

# pNiFty2-56K-SEAP

Inducible reporter plasmid selectable with Zeocin™

Catalog code: pnf2-56ksp

**For research use only**

Version 20L03-MM

## PRODUCT INFORMATION

### Contents:

- 20 µg of pNiFty2-56K-SEAP provided as lyophilized DNA
- 1 ml of Zeocin™ (100 mg/ml)

### Storage and stability:

- Product is shipped at room temperature.
- Lyophilized DNA should be stored at -20 °C.
- Resuspended DNA should be stored at -20 °C and is stable for up to 1 year.
- Store Zeocin™ at 4 °C or at -20 °C. The expiry date is specified on the product label.

### Quality control:

- Plasmid construct has been confirmed by restriction analysis and full-length ORF sequencing.
- Plasmid DNA was purified by ion exchange chromatography.

## GENERAL PRODUCT USE

Interferons are key modulators of the immune response. Their pleiotropic activities are mediated by the induction of many IFN-stimulated genes (ISGs). To help study the transcriptional regulation and signal transduction of type I IFNs, InvivoGen provides several reporter systems, called pNiFty2, based on the inducible expression of the secreted embryonic alkaline phosphatase (SEAP) gene. The SEAP gene is cloned under the control of three different promoters that are activated by various transcription factors, such as IRF3, IRF5, IRF7 and NF-κB. pNiFty2-56K-SEAP features the human ISG-56K promoter.

## PLASMID FEATURES

- **hISG-56K prom:** ISG-56K is the prototype ISG which expression is highly increased by Type I IFNs due to the presence of ISRE and IRF7 sites within the promoter<sup>1</sup>. Co-expression of hISG-56K-SEAP with constitutively activated IRF3 (saIRF3) or IRF7 (saIRF7) in HEK293 cells led to a strong increase in SEAP expression.
- **5U-140** is a synthetic 5'UTR containing an intron.
- **SEAP** is a secreted form of human embryonic alkaline phosphatase. Unlike endogenous alkaline phosphatases, SEAP is extremely heat stable and resistant to the inhibitor L-homoarginine. It catalyses the hydrolysis of pNitrophenyl phosphate (pNpp) producing a yellow end product. SEAP expression can be readily quantified by collecting samples of culture medium and measuring the hydrolysis of pNpp with a spectrophotometer at 405 nm.
- **SV40 pAn:** The Simian Virus 40 late polyadenylation signal enables efficient cleavage and polyadenylation reactions resulting in high levels of steady-state mRNA.
- **hEF1/HTLV prom** is a composite promoter comprising the Elongation Factor-1α (EF-1α) core promoter<sup>2</sup> and the R segment and part of the U5 sequence (R-U5') of the Human T-Cell Leukemia Virus (HTLV) Type 1 Long Terminal Repeat<sup>3</sup>. The EF-1α promoter exhibits a strong activity and yields long lasting expression of a transgene in vivo. The R-U5' has been coupled to the EF-1α core promoter to enhance stability of RNA.

- **EM7** is a bacterial promoter that enables the constitutive expression of the Zeocin™ antibiotic resistance gene in *E. coli*.

**• Zeo:** Resistance to the antibiotic Zeocin™ is conferred by the *Sh ble* gene from *Streptallocteichus hindustanus*. The *Sh ble* gene is driven by the CMV enhancer/promoter in tandem with the bacterial EM7 promoter allowing selection in both mammalian cells and *E. coli*.

**• BGlo pAn:** The human beta-globin 3'UTR and polyadenylation sequence allows efficient arrest of the transgene transcription<sup>4</sup>.

**• pMB1 Ori** is a minimal *E. coli* origin of replication with the same activity as the longer Ori.

**1. Der SD. et al. 1998.** Identification of genes differentially regulated by interferon alpha, beta, or gamma using oligonucleotide arrays. PNAS. 95(26):15623-8. **2. Kim DW. et al. 1990.** Use of the human elongation factor 1 alpha promoter as a versatile and efficient expression system. Gene 91(2): 217-23. **3. Takebe Y. et al. 1988.** SR alphapromoter: an efficient and versatile mammalian cDNA expression system composed of the simian virus 40 early promoter and the R-U5 segment of human T-cell leukemia virus type 1 long terminal repeat. Mol Cell Biol. 8(1):466-72. **4. Yu J & Russell JE. 2001.** Structural and functional analysis of an mRNP complex that mediates the high stability of human beta-globin mRNA. Mol Cell Biol. 21(17):5879-88.

## METHODS

### Plasmid resuspension

Quickly spin the tube containing the lyophilized plasmid to pellet the DNA. To obtain a plasmid solution at 1 µg/µl, resuspend the DNA in 20 µl of sterile H<sub>2</sub>O. Store resuspended plasmid at -20 °C.

### Plasmid amplification and cloning

Plasmid amplification and cloning can be performed in *E. coli* GT116 or in other commonly used laboratory *E. coli* strains, such as DH5α.

### Zeocin™ usage

This antibiotic can be used for *E. coli* at 25 µg/ml in liquid or solid media and at 50-200 µg/ml to select Zeocin™-resistant mammalian cells.

## TECHNICAL SUPPORT

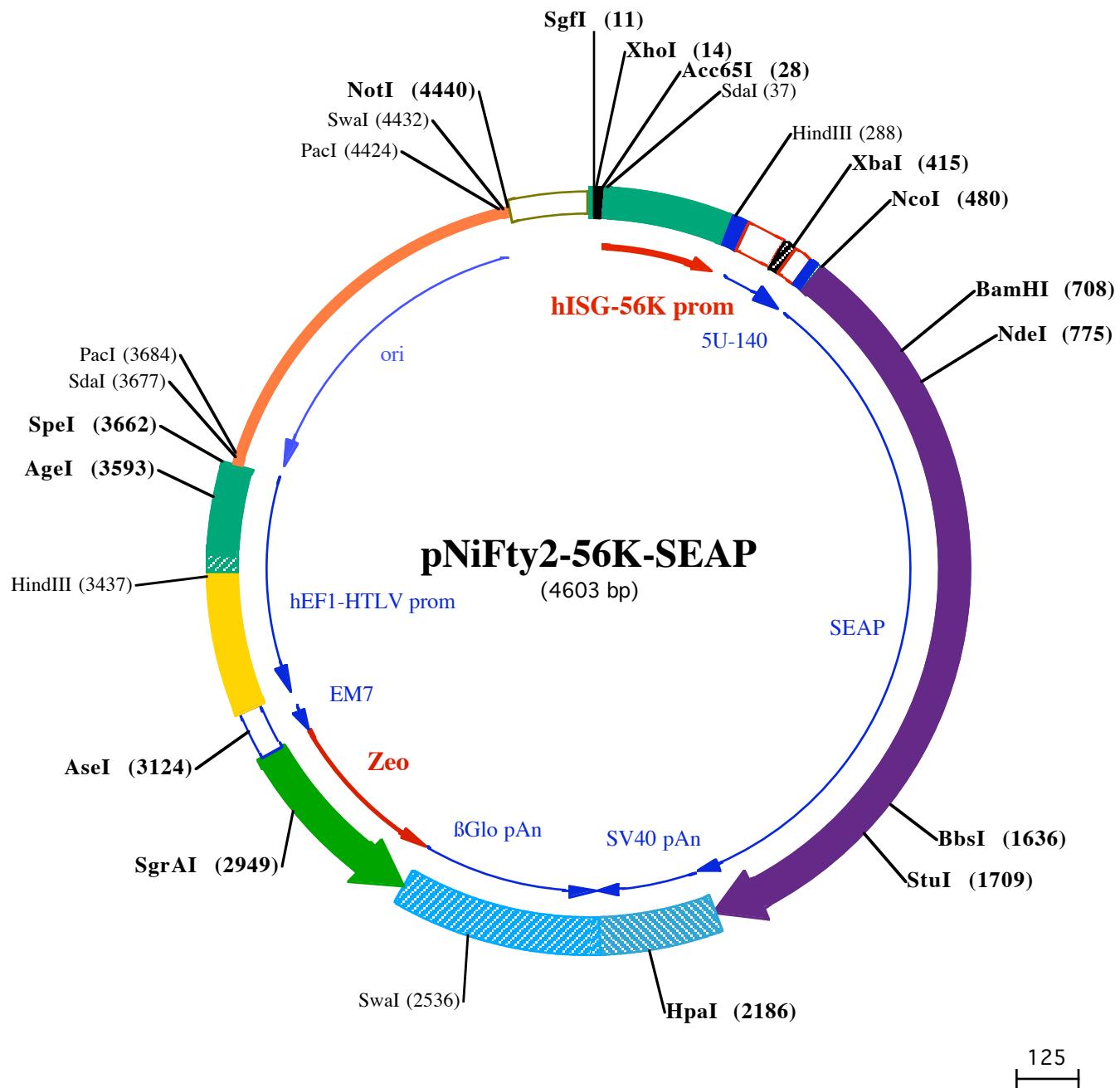
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InvivoGen Europe: +33 (0) 5-62-71-69-39

InvivoGen Hong Kong : +852 3-622-34-80

E-mail: info@invivogen.com



**XbaI (14)**                   **SdaI (37)**

1 **GGATCT** GCGATCGCTGAGTGAATTCTGGTACCTGCAGGACTAGAAACATCTATGGTTGAGGTCTGAGTTTATCTGTTTAAATAGAAACAAGTT

**SgfI (11)**                   **Acc65I (28)**

101 **CATCCCCACCCCCCCCCTCAGCAGGAATTCCTAGCTTAGTTCACTTCCCTTCGTTCCTAGGTTCCA** ACTTGCAAGGACACACCCACA

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**HindIII (288)**

201 **GCTTACACCATTGGCTGCTGTTAGCTCCTTATAAACACTGTCTGGGTTAAACGTA** ACTGAAAATCCACAAGACAGAATAGCAAGCTCTGCCT

301 **CTCCCTCTGTGAGTTTgtaagtactgactgtctatgcctggaaagggtggcaggagatggggcagtgcaggaaaagtggcactatgaacccTGCA**

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**XbaI (415)**                   **NcoI (480)**

401 **GCCCTAGGAATGCATCTAGCaattgtactaacctcttccttccctgcacag** GTTGGTGTACAGTAGCTTCCACCATGGCTCTGGGCCCTGCA  
1► Met Val Leu Gl y Pro Cys M

501 **TGCTGCTGCTGCTGCTGCTGGGCCCTGAGGCTCACGCTCTCCCTGGCATCATCCCTGGCAGTTGAGGAGGAGAACCCGACTCTGGAAACCGCAGGAGCAGC**  
7► etLeuLeuLeuLeuLeuLeuGl yLeuArgLeuGl nLeuSerLeuGl yIlelleProValGl uGl uGl uAsnProAspPheTrpAsnArgGl uAl aAl

601 **CGAGGCCCTGGTGGCCCAAGAACGCTGAGCCTGACAGACAGCCGCAAGAACCTCATCTCTCTGGCAGTGGATGGGGTGTCTACGGTGACA**  
40► aGl uAl aLeuGl yAl aAl aLysLysLeuGl nProAl aGl nThr Al aAl aLysAsnLeuI IlellePheLeuGl yAspGl yMet Gl yVal Ser Thr Val Thr

**BamHI (708)**

701 **GCTGCCAGGATCTAAAGGGCAGAAGAGAACAAACTGGGCCCTGAGATAACCCCTGGCTATGGACCGCTTCCATATGGCTCTGTC** AAAGACATACA  
74► Al aAl aArgI IeLeuLysGl yGl nLysLysAspLysLeuGl yProGl uIleProLeuAl aMetAspArgPheProTyrValAl aLeuSer Lys Thr Tyr A

801 **ATGTAGACAAACATGTCAGCAGACTGGAGCCACGCCACGGCTACCTGTGCGGGTCAAGGGCAACTCCAGCAGCATTGGCTGAGTGCAGCCCG**  
107► s nValAspLysHi s Val I ProAspLysHi s Val I aThr Al aThr Al aTy r Al aVal I leSer Val I Me t AsnArgAl aLysLysAl aGl yLysSer Val I Gl yVal Val I leGlyLeuSer Al aAl aAl aAr

901 **CTTTAACAGGTCAACAGCACGGGCAACGAGGTCATCCGTGATGAATCGGCCAAGAACGGAGGAGTCAGTGGAGTGTAAACACACACGA**  
140► gPheAsnGl nCysAsnThr Thr ArgGl yAsnGl uVal I leSer Val I Me t AsnArgAl aLysLysAl aGl yLysSer Val I Gl yVal Val I leGlyLeuSer Al aAl aAl aAr

1001 **GTGAGCACGCCCTGCCAGCGGACCTACGCCAACCGGTGAAACCGCAACTGGTACTCGGACGCCAGCTGGCTGCCCTGGCCAGGGAGGGGTG**  
174► Val Gl nHi s Al aSer ProAl aGl yThr Tyr Al aHi s Thr Val I AsnArgAsnTrpTyrSerAspAl aAspVal ProAl aSer Al aArgGl nGl uGl yCysG

1101 **AGGACATCGCTACGGCTATCTAACATGGACATCTGGATGATCTGGGGTGGAGGCCAAAGTACATGTTCGCATGGGAACCCAGACCCCTGAGTA**  
207► l nAspI I eAl aThr Gl nLeuI I eSer AsnMetAspI I eAspVal I leLeuGl yGl yArgLysTyrMetPheArgMetGl yThr ProAspProGl uTy

1201 **CCCATGACTACAGCCAAGGGTGGACAGCAGCTGGACGGGAAGAATCTGGTGCAGGAATGGCTGGCGAAGGCCAGGGTCCCGTATGTGTGGAACCGC**  
240► r ProAspAspTyrSerAl nGl yGl yThr ArgLeuAspGl yLysAsnLeuVal Gl nGl I leTrpLeuAl aLysArgGl nGl yAl aArgTyrVal TrpAsnArg

1301 **ACTGAGCTCATGCAGGCTTCCCTGGACCCGCTGTGACCCATCTGGGCTCTTGGAGGACATGAAATCAGAGATCCACCGAGACTCCAC**  
274► Thr Gl uLeuMetGl nAl aSer LeuAspProSer Val Thr Hi sLeuM Gl yLeuPheGl uProGl yAspMetLysTyrGl I leHisLysArgAspSer Thr L

1401 **TGGACCCCTCCGTATGGAGATGACAGAGGCTGCCCTGCGCCTGCTGAGCAGGAACCCCGCGGCTCTCTCTTCGTGAGGGTGGTCGATCGACCA**  
307► euAspProSer LeuMetGl uMet Thr Gl uAl aAl aLeuArgLeuSer ArgAspProArgGl yPheLeuPheVal Gl uGl yGl yArgI I eAspHi

1501 **CGGTATCACGAAAGCAGGGCTTACCGGGACTGACTGAGACGATCATGGTCAGCAGCCATTGAGAGGGCGGCCAGCTACCACCGAGGAGACAGC**  
340► sGl yHi sHi sGl uSer ArgAl aTyrArgAl aLeuThr Gl uThr I leMetPheAspAspAl aI leGl uArgAl aGl yGl nLeuThr Ser Gl uGl uAspThr

**BbsI (1636)**

1601 **CTGAGCTCGTACTGCCGACCACTCCACGTCTCTCTGGAGGCTACCCCTCGAGGGAGCTCCATCTCGGCTGGCCCTGGCAAGGCCGG**  
374► LeuSerLeuValThrAl aAspHi sSer HisVal PheSer PheGl yGl yTyrProLeuArgGl ySer Ser I lePheGl yLeuAl aProGl yLysAl aArgA

**StuI (1709)**

1701 **ACAGGAAGGCCACAGGCTCTCTATACGGAAACGGTCCAGGCTATGTGCTCAAGGACGGGCCGGCGATGTTACCGAGAGCGAGAGCGGGAGCCC**  
407► spArgLysAl aTyrThr Val LeuLeuTyrGl yAsnGl yProGl yTyrVal LeuLysAspGl yAl aArgProAspVal Thr Gl uSer Gl uSer Gl ySer Pr

1801 **CGAGTATCGGAGCAGTCAGCTGGACGGCTGGACGGAGACCCCGCAGGGAGACGTGGCGGTTGCGCGCCGGCCAGGGCACCTGGTTCAC**  
440► oGl uTyrArgGl nGl nSerAl aVal I ProLeuAspLysGl uUhr Hi sAl aGl yGl uAspVal Al aVal PheAl aArgGl yProGl nAl aHi sLeuVal Hi s

1901 **GGCGTGGAGGAGCACCTTATAGCGCACGCTATGGCTTCTGCCCTGCGCTGGACGCCCTACCGCCCTGCGACCTGGCGCCCCCGCCGAC**  
474► Gl yVal Gl nGl uGl nThr Phe I leAl aHi sVal MetAl aPheAl aAl aCysLeuGl uProTyrThr Al aCysAspLeuAl aProProAl aGl yThr Thr A

2001 **ACGCCGCACCGGGGGGGTCCCGTCAAGGCTGCTGAGATTGAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTGGACAAACACAACTA**  
507► spAl aAl aHi sProGl yArgSerArgSerLysArgLeuAsp\*\*\*

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**HpaI (2186)**

2101 **GAATGCAGTAAAAAAATGTTTGTGAAATTGTGATGCTATTGCTTATTGTAACCATATAAGCTGCAATAAACAAAGTTAACACAACAAATTG**

2201 **CATTCTTTATGTTCAGGTCAGGGAGGTGTTGGAGGTTAAAGCAAGTAAACCTCTACAAATGTGGATGGAATTCTAAACATAGCAGCATAG**

2301 **CAAACCTTAACCTCCAATCAAGCTCTACTTGAATCCTTCTGAGGGATGAATAAGGCATAGGCATAGGGCTGTCATGTCATTAGCTGTT**

2401 **TGCAAGCTCACCTCTTCATGGAGTTAAGATATAGTGTATTTCCAAGGTTGAACTAGCTCTCATTTATGTTAAATGCACTGACCTCC**

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**SwI (2536)**

2501 **ACATTCCTTTAGTAAAATTCAGAAAATTTAACATCATTCATGCAATGAAAATTAATGTTTATTAGGCAGAACCTGCTAAGGCTCGTCAGGCC**

2601 **TCATAATATCCCCAGTTAGTTGACTAGGAAACAAAGGAACCTTAATAGAAATTGGACAGCAAGAACGGCTTAGCTTCTAGCTTATCTCAGTC**  
127► I •••Gl y•••AspG

2701 **TGCTCTCTGCCACAAAGTCAGGCGAGTGCAGGCGCCGGTGCAGGGCAACTCCGCCACGGCTGCTGCCATCGCTATGGCGGCCGG**  
122► I nGl uGl uAl aVal PheHi sVal CysAsnGl yAl aProAspArgLeuAl aPheGl uArgGl yTrpProGl nGl uGl yI leGl uThr MetAl aProGl ySe

2801 **AGGGTCCCGGAAGGTCGTGACACGACCCCTCGACACTCGGCCAGCTGAGCTGGCAGGCCACCCACCCAGGGCTGGTCCGGCAC**  
89► r Al aAspArgPheAsnThr Ser Val Val Gl uSer TrpGl uAl aTyrLeuGl uAspLeuGl yArgVal TrpVal TrpAl aLeuThr AsnAspProVal Val

**SgrAI (2949)**

2901 **CTGGTCCTGGACCGCGCTGATGACAGGGTACGTCGTCGGACACACCGCGAAGTCGCTCCACGAAGTCCGGAGAACCCGAGCCGGTCGTC**  
56► Gl nAspGl nVal Al aSer I lePheLeuThr Val I AspAspArgVal Val Gl yAl aPheAspAspGl uVal I PheAspArgSer PheGl yLeuArgAspThr T

3001 **CAGAACTCGACCGCTCCGGCAGCTGGCGCGGGTGGAGCACCGGAACGGCACTGGCAACTTGGCCATGATGGCCCTCTATAGTGA** GTCGTATTATACT  
22► r PheGl uVal Al aGl yAl aVal AspArgAl aThr LeuVal ProVal Al aSer Thr LeuLysAl aMet ←

**AseI (3124)**

3101 **ATGCCGATATACTATGCCGATGATTAAATTGCAACTACTGTTGAGGCAGGGTACAGCTTGAGCTGTAACGGCAGAACAGAAAAGCAAAG**

3201 **ACGTAGAGTTGAGCAAGCAGGGTCAAGCAAAGCCTGGAGAGCCGGCTGAGTCTAGGCTCAAGGGAGCGCCGACAAAGGCCGGTCTGACCTGA**

3301 **GCTTAAACTTACCTAGACGGCGAGCTCAGGAGGACCAACAGGGGGAGGGCGAGAACCGCAGTCAACCGCGTGGATGGCGCCTCAGGTAGG**

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**HindIII (3437)**

3401 **GGGGGGGGCGCTGAGAGAGATCGAGCCCCCTCGAGCTCAGCTGTTGCTGGCGCAACCCGTTGCAAAAGAACGTTACGGCAGACTGCA**

AgeI (3593)

3501 CTTATATACGGTCTCCCCACCTCGGGAAAAGGCGGAGCCAGTACAGACATCACTTCCCAGTTACCCGCCACCTCTAGGCACCGGTC

3601 AATTGCCGACCCCTCCCCAACTCTCGGGACTGTGGCGATGTGCGCTTGCCACTGACTAGTGGCCCTGCAGGTTAATTAGAACATGTGAGCA

3701 AAAGGCCAGAAAGGCCAGGAACCGTAAAAGGCCGTTGCTGGCTTTCCATAGGCTCCGCCCTGACGAGCATCACAAAATCGACGCTCAA

3801 GTCAGAGGTGGGAAACCCGACAGGACTATAAAGATACCAGCGTTCCCTGGAAAGCTCCCTCGTGCCTCTCTGTCCGACCCGCCCTACCGG

3901 ATACCTGTCCGCCTTCTCCCTCGGAAGCGTGGCTTCTCATAGCTACGCTGTAGGTATCTCAGTCGGTAGGTAGTCGTTGCTCCAAGCTGGC

4001 TGTGTGACGAACCCCCGTTCAAGCCGACCGCTCGCCTTATCCGTAACATCGTCTGAGTCAACCCGTAAGACACGACTTATGCCACTGGCAG

4101 CAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCCTGCTACAGAGTTCTGAAGTGGCCCTAACTACGGCTACACTAGAAGAACAGTATT

4201 TGGTATCTGCGCTGCTGAAGCCAGTTACCTCGAAAAAGAGTTGGTAGCTCTGATCCGAAACAAACCACCGCTGGTAGCGGTGTTTTTGT

4301 TGCAAGCAGCAGATTACCGCAGAAAAAAAGGATCTAAGAAGATCTTGTATCTTCTACGGGCTGACGCTAGTGAACGAAAACGTTAG

PacI (4424) SwaI (4432) NotI (4440)

4401 GGATTTGGCATGGCTAGTTAATTAACTTAAATCAGCGGCCAATAAAATCTTATTTCATTACATCTGTGTGTTGGTTTTGTGAATCG

4501 TAACTAACATACGCTCTCCATAAAACAAAAGAAACAAAACAAACTAGCAAAATAGGCTGCCCCAGTCAAGTGCAGGTGCCAGAACATTCTATC

4601 GAA