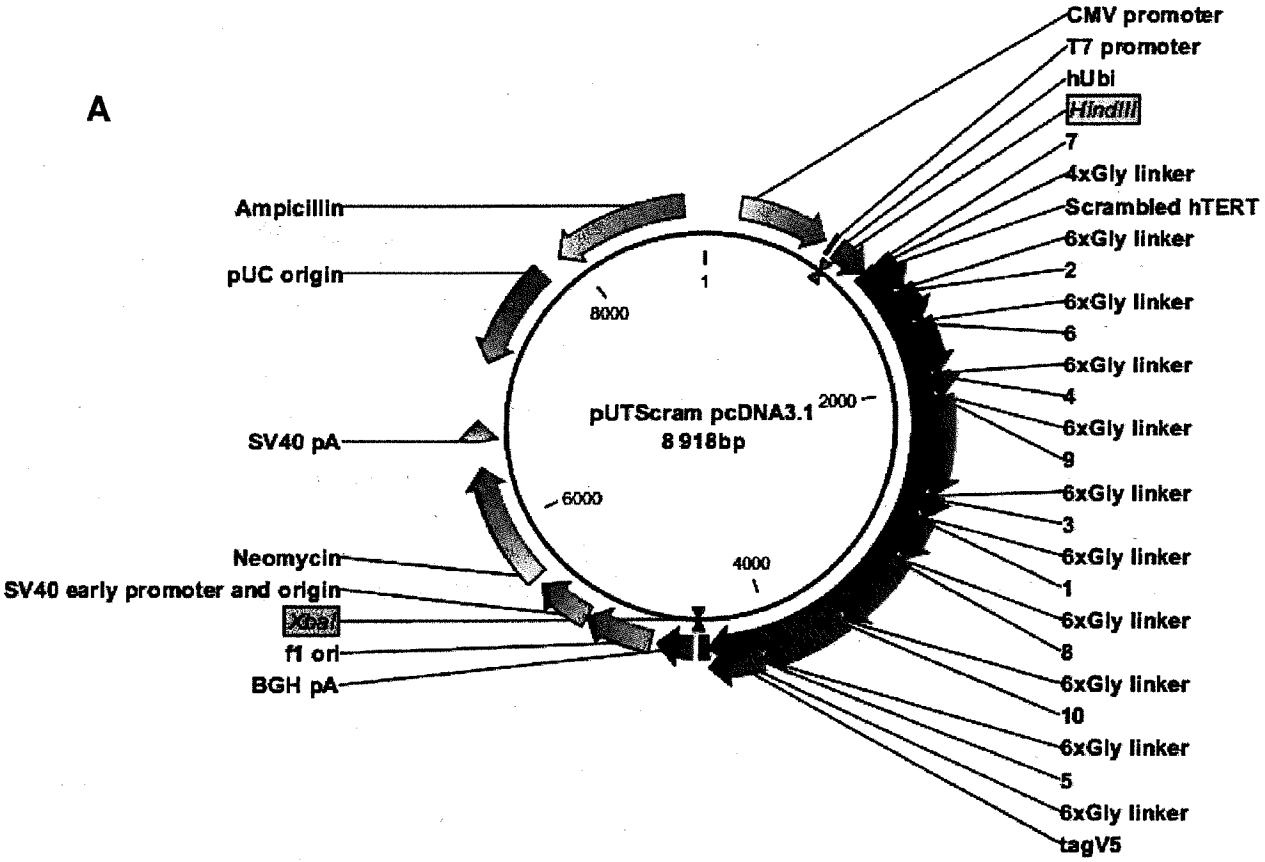
FIGURE 19 cont.

```
     ---------|---------|---------|---------|---------|
3351 gacttacgtcccactcctgggctccctgagaactgctcagacccagcttt 3400
1118  T  Y  V  P  L  L  G  S  L  R  T  A  Q  T  Q  L  S 1134

     ---------|---------|---------|---------|---------|
3401 cccggaagcttccaggcactacccttaccgcactcgaagcagccgccaac 3450
1135   R  K  L  P  G  T  T  L  T  A  L  E  A  A  A  N   1150
                                    hTERT><tag V5
     ---------|---------|---------|---------|---------|
3451 cctgccctgccctccgactttaagactatcctg**gac**ggcaagccaattcc 3500
1151 P  A  L  P  S  D  F  K  T  I  L  D  G  K  P  I  P  1167

                                  >STOP
     ---------|---------|---------|-
3501 taatccattgctgggcctggactcaacttga 3531
1168  N  P  L  L  G  L  D  S  T   □  1176
```

FIGURE 19 cont.


A
CMV promoter
T7 promoter
hUbi
HindIII
7
4xGly linker
Scrambled hTERT
6xGly linker
2
6xGly linker
6
6xGly linker
4
6xGly linker
9
6xGly linker
3
6xGly linker
1
6xGly linker
8
6xGly linker
10
6xGly linker
5
6xGly linker
tagV5
Ampicillin
pUC origin
SV40 pA
Neomycin
SV40 early promoter and origin
XbaI
f1 ori
BGH pA
1
2000
4000
6000
8000
pUTScram pcDNA3.1
8 918bp

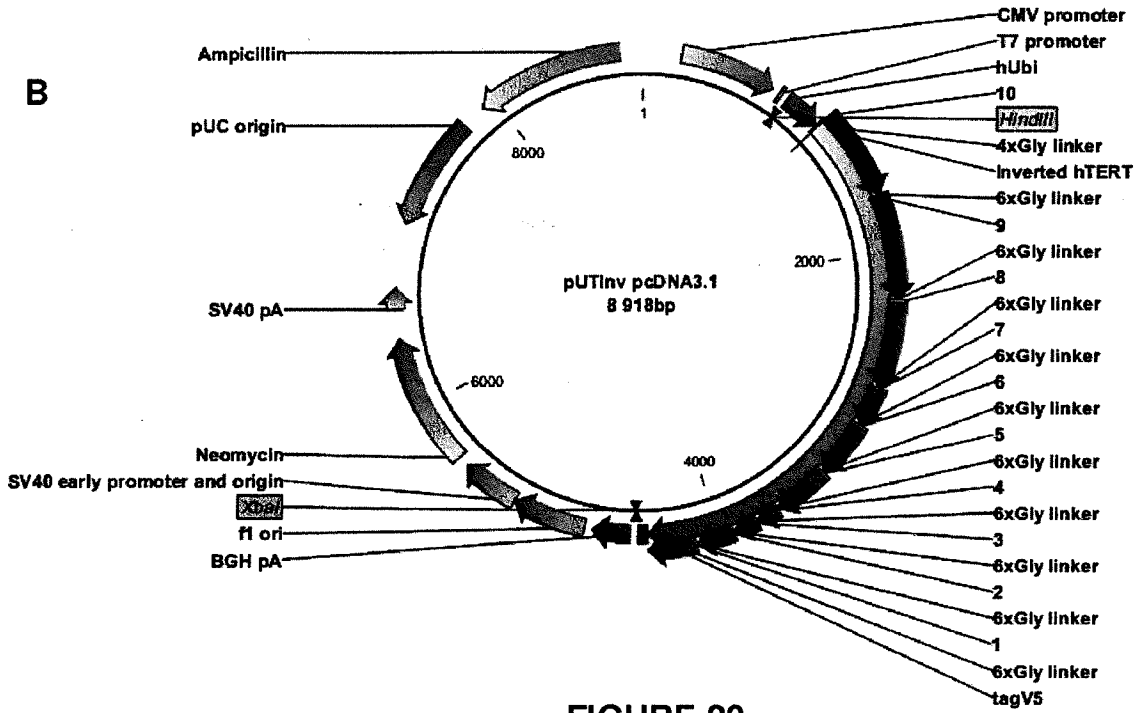
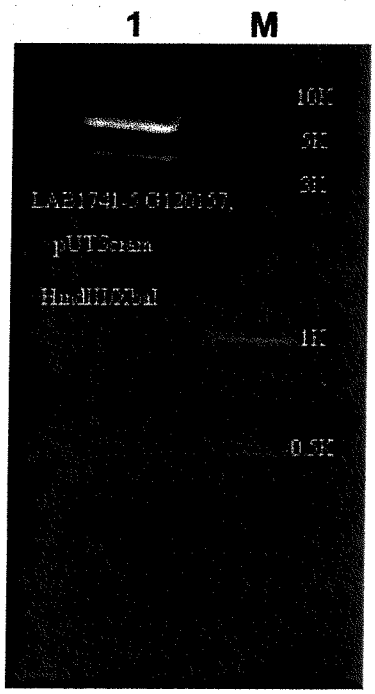

B
CMV promoter
T7 promoter
hUbi
10
HindIII
4xGly linker
Inverted hTERT
6xGly linker
9
6xGly linker
8
6xGly linker
7
6xGly linker
6
6xGly linker
5
6xGly linker
4
6xGly linker
3
6xGly linker
2
6xGly linker
1
6xGly linker
tagV5
Ampicillin
pUC origin
SV40 pA
Neomycin
SV40 early promoter and origin
XbaI
f1 ori
BGH pA
1
2000
4000
6000
8000
pUTinv pcDNA3.1
8 918bp

FIGURE 20

FIGURE 21

A



B

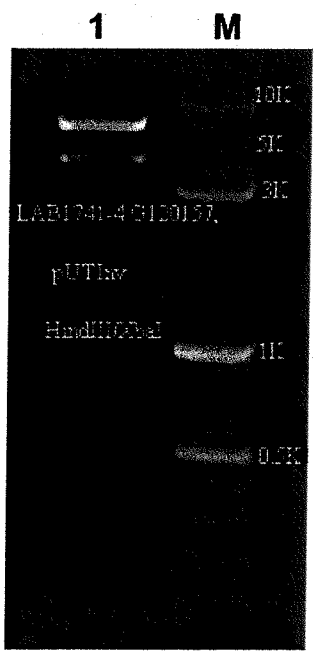


FIGURE 22

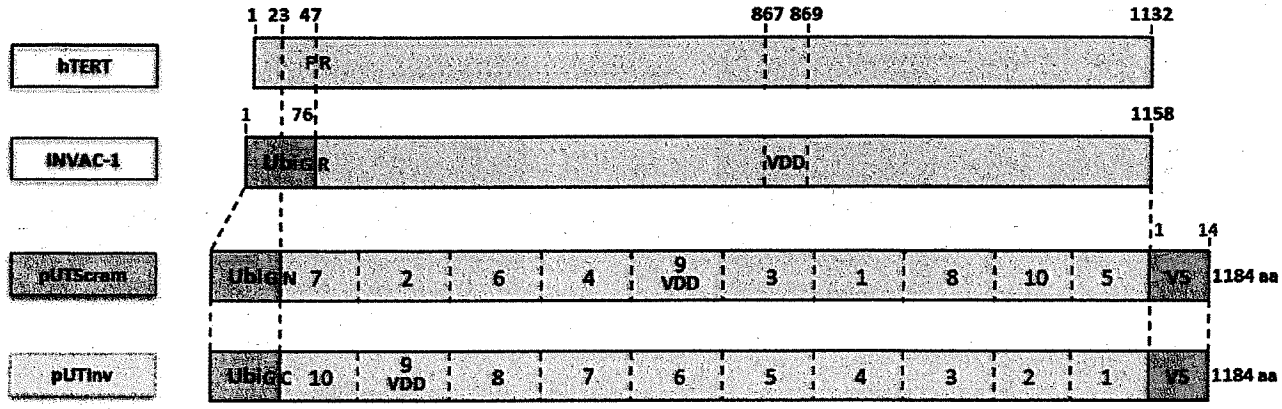

1 23 47
867 869
1132
hTERT
PR
1
76
1158
INVAC-1
UbiG
R
VDD
1
14
pUTScram
UbiG
N
7
2
6
4
9
VDD
3
1
8
10
5
V5
1184 aa
pUTinv
UbiG
C
10
9
VDD
8
7
6
5
4
3
2
1
V5
1184 aa

FIGURE 23

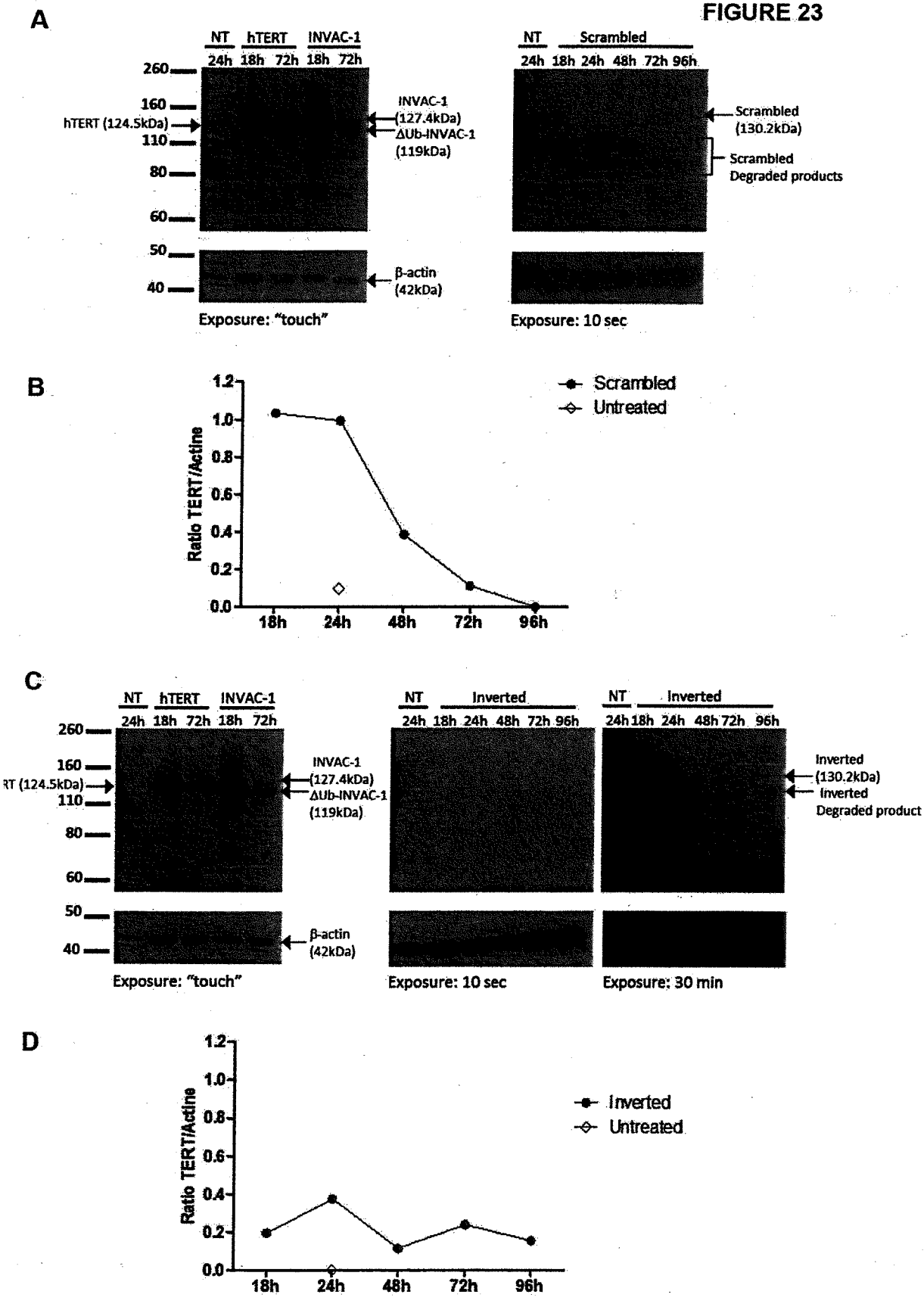

A
NT
hTERT
INVAC-1
24h 18h 72h 18h 72h
260
160
110
80
60
50
40
hTERT (124.5kDa)
INVAC-1
(127.4kDa)
ΔUb-INVAC-1
(119kDa)
β-actin
(42kDa)
Exposure: "touch"
NT
Scrambled
24h 18h 24h 48h 72h 96h
Scrambled
(130.2kDa)
Scrambled
Degraded products
Exposure: 10 sec
B
Scrambled
Untreated
Ratio TERT/Actine
1.2
1.0
0.8
0.6
0.4
0.2
0.0
18h 24h 48h 72h 96h
C
NT
hTERT
INVAC-1
24h 18h 72h 18h 72h
260
160
110
80
60
50
40
INVAC-1
(127.4kDa)
ΔUb-INVAC-1
(119kDa)
β-actin
(42kDa)
Exposure: "touch"
NT
Inverted
24h 18h 24h 48h 72h 96h
Exposure: 10 sec
NT
Inverted
24h 18h 24h 48h 72h 96h
Inverted
(130.2kDa)
Inverted
Degraded product
Exposure: 30 min
D
Inverted
Untreated
Ratio TERT/Actine
1.2
1.0
0.8
0.6
0.4
0.2
0.0
18h 24h 48h 72h 96h

FIGURE 24

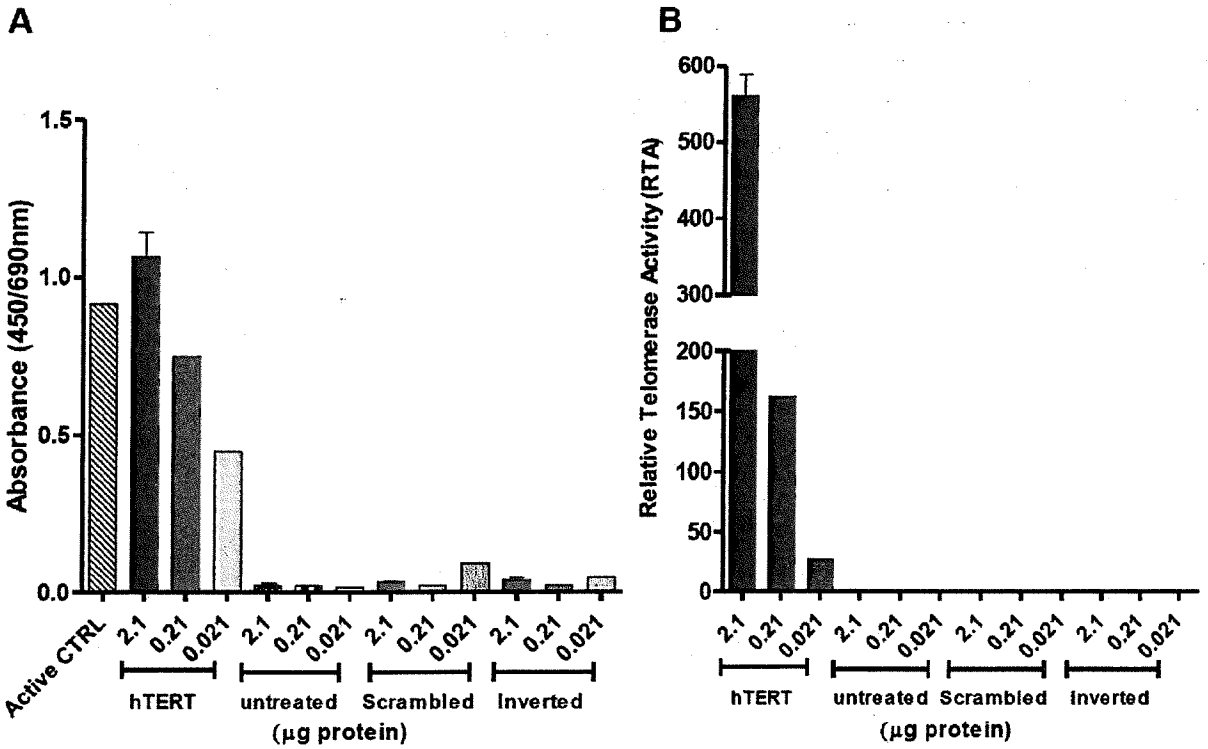
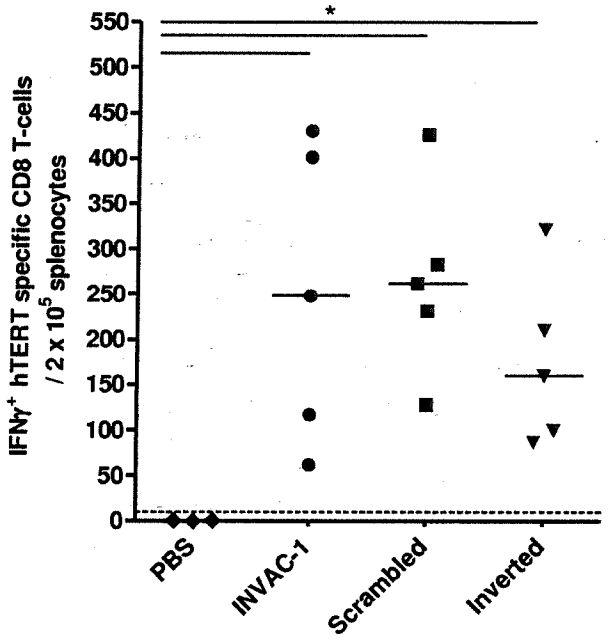
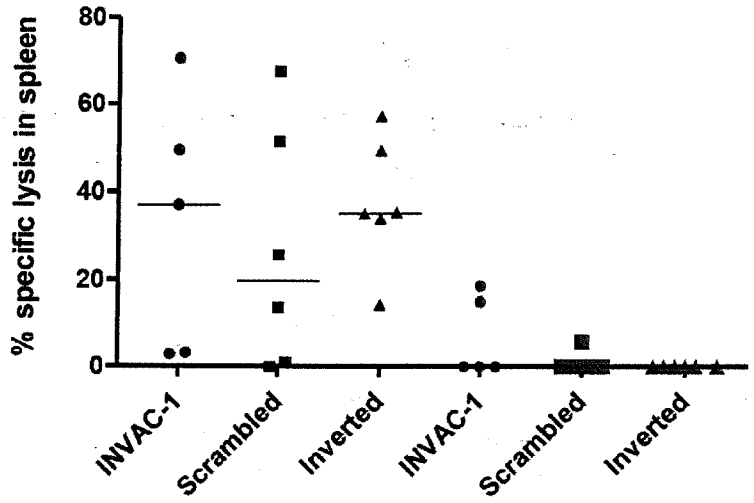

A
Absorbance (450/690nm)
1.5
1.0
0.5
0.0
Active CTRL
2.1
0.21
0.021
hTERT
untreated
Scrambled
Inverted
(µg protein)
B
Relative Telomerase Activity (RTA)
600
500
400
300
200
150
100
50
0
hTERT
untreated
Scrambled
Inverted
(µg protein)

FIGURE 25



n=5
Mann-Whitney test
** p. value < 0.05*

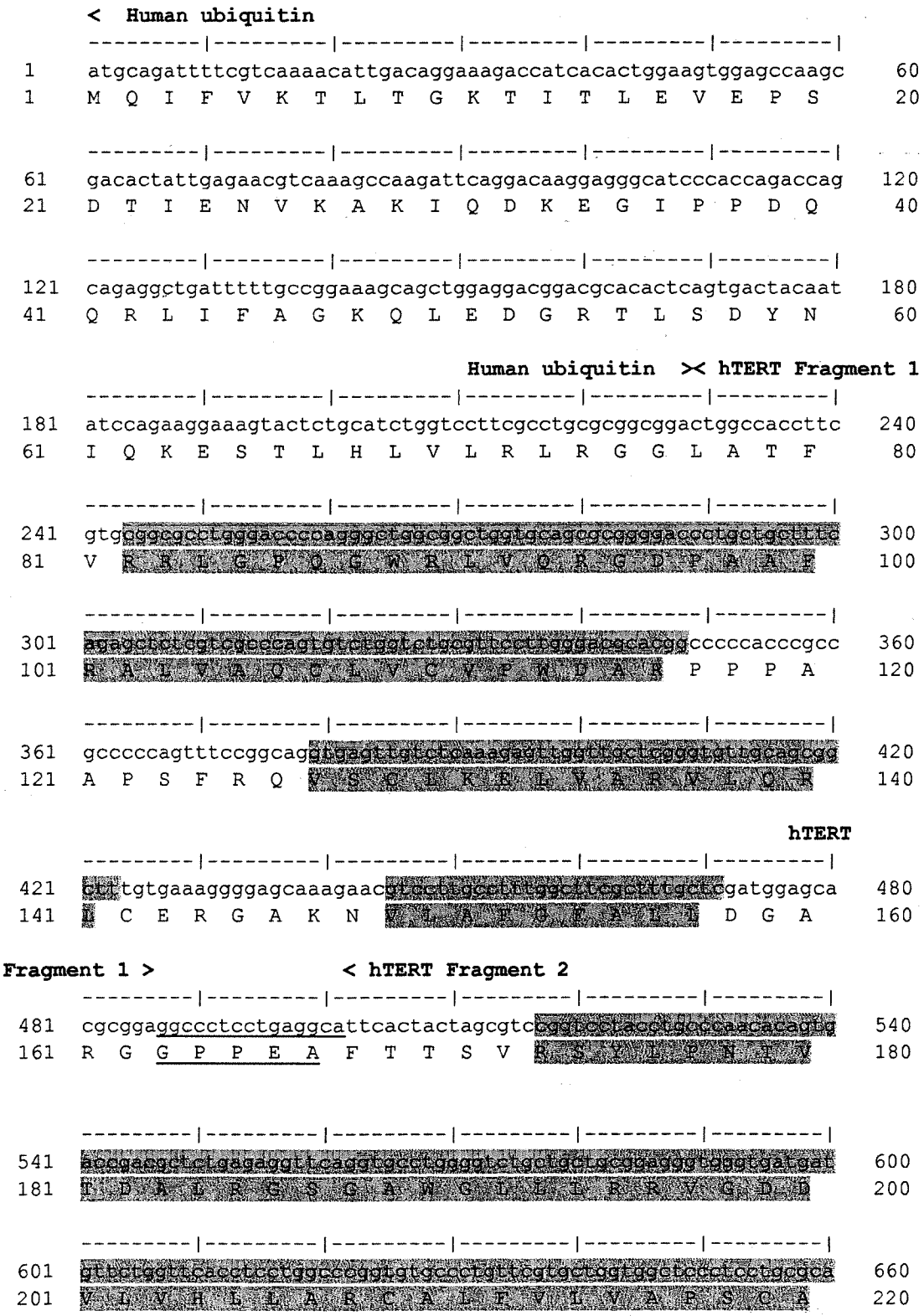
FIGURE 26

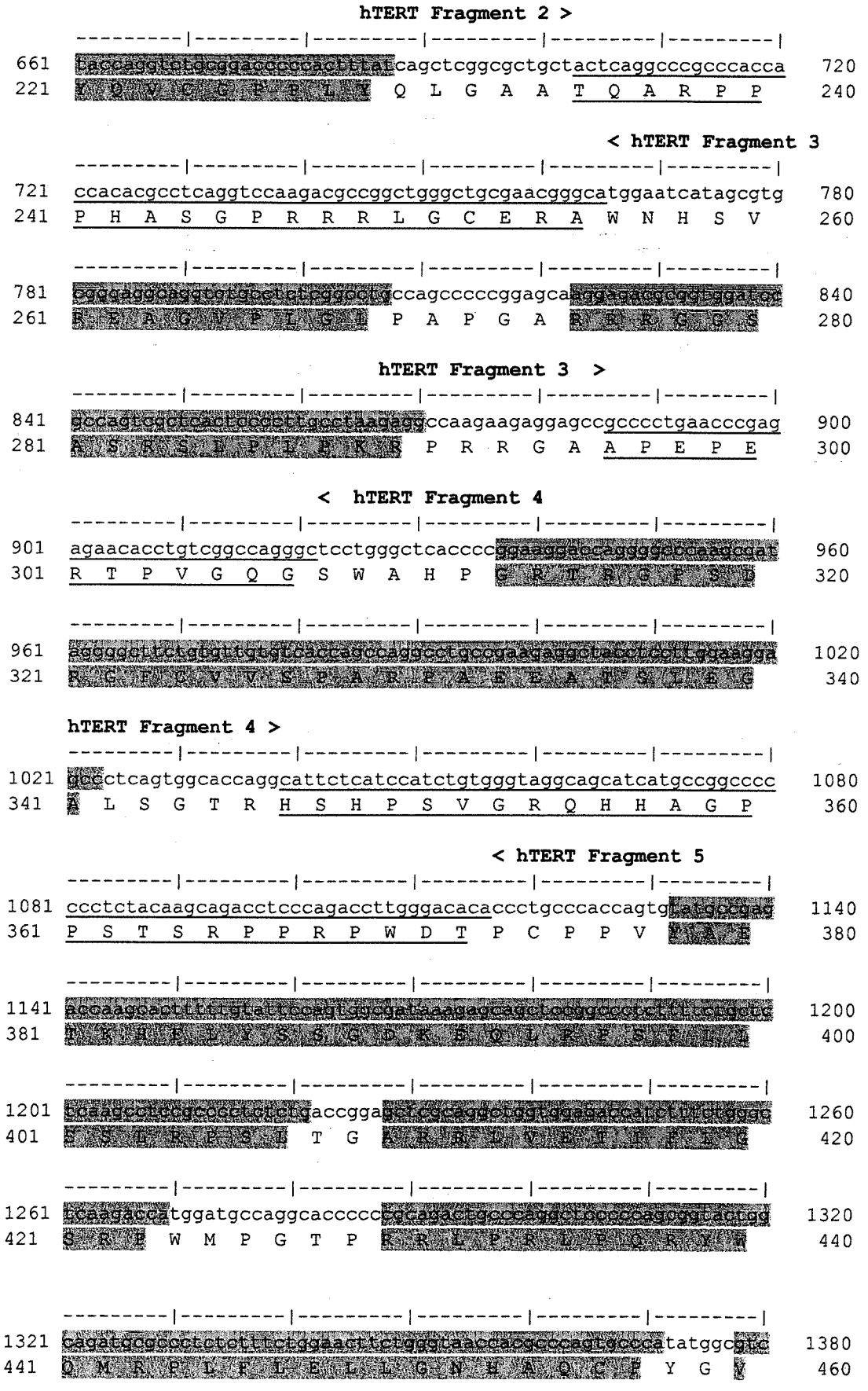


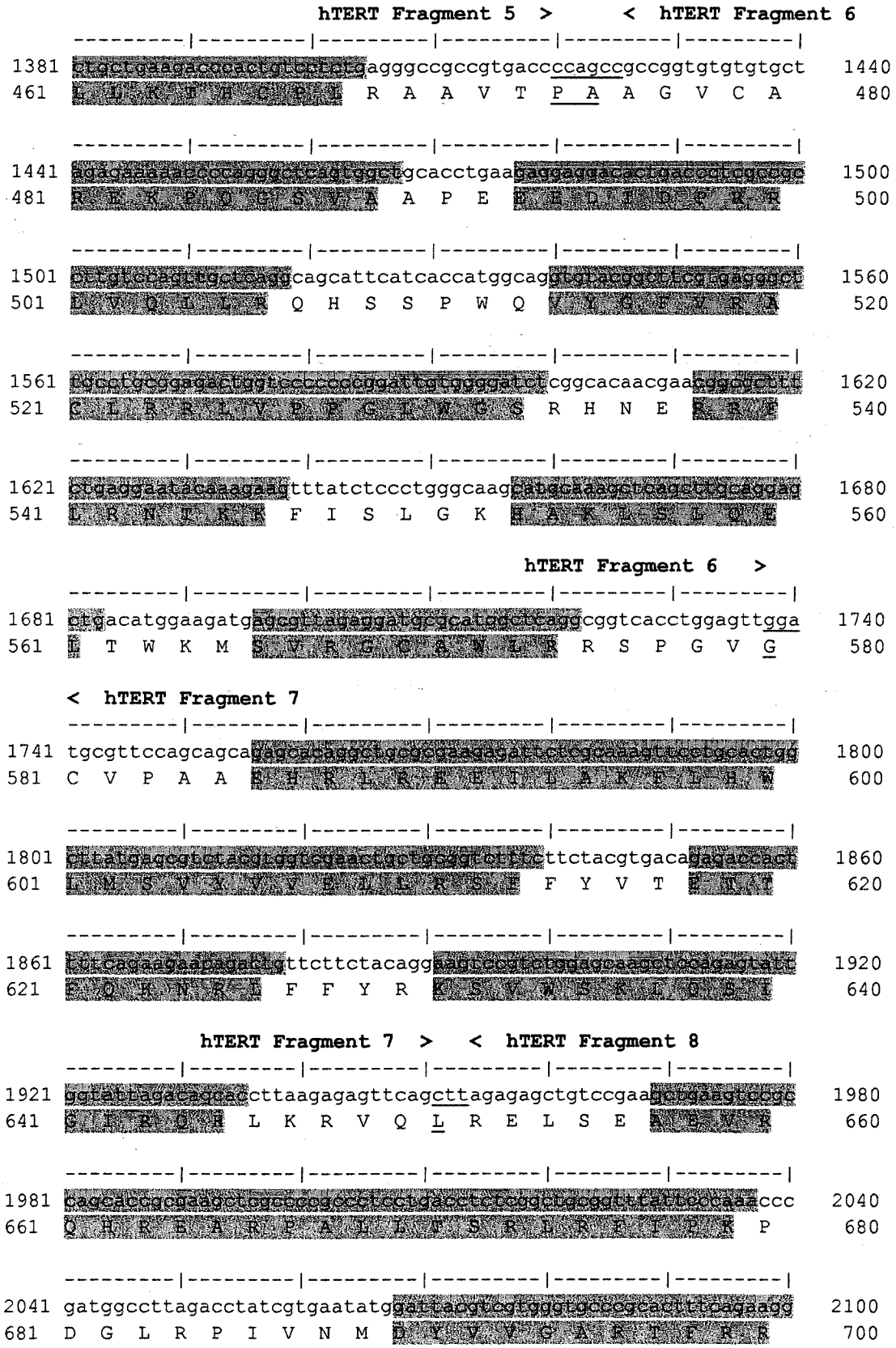
n=4-6
Kruskal-Wallis test
Dunn's correction

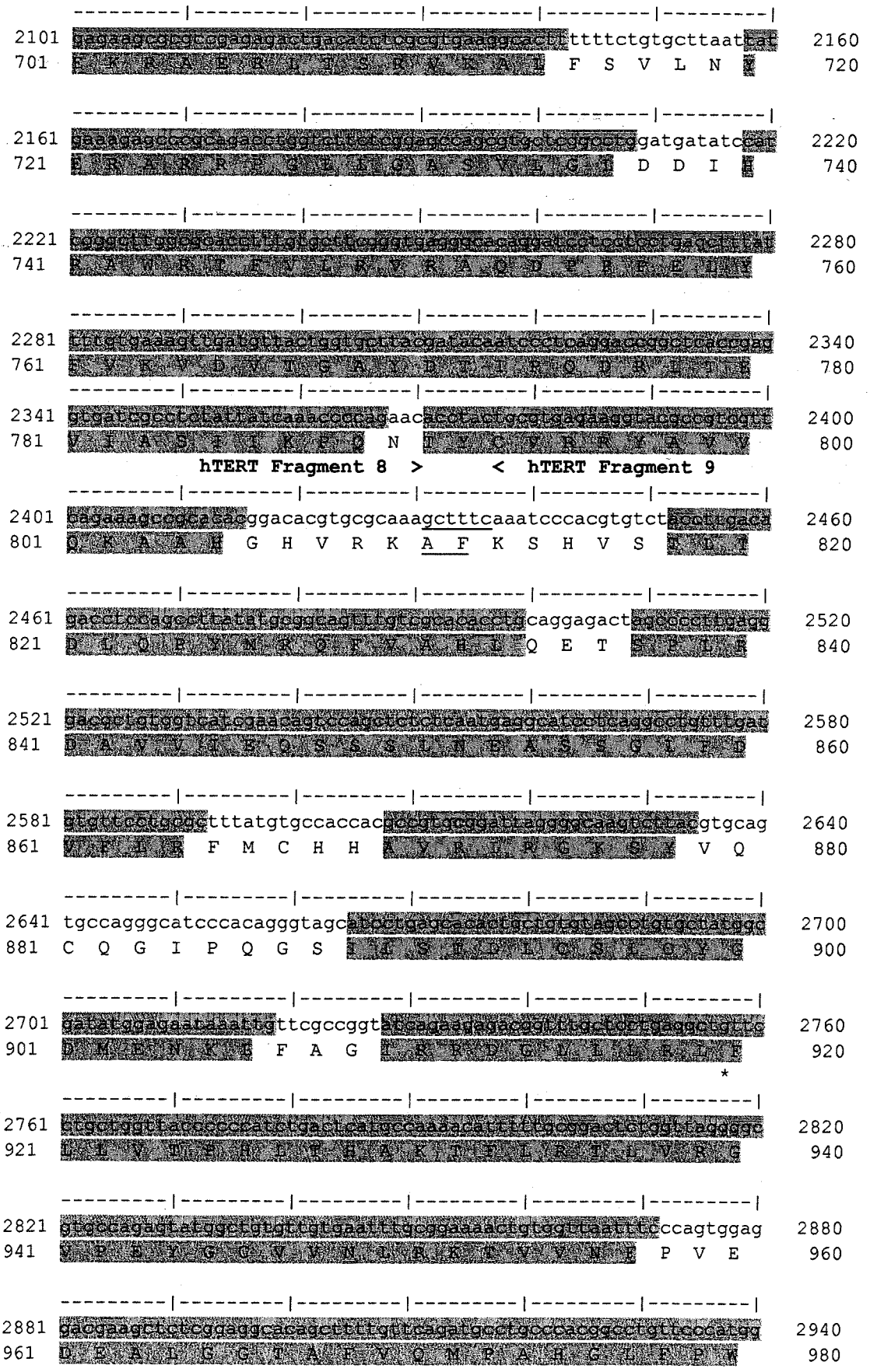
p351
p1123

Figure 27


< Human ubiquitin
Human ubiquitin >< hTERT Fragment 1
hTERT
Fragment 1 >
< hTERT Fragment 2


hTERT Fragment 2 >
661 taccaggtntgcggatgcccccacttlatcagctcggcgctgctactcaggcccgcccacca 720
221 Y Q V C G P P L Y Q L G A A T Q A R P P 240
< hTERT Fragment 3
721 ccacacgcctcaggtccaagacgccggctgggctgcgaacgggcatggaatcatagcgtg 780
241 P H A S G P R R R L G C E R A W N H S V 260
781 cgggaggcaggtgrgcctatrggcctgccagcccccggagcaggaggaccgcggtggatcc 840
261 R E A G V P L G L P A P G A R R R G G S 280
hTERT Fragment 3 >
841 gccagtcgctcactcccttgcctaagaggccaagaagaggagccgcccctgaacccgag 900
281 A S R S P P L P R S P R R G A A P E P E 300
< hTERT Fragment 4
901 agaacacctgtcggccagggctcctgggctcaccccggaaggaccaggggcccaagcgat 960
301 R T P V G Q G S W A H P G R T R G P S D 320
961 aggggcttctgtgttgtgtcaccagccaggcctgccgaagaggctacctccttggaaggga 1020
321 R G F C V V S P A R P A E E A T S L E G 340
hTERT Fragment 4 >
1021 gccctcagtggcaccaggcattctcatccatctgtgggtaggcagcatcatgccggcccc 1080
341 A L S G T R H S H P S V G R Q H H A G P 360
< hTERT Fragment 5
1081 ccctctacaagcagacctcccagaccttgggacacaccctgcccaccagtgtatgccgag 1140
361 P S T S R P P R P W D T P C P P V Y A E 380
1141 accaagcactttttgtatttccagtggcgatcaaagagcagctccggccctcttttctgctc 1200
381 T K H F L Y S S G D K E Q L R P S F L L 400
1201 tcaagcctccgcccctctctgaccggagctcgcaggctggtggaagccatcttttctgggc 1260
401 S S L R P S L T G A R R L V E T I F L G 420
1261 tcaagaccatggatgccaggcaccccccgcagactgcccaggctccccccagccgctagtgg 1320
421 S R P W M P G T P R R L P R L P Q R Y W 440
1321 cagatgcggcctctctttctggaacttctgggtaaccacgcccagtgcccatatggcgtc 1380
441 Q M R P L F L E L L G N H A Q C P Y G V 460


hTERT Fragment 5 >
< hTERT Fragment 6
hTERT Fragment 6 >
< hTERT Fragment 7
hTERT Fragment 7 >
< hTERT Fragment 8


hTERT Fragment 8 >
< hTERT Fragment 9

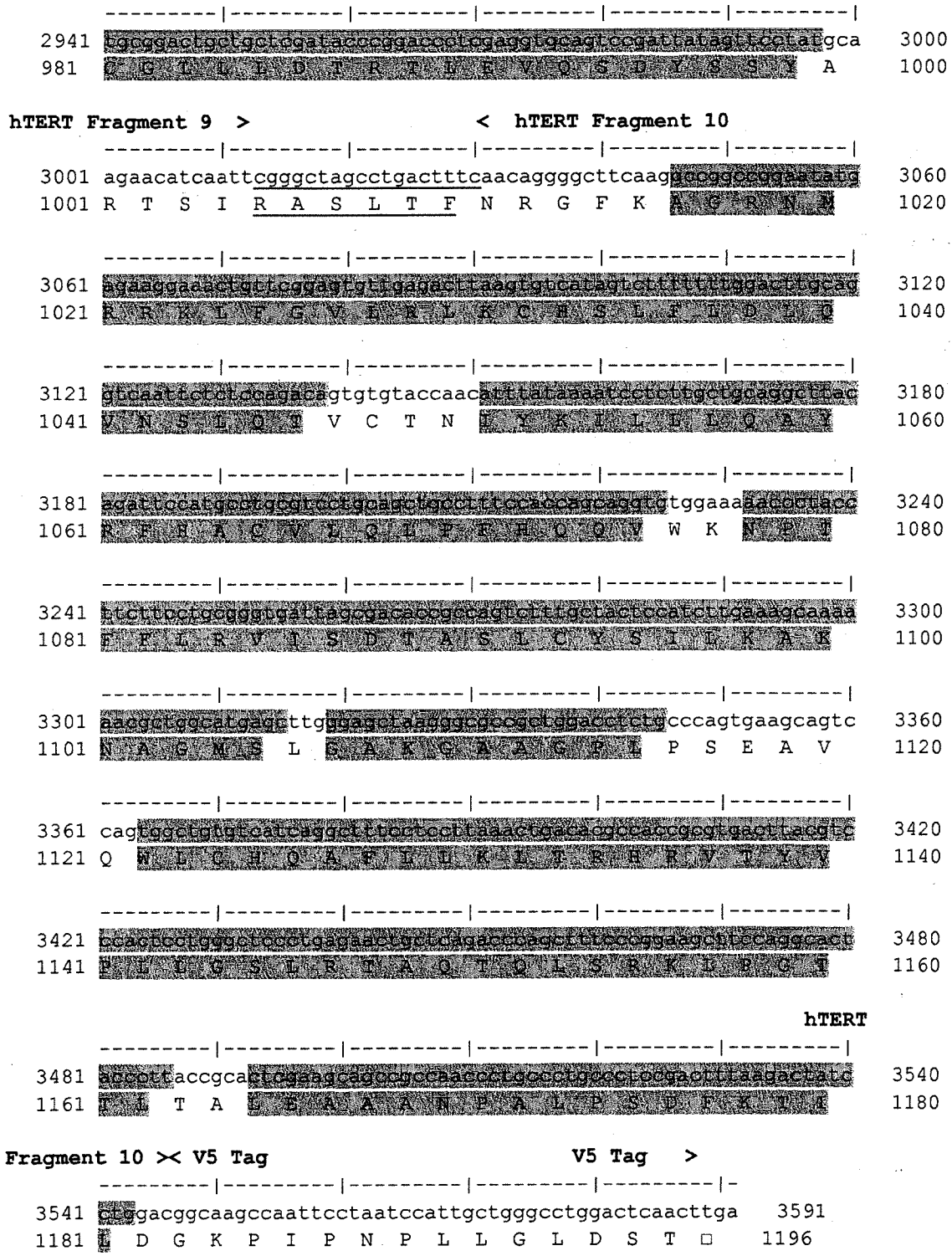

2941 tgcggactgctgctcgataccccgaccctcgaggtgcagtccgattatagttcctatgca 3000
981 C G T L L D T R T L E V Q S D Y S S Y A 1000
hTERT Fragment 9 > < hTERT Fragment 10
3001 agaacatcaattcgggctagcctgactttcaacaggggcttcaaggccggccggaatatg 3060
1001 R T S I R A S L T F N R G F K A G R N M 1020
3061 agaaggaaactgttcggagtgttgagacttaagtgtcatagtctttttttggacttgcag 3120
1021 R R K L F G V L R L K C H S L F L D L Q 1040
3121 gtcaattcctcttccagacagtgtgtaccaacatttataaaatcctcttgctgcaggcttac 3180
1041 V N S L Q T V C T N I Y K I L L L Q A Y 1060
3181 agattccatgcctgcgtcctgcaagctgccttccaccagcaggtgtggaaaaacccctacc 3240
1061 R F H N A C V L Q L P F H Q Q V W K N P T 1080
3241 ttcttcctgcgggtgattagcgacaccgccagtctttgctactccatcttgaaagcaaaa 3300
1081 F F L R V T S D T A S L C Y S I L K A K 1100
3301 aaggctggcatgagcttgggagctaaaggcgccgctggacctctgcccagtgaagcagtc 3360
1101 N A G M S L G A K G A A G P L P S E A V 1120
3361 cagtggctgtgtcatcaggctttcctccttaaacttgaccagccaccgcgtgaccttacgtc 3420
1121 Q W L C H Q A F L L K L T R H R V T Y V 1140
3421 ccactcctgggctccctgaggaactgctccagaccgagcttctccgggaagcttccaggcact 3480
1141 P L L G S L R T A Q T Q L S R K L P G T 1160
hTERT
3481 accgttaccgcactcgaagcagccgccaacccgtgccctgccttccgacttttaagactatc 3540
1161 T L T A L E A A A N P A L P S D F K T I 1180
Fragment 10 >< V5 Tag V5 Tag >
3541 ctggacggcaagccaattcctaatccattgctgggcctggactcaacttga 3591
1181 L D G K P I P N P L L G L D S T □ 1196

Figure 28

```
     < Human ubiquitin
     ---------|---------|---------|---------|---------|
   1 atgcagattttcgtcaaaacattgacaggaaagaccatcacactggaagt 50
   1 M  Q  I  F  V  K  T  L  T  G  K  T  I  T  L  E  V 17

     ---------|---------|---------|---------|---------|
  51 ggagccaagcgacactattgagaacgtcaaagccaagattcaggacaagg 100
  18  E  P  S  D  T  I  E  N  V  K  A  K  I  Q  D  K  E 34

     ---------|---------|---------|---------|---------|
 101 agggcatcccaccagaccagcagaggctgatttttgccggaaagcagctg 150
  35   G  I  P  P  D  Q  Q  R  L  I  F  A  G  K  Q  L  50

     ---------|---------|---------|---------|---------|
 151 gaggacggacgcacactcagtgactacaatatccagaaggaaagtactct 200
  51 E  D  G  R  T  L  S  D  Y  N  I  Q  K  E  S  T  L 67

                Human ubiquitin  >< G linker >< hTERT
     ---------|---------|---------|---------|---------|
 201 gcatctggtccttcgcctgcgcggcggaGGTGGAGGTGGAtgcgttccag 250
  68  H  L  V  L  R  L  R  G  G  G  G  G  G  C  V  P  A 84

     Fragment 7
     ---------|---------|---------|---------|---------|
 251 cagcagagcacaggctgcgcgaagagattctcgcaaagttcctgcactgg 300
  85   A  E  H  R  L  R  E  E  I  L  A  K  F  L  H  W   100

     ---------|---------|---------|---------|---------|
 301 cttatgagcgtctacgtggtcgaactgctgcggtctttcttctacgtgac 350
 101 L  M  S  V  Y  V  V  E  L  L  R  S  F  F  Y  V  T 117

     ---------|---------|---------|---------|---------|
 351 agagaccacttttcagaagaacagactgttcttctacaggaagtccgtct 400
 118  E  T  T  F  Q  K  N  R  L  F  F  Y  R  K  S  V  W 134

                                        hTERT Fragment 7 >
     ---------|---------|---------|---------|---------|
 401 ggagcaagctccagagtattggtattagacagcaccttaagagagttcag 450
 135   S  K  L  Q  S  I  G  I  R  Q  H  L  K  R  V  Q   150

     <    G linker    >< hTERT Fragment 2
     ---------|---------|---------|---------|---------|
 451 GGAGGTGGTGGAGGTGGAttcactactagcgtccggtcctacctgcccaa 500
 151 G  G  G  G  G  G  F  T  T  S  V  R  S  Y  L  P  N 167

     ---------|---------|---------|---------|---------|
 501 cacagtgaccgacgctctgagaggttcaggtgcctggggtctgctgctgc 550
 168  T  V  T  D  A  L  R  G  S  G  A  W  G  L  L  L  R 184

     ---------|---------|---------|---------|---------|
 551 ggagggtgggtgatgatgttctggttcacctcctggcccggtgtgccctg 600
 185   R  V  G  D  D  V  L  V  H  L  L  A  R  C  A  L   200
```

```
    ---------|---------|---------|---------|---------|
601 ttcgtgctggtggctccctcctgcgcataccaggtctgcggacccccact 650
201 F  V  L  V  A  P  S  C  A  Y  Q  V  C  G  P  P  L  217

     hTERT Fragment 2 ><    G linker    >< hTERT
    ---------|---------|---------|---------|---------|
651 ttatcagctcggcgctgctGGTGGAGGTGGTGGAGGTgccggtgtgtgtg 700
218  Y  Q  L  G  A  A  G  G  G  G  G  G  A  G  V  C  A 234

    Fragment 6
    ---------|---------|---------|---------|---------|
701 ctagagaaaaaccccagggctcagtggctgcacctgaagaggaggacact 750
235   R  E  K  P  Q  G  S  V  A  A  P  E  E  E  D  T   250

    ---------|---------|---------|---------|---------|
751 gaccctcgccgccttgtccagttgctcaggcagcattcatcaccatggca 800
251 D  P  R  R  L  V  Q  L  L  R  Q  H  S  S  P  W  Q  267

    ---------|---------|---------|---------|---------|
801 ggtgtacggcttcgtgagggcttgcctgcggagactggtccccccggat 850
268  V  Y  G  F  V  R  A  C  L  R  R  L  V  P  P  G  L 284

    ---------|---------|---------|---------|---------|
851 tgtggggatctcggcacaacgaacggcgctttctgaggaatacaaagaag 900
285   W  G  S  R  H  N  E  R  R  F  L  R  N  T  K  K   300

    ---------|---------|---------|---------|---------|
901 tttatctccctgggcaagcatgcaaagctcagcttgcaggagctgacatg 950
301 F  I  S  L  G  K  H  A  K  L  S  L  Q  E  L  T  W  317

                                        hTERT Fragment 6 ><
    ---------|---------|---------|---------|---------|
951 gaagatgagcgttagaggatgcgcatggctcaggcggtcacctggagttG 1000
318  K  M  S  V  R  G  C  A  W  L  R  R  S  P  G  V  G 334

   G linker          >< hTERT Fragment 4
    ---------|---------|---------|---------|---------|
1001 GAGGTGGAGGTGGAGGAtcctgggctcaccccggaaggaccaggggccca 1050
335   G  G  G  G  G  S  W  A  H  P  G  R  T  R  G  P   350

    ---------|---------|---------|---------|---------|
1051 agcgataggggcttctgtgttgtgtcaccagccaggcctgccgaagaggc 1100
351 S  D  R  G  F  C  V  V  S  P  A  R  P  A  E  E  A  367

              hTERT Fragment 4     ><    G linker
    ---------|---------|---------|---------|---------|
1101 tacctccttggaaggagccctcagtggcaccaggGGTGGTGGAGGTGGAG 1150
368  T  S  L  E  G  A  L  S  G  T  R  G  G  G  G  G  G 384

     ><   hTERT Fragment 9
    ---------|---------|---------|---------|---------|
1151 GAaaatcccacgtgtctaccttgacagacctccagccttatatgcggcag 1200
385   K  S  H  V  S  T  L  T  D  L  Q  P  Y  M  R  Q   400
```

```
     ---------|---------|---------|---------|---------|
1201 tttgtcgcacacctgcaggagactagccccttgagggacgctgtggtcat 1250
 401 F  V  A  H  L  Q  E  T  S  P  L  R  D  A  V  V  I  417

     ---------|---------|---------|---------|---------|
1251 cgaacagtccagctctctcaatgaggcatcctcaggcctgtttgatgtgt 1300
 418  E  Q  S  S  S  L  N  E  A  S  S  G  L  F  D  V  F 434

     ---------|---------|---------|---------|---------|
1301 tcctgcgctttatgtgccaccacgccgtgcggattaggggcaagtcttac 1350
 435   L  R  F  M  C  H  H  A  V  R  I  R  G  K  S  Y   450

     ---------|---------|---------|---------|---------|
1351 gtgcagtgccagggcatcccacagggtagcatcctgagcacactgctgtg 1400
 451 V  Q  C  Q  G  I  P  Q  G  S  I  L  S  T  L  L  C  467

     ---------|---------|---------|---------|---------|
1401 tagcctgtgctatggcgatatggagaataaattgttcgccggtatcagaa 1450
 468  S  L  C  Y  G  D  M  E  N  K  L  F  A  G  I  R  R 484

     ---------|---------|---------|---------|---------|
1451 gagacggtttgctcctgaggctgttcctgctggttacccccatctgact 1500
 485   D  G  L  L  L  R  L  F  L  L  V  T  P  H  L  T   500
                          *
     ---------|---------|---------|---------|---------|
1501 catgccaaaacatttttgcggactctggttaggggcgtgccagagtatgg 1550
 501 H  A  K  T  F  L  R  T  L  V  R  G  V  P  E  Y  G  517

     ---------|---------|---------|---------|---------|
1551 ctgtgttgtgaatttgcggaaaactgtggttaatttcccagtggaggacg 1600
 518  C  V  V  N  L  R  K  T  V  V  N  F  P  V  E  D  E 534

     ---------|---------|---------|---------|---------|
1601 aagctctcggaggcacagcttttgttcagatgcctgcccacggcctgttc 1650
 535   A  L  G  G  T  A  F  V  Q  M  P  A  H  G  L  F   550

     ---------|---------|---------|---------|---------|
1651 ccatggtgcggactgctgctcgatacccggaccctcgaggtgcagtccga 1700
 551 P  W  C  G  L  L  L  D  T  R  T  L  E  V  Q  S  D  567
            hTERT Fragment 9   ><    G linker    >< hTERT
     ---------|---------|---------|---------|---------|
1701 ttatagttcctatgcaagaacatcaattGGAGGAGGTGGTGGAGGTtgga 1750
 568  Y  S  S  Y  A  R  T  S  I  G  G  G  G  G  G  W  N 584
     Fragment 3
     ---------|---------|---------|---------|---------|
1751 atcatagcgtgcgggaggcaggtgtgcctctcggcctgccagcccccgga 1800
 585   H  S  V  R  E  A  G  V  P  L  G  L  P  A  P  G   600

     ---------|---------|---------|---------|---------|
1801 gcaaggagacgcggtggatccgccagtcgctcactccccttgcctaagag 1850
 601 A  R  R  R  G  G  S  A  S  R  S  L  P  L  P  K  R  617
```

hTERT Fragment 3 >< G linker >< hTERT Fragment 1

```
---------|---------|---------|---------|---------|
1851 gccaagaagaggagccGGTGGAGGAGGTGGTGGActggccaccttcgtgc 1900
 618  P  R  R  G  A  G  G  G  G  G  G  L  A  T  F  V  R 634

---------|---------|---------|---------|---------|
1901 ggcgcctgggaccccagggctggcggctggtgcagcgcggggaccctgct 1950
 635   R  L  G  P  Q  G  W  R  L  V  Q  R  G  D  P  A   650

---------|---------|---------|---------|---------|
1951 gctttcagagctctcgtcgcccagtgtctggtctgcgttccttgggacgc 2000
 651 A  F  R  A  L  V  A  Q  C  L  V  C  V  P  W  D  A 667

---------|---------|---------|---------|---------|
2001 acggcccccacccgccgcccccagtttccggcaggtgagttgtctcaaag 2050
 668  R  P  P  P  A  A  P  S  F  R  Q  V  S  C  L  K  E 684

---------|---------|---------|---------|---------|
2051 agttggttgctcgggtgttgcagcggctttgtgaaaggggagcaaagaac 2100
 685   L  V  A  R  V  L  Q  R  L  C  E  R  G  A  K  N   700
```

hTERT Fragment 1 >< G linker

```
---------|---------|---------|---------|---------|
2101 gtccttgcctttggcttcgctttgctcgatggagcacgcggaGGAGGTGG 2150
 701 V  L  A  F  G  F  A  L  L  D  G  A  R  G  G  G  G 717
```

>< hTERT Fragment 8

```
---------|---------|---------|---------|---------|
2151 TGGAGGTGGAagagagctgtccgaagctgaagtccgccagcaccgcgaag 2200
 718  G  G  G  R  E  L  S  E  A  E  V  R  Q  H  R  E  A 734

---------|---------|---------|---------|---------|
2201 ctcgccccgccctcctgacctctcggctgcggtttattcccaaacccgat 2250
 735   R  P  A  L  L  T  S  R  L  R  F  I  P  K  P  D   750

---------|---------|---------|---------|---------|
2251 ggccttagacctatcgtgaatatggattacgtcgtgggtgcccgcacttt 2300
 751 G  L  R  P  I  V  N  M  D  Y  V  V  G  A  R  T  F 767

---------|---------|---------|---------|---------|
2301 cagaagggagaagcgcgccgagagactgacatctcgcgtgaaggcacttt 2350
 768  R  R  E  K  R  A  E  R  L  T  S  R  V  K  A  L  F 784

---------|---------|---------|---------|---------|
2351 tttctgtgcttaattatgaaagagcccgcagacctggtcttctcggagcc 2400
 785   S  V  L  N  Y  E  R  A  R  R  P  G  L  L  G  A   800

---------|---------|---------|---------|---------|
2401 agcgtgctcggcctggatgatatccatcgggcttggcgcacctttgtgct 2450
 801 S  V  L  G  L  D  D  I  H  R  A  W  R  T  F  V  L 817
```

```
         ---------|---------|---------|---------|---------|
2451 tcgggtgagggcacaggatcctcctcctgagctttatttttgtgaaagttg 2500
 818  R  V  R  A  Q  D  P  P  P  E  L  Y  F  V  K  V  D 834

         ---------|---------|---------|---------|---------|
2501 atgttactggtgcttacgatacaatccctcaggaccggctcaccgaggtg 2550
 835   V  T  G  A  Y  D  T  I  P  Q  D  R  L  T  E  V  850

         ---------|---------|---------|---------|---------|
2551 atcgcctctattatcaaaccccagaacacctactgcgtgagaaggtacgc 2600
 851 I  A  S  I  I  K  P  Q  N  T  Y  C  V  R  R  Y  A 867

                              hTERT Fragment 8  ><  G linker
         ---------|---------|---------|---------|---------|
2601 cgtcgttcagaaagccgcacacggacacgtgcgcaaaGGTGGAGGAGGTG 2650
 868  V  V  Q  K  A  A  H  G  H  V  R  K  G  G  G  G  G 884

            ><   hTERT Fragment 10
         ---------|---------|---------|---------|---------|
2651 GTGGAaacagggggcttcaaggccggccggaatatgagaaggaaactgttc 2700
 885   G  N  R  G  F  K  A  G  R  N  M  R  R  K  L  F   900

         ---------|---------|---------|---------|---------|
2701 ggagtgttgagacttaagtgtcatagtctttttttggacttgcaggtcaa 2750
 901 G  V  L  R  L  K  C  H  S  L  F  L  D  L  Q  V  N 917

         ---------|---------|---------|---------|---------|
2751 ttctctccagacagtgtgtaccaacatttataaaatcctcttgctgcagg 2800
 918  S  L  Q  T  V  C  T  N  I  Y  K  I  L  L  L  Q  A 934

         ---------|---------|---------|---------|---------|
2801 cttacagattccatgcctgcgtcctgcagctgcctttccaccagcaggtg 2850
 935   Y  R  F  H  A  C  V  L  Q  L  P  F  H  Q  Q  V   950

         ---------|---------|---------|---------|---------|
2851 tggaaaaaccctaccttcttcctgcgggtgattagcgacaccgccagtct 2900
 951 W  K  N  P  T  F  F  L  R  V  I  S  D  T  A  S  L 967

         ---------|---------|---------|---------|---------|
2901 ttgctactccatcttgaaagcaaaaaacgctggcatgagcttgggagcta 2950
 968  C  Y  S  I  L  K  A  K  N  A  G  M  S  L  G  A  K 984

         ---------|---------|---------|---------|---------|
2951 agggcgccgctggacctctgcccagtgaagcagtccagtggctgtgtcat 3000
 985   G  A  A  G  P  L  P  S  E  A  V  Q  W  L  C  H   1000

         ---------|---------|---------|---------|---------|
3001 caggctttcctccttaaactgacacgccaccgcgtgacttacgtcccact 3050
1001 Q  A  F  L  L  K  L  T  R  H  R  V  T  Y  V  P  L 1017

         ---------|---------|---------|---------|---------|
3051 cctgggctccctgagaactgctcagacccagctttcccggaaacttccag 3100
1018  L  G  S  L  R  T  A  Q  T  Q  L  S  R  K  L  P  G 1034
```

```
     ---------|---------|---------|---------|---------|
3101 gcactacccttaccgcactcgaagcagccgccaaccctgccctgccctcc 3150
1035   T  T  L  T  A  L  E  A  A  A  N  P  A  L  P  S   1050

      hTERT Fragment 10  ><    G linker    ><  hTERT
     ---------|---------|---------|---------|---------|
3151 gactttaagactatcctggacGGAGGTGGAGGTGGAGGTcccctgcccacc 3200
1051 D  F  K  T  I  L  D  G  G  G  G  G  G  P  C  P  P  1067

     Fragment 5
     ---------|---------|---------|---------|---------|
3201 agtgtatgccgagaccaagcacttttgtattccagtggcgataaagagc 3250
1068  V  Y  A  E  T  K  H  F  L  Y  S  S  G  D  K  E  Q 1084

     ---------|---------|---------|---------|---------|
3251 agctccggccctcttttctgctctcaagcctccgcccctctctgaccgga 3300
1085   L  R  P  S  F  L  L  S  S  L  R  P  S  L  T  G   1100

     ---------|---------|---------|---------|---------|
3301 gctcgcaggctggtggagaccatctttctgggctcaagaccatggatgcc 3350
1101 A  R  R  L  V  E  T  I  F  L  G  S  R  P  W  M  P  1117

     ---------|---------|---------|---------|---------|
3351 aggcacccccgcagactgcccaggctcccccagcggtactggcagatgc 3400
1118  G  T  P  R  R  L  P  R  L  P  Q  R  Y  W  Q  M  R 1134

     ---------|---------|---------|---------|---------|
3401 gccctctctttctggaacttctgggtaaccacgcccagtgcccatatggc 3450
1135   P  L  F  L  E  L  L  G  N  H  A  Q  C  P  Y  G   1150

                              hTERT fragment 5   ><  G linker
     ---------|---------|---------|---------|---------|
3451 gtcctgctgaagacccactgtcctctgagggccgccgtgaccGGAGGTGG 3500
1151 V  L  L  K  T  H  C  P  L  R  A  A  V  T  G  G  G  1167

               ><  V5 Tag
     ---------|---------|---------|---------|---------|
3501 TGGAGGAGGTggcaagccaattcctaatccattgctgggcctggactcaa 3550
1168  G  G  G  G  K  P  I  P  N  P  L  L  G  L  D  S  T 1184

V5 Tag ><
     -----
3551 cttga 3555
       □
```

Figure 29

< Human ubiquitin

```
         ---------|---------|---------|---------|---------|
       1 atgcagattttcgtcaaaacattgacaggaaagaccatcacactggaagt 50
       1 M  Q  I  F  V  K  T  L  T  G  K  T  I  T  L  E  V 17

         ---------|---------|---------|---------|---------|
      51 ggagccaagcgacactattgagaacgtcaaagccaagattcaggacaagg 100
      18  E  P  S  D  T  I  E  N  V  K  A  K  I  Q  D  K  E 34

         ---------|---------|---------|---------|---------|
     101 agggcatcccaccagaccagcagaggctgatttttgccggaaagcagctg 150
      35   G  I  P  P  D  Q  Q  R  L  I  F  A  G  K  Q  L  50

         ---------|---------|---------|---------|---------|
     151 gaggacggacgcacactcagtgactacaatatccagaaggaaagtactct 200
      51 E  D  G  R  T  L  S  D  Y  N  I  Q  K  E  S  T  L 67
```

Human ubiquitin >< G linker >< hTERT

```
         ---------|---------|---------|---------|---------|
     201 gcatctggtccttcgcctgcgcggc**gga**GGTGGAGGTGGA**aac**aggggct 250
      68  H  L  V  L  R  L  R  G  G  G  G  G  G  N  R  G  F 84
```

Fragment 10

```
         ---------|---------|---------|---------|---------|
     251 tcaaggccggccggaatatgagaaggaaactgttcggagtgttgagactt 300
      85   K  A  G  R  N  M  R  R  K  L  F  G  V  L  R  L  100

         ---------|---------|---------|---------|---------|
     301 aagtgtcatagtctttttttggacttgcaggtcaattctctccagacagt 350
     101 K  C  H  S  L  F  L  D  L  Q  V  N  S  L  Q  T  V 117

         ---------|---------|---------|---------|---------|
     351 gtgtaccaacatttataaaatcctcttgctgcaggcttacagattccatg 400
     118  C  T  N  I  Y  K  I  L  L  L  Q  A  Y  R  F  H  A 134

         ---------|---------|---------|---------|---------|
     401 cctgcgtcctgcagctgcctttccaccagcaggtgtggaaaaaccctacc 450
     135   C  V  L  Q  L  P  F  H  Q  Q  V  W  K  N  P  T  150

         ---------|---------|---------|---------|---------|
     451 ttcttcctgcgggtgattagcgacaccgccagtctttgctactccatctt 500
     151 F  F  L  R  V  I  S  D  T  A  S  L  C  Y  S  I  L 167

         ---------|---------|---------|---------|---------|
     501 gaaagcaaaaaacgctggcatgagcttgggagctaagggcgccgctggac 550
     168  K  A  K  N  A  G  M  S  L  G  A  K  G  A  A  G  P 184

         ---------|---------|---------|---------|---------|
     551 ctctgcccagtgaagcagtccagtggctgtgtcatcaggctttcctcctt 600
     185   L  P  S  E  A  V  Q  W  L  C  H  Q  A  F  L  L  200
```

```
         ---------|---------|---------|---------|---------|
601 aaactgacacgccaccgcgtgacttacgtcccactcctgggctccctgag 650
201 K  L  T  R  H  R  V  T  Y  V  P  L  L  G  S  L  R  217

         ---------|---------|---------|---------|---------|
651 aactgctcagacccagctttcccggaaacttccaggcactacccttaccg 700
218  T  A  Q  T  Q  L  S  R  K  L  P  G  T  T  L  T  A 234
                                                    hTERT
         ---------|---------|---------|---------|---------|
701 cactcgaagcagccgccaaccctgccctgccctccgactttaagactatc 750
235   L  E  A  A  A  N  P  A  L  P  S  D  F  K  T  I   250
```

Fragment 10 >< G linker >< hTERT Fragment 9

```
         ---------|---------|---------|---------|---------|
751 ctg**gac**GGAGGTGGTGGAGGTGGA**aaa**tcccacgtgtctaccttgacaga 800
251 L  D  G  G  G  G  G  G  K  S  H  V  S  T  L  T  D  267

         ---------|---------|---------|---------|---------|
801 cctccagccttatatgcggcagtttgtcgcacacctgcaggagactagcc 850
268  L  Q  P  Y  M  R  Q  F  V  A  H  L  Q  E  T  S  P 284

         ---------|---------|---------|---------|---------|
851 ccttgagggacgctgtggtcatcgaacagtccagctctctcaatgaggca 900
285   L  R  D  A  V  V  I  E  Q  S  S  S  L  N  E  A   300

         ---------|---------|---------|---------|---------|
901 tcctcaggcctgtttgatgtgttcctgcgctttatgtgccaccacgccgt 950
301 S  S  G  L  F  D  V  F  L  R  F  M  C  H  H  A  V  317

         ---------|---------|---------|---------|---------|
951 gcggattaggggcaagtcttacgtgcagtgccagggcatcccacagggta 1000
318  R  I  R  G  K  S  Y  V  Q  C  Q  G  I  P  Q  G  S 334

         ---------|---------|---------|---------|---------|
1001 gcatcctgagcacactgctgtgtagcctgtgctatggcgatatggagaat 1050
335   I  L  S  T  L  L  C  S  L  C  Y  G  D  M  E  N   350

         ---------|---------|---------|---------|---------|
1051 aaattgttcgccggtatcagaagagacggtttgctcctgaggctgttcct 1100
351 K  L  F  A  G  I  R  R  D  G  L  L  L  R  L  F  L  367
                                                  *
         ---------|---------|---------|---------|---------|
1101 gctggttacccccccatctgactcatgccaaaacatttttgcggactctgg 1150
368  L  V  T  P  H  L  T  H  A  K  T  F  L  R  T  L  V 384

         ---------|---------|---------|---------|---------|
1151 ttaggggcgtgccagagtatggctgtgttgtgaatttgcggaaaactgtg 1200
385   R  G  V  P  E  Y  G  C  V  V  N  L  R  K  T  V   400

         ---------|---------|---------|---------|---------|
1201 gttaatttcccagtggaggacgaagctctcggaggcacagcttttgttca 1250
401 V  N  F  P  V  E  D  E  A  L  G  G  T  A  F  V  Q  417
```

```
         ---------|---------|---------|---------|---------|
1251 gatgcctgcccacggcctgttcccatggtgcggactgctgctcgataccc 1300
 418  M  P  A  H  G  L  F  P  W  C  G  L  L  L  D  T  R 434
                                    hTERT Fragment 9  >
         ---------|---------|---------|---------|---------|
1301 ggaccctcgaggtgcagtccgattatagttcctatgcaagaacatcaatt 1350
 435   T  L  E  V  Q  S  D  Y  S  S  Y  A  R  T  S  I   450
      <    G linker    ><  hTERT Fragment 8
         ---------|---------|---------|---------|---------|
1351 GGTGGAGGTGGTGGAGGTagagagctgtccgaagctgaagtccgccagca 1400
 451 G  G  G  G  G  G  R  E  L  S  E  A  E  V  R  Q  H  467

         ---------|---------|---------|---------|---------|
1401 ccgcgaagctcgccccgccctcctgacctctcggctgcggtttattccca 1450
 468  R  E  A  R  P  A  L  L  T  S  R  L  R  F  I  P  K 484

         ---------|---------|---------|---------|---------|
1451 aacccgatggccttagacctatcgtgaatatggattacgtcgtgggtgcc 1500
 485   P  D  G  L  R  P  I  V  N  M  D  Y  V  V  G  A   500

         ---------|---------|---------|---------|---------|
1501 cgcactttcagaagggagaagcgcgccgagagactgacatctcgcgtgaa 1550
 501 R  T  F  R  R  E  K  R  A  E  R  L  T  S  R  V  K  517

         ---------|---------|---------|---------|---------|
1551 ggcacttttttctgtgcttaattatgaaagagcccgcagacctggtcttc 1600
 518  A  L  F  S  V  L  N  Y  E  R  A  R  R  P  G  L  L 534

         ---------|---------|---------|---------|---------|
1601 tcggagccagcgtgctcggcctggatgatatccatcgggcttggcgcacc 1650
 535   G  A  S  V  L  G  L  D  D  I  H  R  A  W  R  T   550

         ---------|---------|---------|---------|---------|
1651 tttgtgcttcgggtgagggcacaggatcctcctcctgagctttatttttgt 1700
 551 F  V  L  R  V  R  A  Q  D  P  P  P  E  L  Y  F  V  567

         ---------|---------|---------|---------|---------|
1701 gaaagttgatgttactggtgcttacgatacaatccctcaggaccggctca 1750
 568  K  V  D  V  T  G  A  Y  D  T  I  P  Q  D  R  L  T 584

         ---------|---------|---------|---------|---------|
1751 ccgaggtgatcgcctctattatcaaaccccagaacacctactgcgtgaga 1800
 585   E  V  I  A  S  I  I  K  P  Q  N  T  Y  C  V  R   600

                                  hTERT Fragment 8   >< G
         ---------|---------|---------|---------|---------|
1801 aggtacgccgtcgttcagaaagccgcacacggacacgtgcgcaaaGGAGG 1850
 601 R  Y  A  V  V  Q  K  A  A  H  G  H  V  R  K  G  G  617

       linker    >< hTERT Fragment 7
         ---------|---------|---------|---------|---------|
1851 TGGAGGTGGAGGAtgcgttccagcagcagagcacaggctgcgcgaagaga 1900
 618  G  G  G  G  C  V  P  A  A  E  H  R  L  R  E  E  I 634
```

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         ---------|---------|---------|---------|---------|
    1901 ttctcgcaaagttcctgcactggcttatgagcgtctacgtggtcgaactg 1950
     635   L  A  K  F  L  H  W  L  M  S  V  Y  V  V  E  L   650

         ---------|---------|---------|---------|---------|
    1951 ctgcggtctttcttctacgtgacagagaccacttttcagaagaacagact 2000
     651 L  R  S  F  F  Y  V  T  E  T  T  F  Q  K  N  R  L  667

         ---------|---------|---------|---------|---------|
    2001 gttcttctacaggaagtccgtctggagcaagctccagagtattggtatta 2050
     668  F  F  Y  R  K  S  V  W  S  K  L  Q  S  I  G  I  R 684

              hTERT Fragment 7 ><    G linker    >< hTERT
         ---------|---------|---------|---------|---------|
    2051 gacagcaccttaagagagttcagGGTGGTGGAGGTGGAGGAgccggtgtg 2100
     685   Q  H  L  K  R  V  Q  G  G  G  G  G  G  A  G  V   700

         Fragment 6
         ---------|---------|---------|---------|---------|
    2101 tgtgctagagaaaaaccccagggctcagtggctgcacctgaagaggagga 2150
     701 C  A  R  E  K  P  Q  G  S  V  A  A  P  E  E  E  D  717

         ---------|---------|---------|---------|---------|
    2151 cactgaccctcgccgccttgtccagttgctcaggcagcattcatcaccat 2200
     718  T  D  P  R  R  L  V  Q  L  L  R  Q  H  S  S  P  W 734

         ---------|---------|---------|---------|---------|
    2201 ggcaggtgtacggcttcgtgagggcttgcctgcggagactggtcccccc 2250
     735   Q  V  Y  G  F  V  R  A  C  L  R  R  L  V  P  P   750

         ---------|---------|---------|---------|---------|
    2251 ggattgtggggatctcggcacaacgaacggcgctttctgaggaatacaaa 2300
     751 G  L  W  G  S  R  H  N  E  R  R  F  L  R  N  T  K  767

         ---------|---------|---------|---------|---------|
    2301 gaagtttatctccctgggcaagcatgcaaagctcagcttgcaggagctga 2350
     768  K  F  I  S  L  G  K  H  A  K  L  S  L  Q  E  L  T 784

                                                    hTERT
         ---------|---------|---------|---------|---------|
    2351 catggaagatgagcgttagaggatgcgcatggctcaggcggtcacctgga 2400
     785   W  K  M  S  V  R  G  C  A  W  L  R  R  S  P  G   800

Fragment 6 ><    G linker    >< hTERT Fragment 5
         ---------|---------|---------|---------|---------|
    2401 gttGGAGGAGGTGGTGGAGGTcccctgcccaccagtgtatgccgagaccaa 2450
     801 V  G  G  G  G  G  G  P  C  P  P  V  Y  A  E  T  K  817

         ---------|---------|---------|---------|---------|
    2451 gcacttttgtattccagtggcgataaagagcagctccggccctcttttc 2500
     818  H  F  L  Y  S  S  G  D  K  E  Q  L  R  P  S  F  L 834
```

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         ---------|---------|---------|---------|---------|
2501 tgctctcaagcctccgcccctctctgaccggagctcgcaggctggtggag 2550
 835   L  S  S  L  R  P  S  L  T  G  A  R  R  L  V  E   850

         ---------|---------|---------|---------|---------|
2551 accatctttctgggctcaagaccatggatgccaggcacccccgcagact 2600
 851 T  I  F  L  G  S  R  P  W  M  P  G  T  P  R  R  L  867

         ---------|---------|---------|---------|---------|
2601 gcccaggctcccccagcggtactggcagatgcgccctctctttctggaac 2650
 868  P  R  L  P  Q  R  Y  W  Q  M  R  P  L  F  L  E  L 884

         ---------|---------|---------|---------|---------|
2651 ttctgggtaaccacgcccagtgcccatatggcgtcctgctgaagacccac 2700
 885   L  G  N  H  A  Q  C  P  Y  G  V  L  L  K  T  H   900

              hTERT Fragment 5 ><    G linker    >< hTERT
         ---------|---------|---------|---------|---------|
2701 tgtcctctgagggccgccgtgaccGGTGGAGGAGGTGGTGGAtcctgggc 2750
 901 C  P  L  R  A  A  V  T  G  G  G  G  G  G  S  W  A  917

         Fragment 4
         ---------|---------|---------|---------|---------|
2751 tcaccccggaaggaccaggggcccaagcgataggggcttctgtgttgtgt 2800
 918  H  P  G  R  T  R  G  P  S  D  R  G  F  C  V  V  S 934

         ---------|---------|---------|---------|---------|
2801 caccagccaggcctgccgaagaggctacctccttggaaggagccctcagt 2850
 935   P  A  R  P  A  E  E  A  T  S  L  E  G  A  L  S   950

hTERT Fragment 4 ><    G linker    >< hTERT Fragment 3
         ---------|---------|---------|---------|---------|
2851 ggcaccaggGGAGGTGGTGGAGGTGGAtggaatcatagcgtgcgggaggc 2900
 951 G  T  R  G  G  G  G  G  G  W  N  H  S  V  R  E  A  967

         ---------|---------|---------|---------|---------|
2901 aggtgtgcctctcggcctgccagcccccggagcaaggagacgcggtggat 2950
 968  G  V  P  L  G  L  P  A  P  G  A  R  R  R  G  G  S 984

                                        hTERT Fragment 3 ><
         ---------|---------|---------|---------|---------|
2951 ccgccagtcgctcactccccttgcctaagaggccaagaagaggagccGGT 3000
 985   A  S  R  S  L  P  L  P  K  R  P  R  R  G  A  G   1000

          G linker    >< hTERT Fragment 2
         ---------|---------|---------|---------|---------|
3001 GGAGGAGGTGGTGGAttcactactagcgtccggtcctacctgcccaacac 3050
1001 G  G  G  G  G  F  T  T  S  V  R  S  Y  L  P  N  T  1017

         ---------|---------|---------|---------|---------|
3051 agtgaccgacgctctgagaggttcaggtgcctggggtctgctgctgcgga 3100
1018  V  T  D  A  L  R  G  S  G  A  W  G  L  L  L  R  R 1034
```

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     ---------|---------|---------|---------|---------|
3101 gggtgggtgatgatgttctggttcacctcctggcccggtgtgccctgttc 3150
1035   V  G  D  D  V  L  V  H  L  L  A  R  C  A  L  F   1050

     ---------|---------|---------|---------|---------|
3151 gtgctggtggctccctcctgcgcataccaggtctgcggacccccacttta 3200
1051 V  L  V  A  P  S  C  A  Y  Q  V  C  G  P  P  L  Y  1067

  hTERT Fragment 2 ><    G linker    >< hTERT Fragment 1
     ---------|---------|---------|---------|---------|
3201 tcagctcggcgctgctGGAGGTGGAGGTGGAGGTctggccaccttcgtgc 3250
1068  Q  L  G  A  A  G  G  G  G  G  G  L  A  T  F  V  R 1084

     ---------|---------|---------|---------|---------|
3251 ggcgcctgggaccccagggctggcggctggtgcagcgcggggaccctgct 3300
1085   R  L  G  P  Q  G  W  R  L  V  Q  R  G  D  P  A   1100

     ---------|---------|---------|---------|---------|
3301 gctttcagagctctcgtcgcccagtgtctggtctgcgttccttgggacgc 3350
1101 A  F  R  A  L  V  A  Q  C  L  V  C  V  P  W  D  A  1117

     ---------|---------|---------|---------|---------|
3351 acggcccccacccgccgcccccagtttccggcaggtgagttgtctcaaag 3400
1118  R  P  P  P  A  A  P  S  F  R  Q  V  S  C  L  K  E 1134

     ---------|---------|---------|---------|---------|
3401 agttggttgctcgggtgttgcagcggctttgtgaaaggggagcaaagaac 3450
1135   L  V  A  R  V  L  Q  R  L  C  E  R  G  A  K  N   1150

                              hTERT Fragment 1 ><   G
     ---------|---------|---------|---------|---------|
3451 gtccttgcctttggcttcgctttgctcgatggagcacgcggaGGAGGTGG 3500
1151 V  L  A  F  G  F  A  L  L  D  G  A  R  G  G  G  G  1167

     linker   >< V5 Tag
     ---------|---------|---------|---------|---------|
3501 TGGAGGAGGTggcaagccaattcctaatccattgctgggcctggactcaa 3550
1168  G  G  G  G  K  P  I  P  N  P  L  L  G  L  D  S  T 1184

V5 Tag ><
     -----
3551 cttga 3555
       □
```