

pFUSE-SEAP-hG2-Fc

Plasmid designed for the expression of a SEAP-Fc Fusion protein

Catalog # pfuse-hsp

For research use only

Version 22H30-MM

PRODUCT INFORMATION

Content:

- 20 µg of pFUSE-SEAP-hG2-Fc plasmid 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 and is stable 3 months.
- Resuspended DNA should be stored at -20°C and is stable 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 sequencing.
- Plasmid DNA was purified by ion exchange chromatography and lyophilized.

GENERAL PRODUCT USE

pFUSE-Fc is a family of plasmid developed to facilitate the construction of Fc-Fusion proteins by fusing a sequence encoding a given protein to the Fc region of an immunoglobulin.

pFUSE-Fc plasmids yield high levels of Fc-Fusion proteins. The level of expression is usually in the µg/mL range. They can be transfected in a variety of mammalian cells, including myeloma cell lines, CHO cells, monkey COS cells and human embryonic kidney (HEK)293 cells. These cells are commonly used in protein purification systems.

pFUSE-SEAP-hFc plasmids allow the production of SEAP-Fc fusion proteins. This plasmid can be used to make recombinant SEAP-Fc fusion proteins or can be used as a transfection control in experiments with other pFUSE-hFc constructs. Quantification of SEAP-Fc expression can be determined using QUANTI-Blue™ Solution (cat. code: rep-qbs).

PLASMID FEATURES

- **hEF1-HTLV prom** is a composite promoter comprising the Elongation Factor-1α (EF-1α) core promoter¹ and the R segment and part of the U5 sequence (R-U5') of the Human T-Cell Leukemia Virus (HTLV) Type 1 Long Terminal Repeat². 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.
- **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.
- **hIgG2 Fc (human):** The Fc region of human IgG2 comprises the CH2 and CH3 domains of the IgG heavy chain and the hinge region. The hinge serves as a flexible spacer between the two parts of the Fc-Fusion protein, allowing each part of the molecule to function independently.

• **SV40 pAn:** the Simian Virus 40 late polyadenylation signal enables efficient cleavage and polyadenylation reactions resulting in high levels of steady-state mRNA³.

• **ori:** a minimal *E. coli* origin of replication to limit vector size, but with the same activity as the longer Ori.

• **CMV enh / hFerL prom:** This composite promoter combines the human cytomegalovirus immediate-early gene 1 enhancer and the core promoter of the human ferritin light chain gene. This ubiquitous promoter drives the expression of the Zeocin®-resistance gene in mammalian cells.

• **EM2KC** is a bacterial promoter that enables the constitutive expression of the antibiotic resistance gene in *E. coli*. EM2KC is located within an intron and is spliced out in mammalian cells.

• **Zeo:** Resistance to Zeocin® is conferred by the *Sh ble* gene from *Streptallotheichus hindustanus*. The same resistance gene confers selection in both mammalian cells and *E. coli*.

• **βGlo pAn:** The human beta-globin 3'UTR and polyadenylation sequence allows efficient arrest of the transgene transcription⁴.

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 H₂O. Store resuspended plasmid at -20 °C.

Plasmid amplification and cloning

Plasmid amplification and cloning can be performed in *E. coli* GT116 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.

References:

1. Kim, D.W. *et al.* (1990). Gene 2: 217-223.
2. Takebe, Y. *et al.* (1988). Mol. Cell Biol. 1: 466-472.
3. Carswell, S., and Alwine, J.C. (1989). Mol. Cell Biol. 10: 4248-4258.
4. Yu J & Russell JE. (2001). Mol Cell Biol, 21(17):5879-88.

TECHNICAL SUPPORT

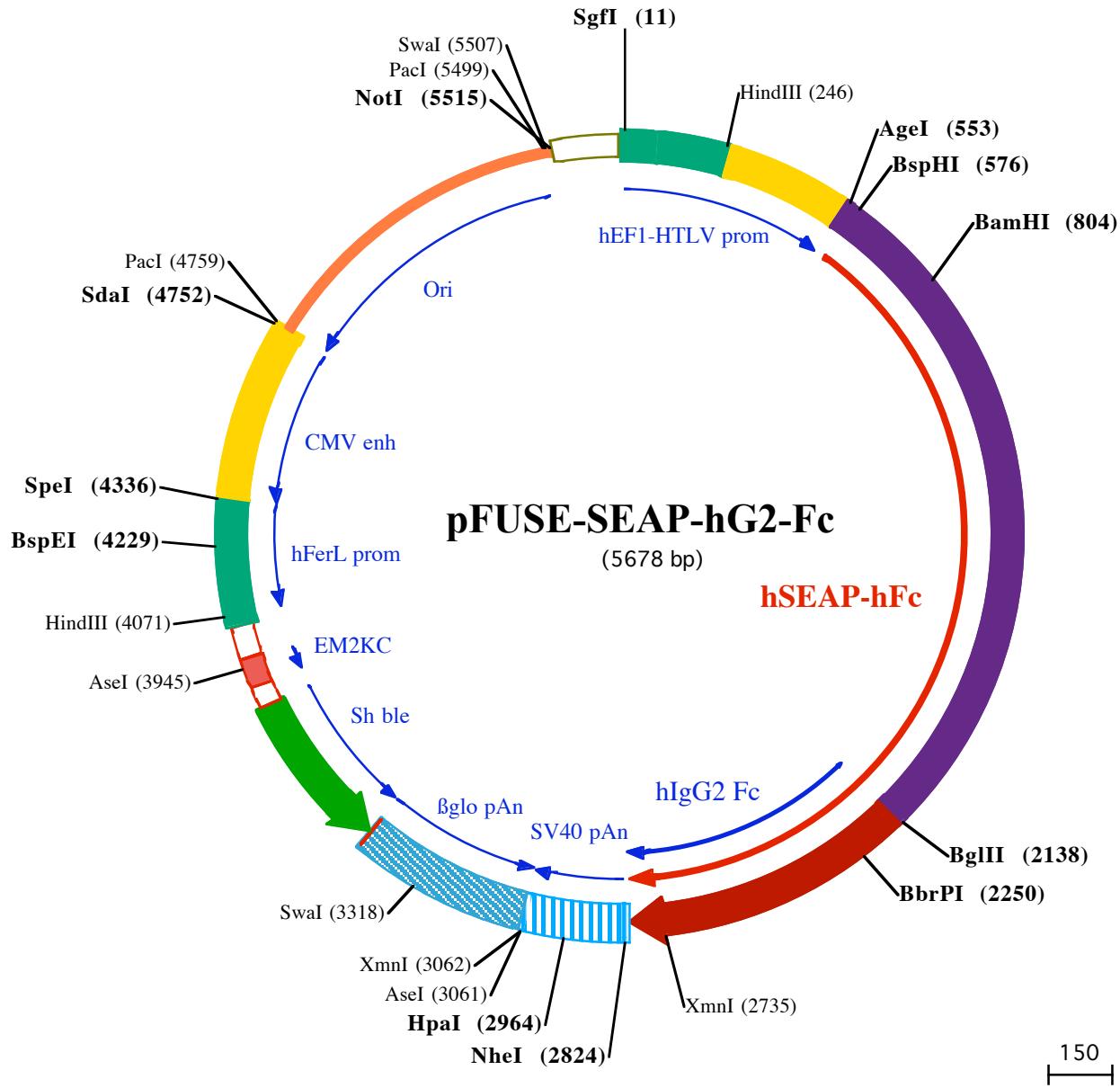
InvivoGen USA (Toll-Free): 888-457-5873

InvivoGen USA (International): +1 (858) 457-5873

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

InvivoGen Asia: +852 3622-3480

E-mail: info@invivogen.com



SgII (11)

1 GGATCTGCGATCGTCCGGTCCCCGTAGGGCAGAGGCACATGCCACAGTCCCAGAAGTTGGGGGAGGGTCGGCAATTGAACGGGTGCTA
 101 GAGAAGGTGGCGGGGTAACGGAAAGTGATGTCGTACTGGCTCGCCTTTCCCAGGGTGGGGAGAACGTATAAGTCAGTAGTCGC

HindIII (246)
 201 GTGAACTCTTTTCGCAACGGTTGCCAGAACACAGCTGAAGCTCGAGGGCTCGCATCTCCTCACGCCGCCCTACCTGAGGCC
 301 GCCATCCACGCCGGTGGCTCGCTGCCCTCCGCCCTGGCTCTGAACCTGCCTCCAGCCTCTAGTTAAAGTCAGGTCAGGTCAGACC
 401 GGGCCTTGTCCGGCGCTCCCTGGAGCCTACCTAGACTCAGCGGCTCTCACGCCCTGACCCCTGCTGCTCAACTACGTTGCTT

AgeI (553)**BspHI (576)**

501 TCTGTTCTGCCGTTACAGATCCAAGCTGACCGGCCCTACCTGAGATCACCGGTTCACTGAGGAGGACATCATGATCTGGGCCCTGCATGCT
 1► Met I I eLeuGI y ProCysMetLe
 601 GCTGCTGCTGCTGCTGGGCTGAGGCTACAGCTCCGGCATCTGGGCACTCCAGTGGAGGAGAACCCGGACTCTGGAAACCCGGAGGCCAG
 8► uLeuLeuLeuLeuLeuLeuGl yLeuArgLeuGl nLeuSerLeuGl l I eI eProValGl uGl uAsnProAspPheTrpAsnArgGl uAl aAl aGl u
 701 GCCTGGTGGCCCAAAGACTGCAAGCAGCCAAACCTCATCTCCGGGATGGATGGGGTGTCTACGGTGACAGCTG
 42► Al aLeuGl yAl aAl aLysLysLeuGl nProAl aGl nThr Al aAl aLysAsnLeuI l eI ePheLeuGl yAspGl yMetGl yVal Ser Thr Val Thr Al aA
 BamHI (804)
 801 CCAGGATCTAAAGGGCAGAAGAGACAACTGGGCCCTGAGATACCCCTGGCTATGGACCGCTTCCCATATGGGCTCTGTCCAAGACATACAATGT
 75► IaArgI l eLeuLysGl yGl nLysLysAspLysLeuGl yProGl uI l eProLeuAl aMetAspArgPheProTyrValAl aLeuSerLysThr TyrAsnVa
 901 AGACAAACATGTGCCAGACAGTGGGCCACAGCACGGCCACCTGTGGGGTCAAGGGCAACTTCCAGACCATTGGCTGAGTGCAGCCGCCCTT
 108► IAspLysHisVal ProAspSerGl yAl aThr Al aThr Al aTyrLeuCysGl yVal LysGl yAsnPheGl nThr l I eGl yLeuSerAl aAl aAl aArgPhe
 1001 AACAGTCAACGACAGCCGCAACGGCTACCTCCGGATGAACTGGGCAAGAACAGGGAGCTGGGAGTGGTAACCAACACAGATGTC
 142► AsnGl nCysAsnThr Th ArgGl yAsnGl uVal l I eSerValMetAsnArgAl aLysLysVal Gl yVal Val Thr Th ArgVal G
 1101 AGACGCTTCGCCGGGCAACCTGGGCCACAGGGCAACTGGTACTCGGACGCCAGCTGGCTGCCTCGGCCGCCAGGGGGTGCAGGAG
 175► IaHisAl aSer ProAl aGl yThr TyrAl aHi sThr Val AsnArgAsnTrpTyrSerAspAl aAspVal ProAl aSer Al aArgGl nGl uGl yCysGl nAs
 1201 CATCGCTACGCACTCATCTCCACATGGACATTGATGATCTGGGTTGGAGGCGAAAGTACATGTTTCGATGGAAACCCAGACCCCTGAGTACCCA
 208► pI eLeuAl aThr Gl nLeuI l eSerAsnMetAspI l eAspVal l eLeuGl yGl yGlyArgLysTyrMetArgMetGl yThr ProAspProGl uTyrPro
 1301 GATGACTACAGGCAAGGTTGGGACAGGCTGGACGGAGAATCTGGTGCAGGAATGGCTGGCGAAGGCCAGGGTGGCCGATGTGGAACCGCAGT
 242► AspAspTyrSerGl nGl yGl yThr ArgLeuAspGl yLysAsnLeuValGl nGl uTrpLeuAl aLysArgGl nGl yAl aArgTyrVal TrpAsnArgThr G
 1401 AGCTCATGAGGCTCCCTGGACCCGCTGTGACCCATCTCATGGGCTCTTGAGGCTGGAGACATGAAATACGAGATCCACGAGACTCCACACTGGA
 275► IuLeuMetGl nAl aSer LeuAspProSerValThrHi LeuMetGl yLeuPheGl uProMet yLysTyrGl l eHi sArgAspSerThrLeuAs
 1501 CCCCTCTGTGGAGATGACAGGGCTGCCCCTGGCTGAGCAGGAACCCCCGGGCTCTCTCTCTGGGAGGGTGGTCATGACCCACGGT
 308► pProSerLeuMetGl uMetThrGl uAl aAl aLeuArgLeuSerArgAsnProArgGl yPhePheLeuPheValGl uGl yGl yArgI l eAspH i sGl y
 1601 CATACGAAAGCAGGGCTTACCGGGCACTGACTGAGACGATCATGGTGCAGCACGCCATTGAGAGGGCGGGCAGCTCACAGCAGGGAGACACGCTGA
 342► HiShiGl sGl sUser ArgAl aTyrArgAl aLeuThrGl uThrMetPheAspAspAl aIleGl uAl aGl yGl nLeuThrSerGl uGl uAspThrLeuS
 1701 GCCTCGTACTGCCGACCCATCCCAGTCTCTCTGGAGGCTACCCCTCGAGGGAGCTCATCTGGGCTGGGGCTGGCAAGGCCGGCAG
 375► erLeuValThrAl aAspH i sSer H i sVal PheSerPheGl yGl yTyrProLeuArgGl ySerSer l I ePheGl yLeuAl aProGl yLeuAl aArgAspAr
 1801 GAAGGCCTACCGGCTCTTACGGAAACGGTCAGGCTATGGCTCAAGGACGGCCGGGGATGTTACCGAGAGCAGAGCGGGAGCCCCGAG
 408► gLysAl aTyrThr ValLeuLeuTyrGl yAsnGl yProGl yTyrValLeuLysAspGl yAl aArgPheProValThrGl uSerGl uSerProGl u
 1901 TATCGGCAGCTAGCTGGCCCTGGACGAAGAGACCCAGCCGGAGGACGCTGGCGTGGCTGGCGGGCCCGAGGGCAGCTGGTTACGGCG
 442► TyrArgGl nGl nSerAl aValI ProlLeuAspGl uGl uThrHi sAl aGl yGl uAspValAl aValPheAl aArgGl yProGl nAl aHi sLeuValHi sGl yV
 2001 TGAGGAGCAGCTTACAGCGCATGGCTCGCCGCTGGAGGCCATACCGCCTGCGACCTGGGCCCGCCGACCACCGAC
 475► al Gl nGl uGl nThr Phel l eAl aHi sValMetAl aPheAl aAl aCysLeuGl uProTyrThrAl aCysAspLeuAl aProProAl aGl yThr ThrAspAl

BglII (2138)

2101 CGCCGACCCGGGGGGTCCCGGTTCAAGCCTGCTGGATAGCTGTGGAGTGCACCTGCCAGCACACCTGTTGAGACCTTCAGTCTCTTC
 508► aAl aHi sProGl yArgSerArgSerLysArgLeuAspArgSerValGl uCysProProCysProAl aProProValAl aGl yProSerValPheLeuPhe
 1► ValGl uCysProProCysProAl aProProValAl aGl yProSerValPheLeuPhe

BbrPI (2250)

2201 CCCCAAACCAAGGACACCTGATGATCTCCAGAACCCCTGAGGTACCTGCGTGGGGAGCTGAGGCCAGAACCCCCGGGAGTCCAGTCAACT
 542► ProProLysProLysAspThrLeuMetI l eSerArgThrProGl uValThrCysValValAspValSerHi sGl uAspProGl uValGl nPheAsnT
 20► ProProLysProLysAspThrLeuMetI l eSerArgThrProGl uValThrCysValValAspValSerHi sGl uAspProGl uValGl nPheAsnT
 2301 GGTACGTGGACGGCATGGGGTCAATGCCAACAGAACGCCAGGGAGGAGCTCAACAGCACGGTCTGGTGTGGTCAAGCTCACCGTCGTGCA
 575► rPtyValAspGl yMetGl uValHi sAsnAl aLysThrLysProArgGl uGl uGl nPheAsnSerThrPheArgValValSerValLeuThrValValHi
 53► rPtyValAspGl yMetGl uValHi sAsnAl aLysThrLysProArgGl uGl uGl nPheAsnSerThrPheArgValValSerValLeuThrValValHi
 2401 CCAGGACTGGCTGAACGCCAACAGGATCAAAGTCAAGGCTCCACAGCCCCATCGAGAAAACCATCTCCAAACAAAGGGCAGCC
 608► sGl nAspTrpLeuAsnGl yLysGl uTyrLysCysLysValSerAsnLysGl yLeuProAl aProI l eGl uLysThr l I eSerLysThrLysGl yGl nPro
 86► sGl nAspTrpLeuAsnGl yLysGl uTyrLysCysLysValSerAsnLysGl yLeuProAl aProI l eGl uLysThr l I eSerLysThrLysGl yGl nPro
 2501 CGAGAACACAGGTGTACACCCCTGGGGAGAGTACCAAGAACCCAGCTGGCTGGCTGGCTAACAGCTTACCCAGGACA
 642► ArgGl uProGl nValI TyrThrLeuProProSerArgGl uGl uMetThrLysAsnGl nValI SerLeuThrCysLeuValLysGl yPheTyrProSerAspI
 120► ArgGl uProGl nValI TyrThrLeuProProSerArgGl uGl uMetThrLysAsnGl nValI SerLeuThrCysLeuValLysGl yPheTyrProSerAspI
 2601 TCGCCGTGGAGTGGGAGAGCAATGGCAGCGGGAGAACAACTAACAGACCACACCTCCATGCTGGACTCCGACGGCTCTCTCTACAGCAAGCT
 675► IeAl aValGl uTrpGl uSerAsnGl yGl nProGl uAsnAsnTyrLysThrThProMetLeuAspSerAspGl ySerPheLeuTyrSerLysLe
 153► IeAl aValGl uTrpGl uSerAsnGl yGl nProGl uAsnAsnTyrLysThrThProMetLeuAspSerAspGl ySerPheLeuTyrSerLysLe

XmnI (2735)

2701 CACCGTGGACAAGAGCAGGTGGCAGGGGAACCTCTCATGCTCGTATGGCATGAGGCTCTGACAACCAACTACACAGAAGAGCCTCTCCCTG
 708► uThrValAspLysSerArgTrpGl nGl nLysyAsnValPheSerCysSerValMetHi sGl uAl aLeuHi sAsnHi sTyrThrGl nLysSerLeu
 186► uThrValAspLysSerArgTrpGl nGl nLysyAsnValPheSerCysSerValMetHi sGl uAl aLeuHi sAsnHi sTyrThrGl nLysSerLeu

NheI (2824)

2801 TCTCCGGTAAATGAgtgccacGCTAGCTGGCCAGACATGATAAGATACTTGTAGTGGACAAACCAACTAGAATGCAGTAAAAAAATGCTT
 742► SerProGl yLys***
 220► SerProGl yLys***

HpaI (2964)

2901 TATTGTGAAATTGTGATGCTATTGTTATTGTAACCATTATAAGCTCAATAAACAAAGTTAACAAACAATTGATTCTTTATGTTCA
 AseI (3061)
 3001 CAGGGGGAGGTGTGGAGGTTTTAAAGCAAGTAAACCTCTACAAATGTGGATGGAATTAACTCTAAACAGCATAGCAAACACTTAAACCTCAA
 3101 ATCAAGCCTACTGATCCTTCTGAGGGATAAGCATGGCATAGGCTGTTGCCAATGTCATTAGCTGTTGAGCCTCACCTCTT

3201 CATGGAGTTAAGATATAGTGTATTTCCAAGGTTGAACTAGCTCTCATTCTTATGTTAAATGACTGACCTCCACATCCCTTTAGTAA
 SwaI (3318)

3301 AATATTCAAGAAATAATTAAATACATCATTGAATGAAAATAATGTTTTATTAGGCAGAACAGATGCTCAAGGCCCTCATATATCCCCAGTT

3401 TAGTAGTGGACTTAGGAAACAAGGAACCTTAATAGAAATTGGACAGCAAGAAAGCGAGCTCTAGCTTATCCTCAGTCCTGCTCTGCCACAAAG
 125◀•••AspGI nGI uGI uAl aVal PheH
 3501 TGCACGCAGTTGCCGCCGGTGCAGGGCGAACCTCCGCCACGGCTGCTCGCGATCTGGCATGGCCGCCGGAGGCCTCCCGAAGTTCG
 116◀r Val CysAsnGI yAl aP ProAspArgLeuAl aPheGI uArgGI yTrpAl roGI nGI yI l eGI uThr MetAl aProGI ySer Al aAspArgPheAsnTh
 3601 TGGACACGACCTCGGACACTCGGGTACAGCTCGCCAGGCCGACCCACACCCAGGGCTGTTGCGCACCCCTGGTCTGGACCGCCT
 83◀r Ser Val Val GI uSer TrpGI uAl aTyLeuGI uAspLeuGI yArgVal TrpVal TrpAl aLeuThrAsnAspProVal Val GI nAspGI nValAl aSer
 3701 GATGAACAGGGTACAGTCGTCGGACACCCGGCGAACAGTCGTCCTCACGAACTCCGGAGAACCCGAGCCGGTCCAGAACCTCGACCGCTCG
 50◀l PheLeuThr Val AspAspArgVal Val GI yAl aPhePheGI uPheAspArgSer PheGI yLeuArgAspThr TrpPheGI uValAl aGI yA
 3801 GCGACGTCGCGCGGGTGAGCACCGAACGGACTGGTCAACTGGCCATGATGGCTCctgtcaggagaggaaagaagaaggtagtacaatgC
 16◀l aValAspArgAl aThr LeuVal ProValAl aSer Thr LeuLysAl aMet

Ascl (3945)

3901 TATAGTGAGTTGATTATACTATGCAGATATACTATGCCAATGTTAACTAGGGCTGCAgggttcatagtgcactttcctgcactgcccc

HindIII (4071)

4001 atctcctgcccaccctttccaggcatagacagtcaacttgcattttatggcgccctcgaggcaggcgctcgaggcgtcgccatctcggtggcaggA
 4101 ACTCGGAGGGGACGTGGCTAGGGCGTTCTTTATGGCGCCGCCCCTGGAGGCAGGGCGCTCGGGAGGCCTAGCGCCAATCTCGGTGGCAGGA

BspEI (4229)

4201 GCGGGGCCGAAGGCCGTGCTGACCAATCGGAGCACATAGGAGTCTCAGCCCCCGCCCAAAGCAAGGGGAAGTCACGCCCTGAGGCCAGCGT

SphI (4336)

4301 TTGTGAAATGGGGCTTGGGGGGTTGGGGCCCTGACTAGTCAAAACAAACTCCATTGACGTCAATGGGTGGAGACTTGGAAATCCCGTAGTC
 4401 CCGCTATCCACGCCATTGATGACTGCCAAACCGCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAG
 4501 GTCATGTAATGGGCATAATGCCAGGGCCATTACCGTCAATTGGCTCAATAGGGGCGTACTTGGCATATGATACACTTGATGACTGCCAAGTGG
 4601 CAGTTACCGTAATACTCCACCCATTGACGTCAATGGAAAGTCCATTGGCGTTACTATGGAACATACGTATTGACGTCAATGGCGGGGTC

PacI (4759)

SdaI (4752)

4701 GTTGGCGGTAGCCAGGCAGGCCATTACCGTAAGTTATGTAACGCCCTGAGGTTAAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACC
 4801 GTAAAAAGGCCGCGTTGCTGGCTTTCCATAGGCTCCGCCCTGACGAGCATCACAAAATGACGCTCAAGTCAGGGTGGGAAACCCGACAGG
 4901 ACTATAAGATACCAGCGTTCCCTGAAAGCTCCCTGCGCTCTCCGTCCGACCCCTGCCCTTACCGGATACCTGTCGCCCTTCCCTCG
 5001 GGAAGCGTGGCTTCTCATAGCTACGCTGAGGTATCTCAGTCGGTAGGTCTCGTCAAGCTGGCTGTGACGAACCCCCGTTCA
 5101 CCGACCGCTGCGCCTTACCGTAACTATGCTTCTGAGTCAACCCGTAAGACACGACTTATGCCACTGGCAGCAGGACTGGTAACAGGATTAGCAG
 5201 AGCGAGGTATGAGGGCGTACAGAGTTCTGAAGTGGCTACTACGGCTACACTAGAAGAACAGTATTGGTATCTGCCTGCTGAAGCA
 5301 GTTACCTCGGAAAAGAGTTGAGCTCTGATCCGCAAACAAACCCCGCTGGTAGCGTGGTTTTGGCAAGCAGCAGATTACGCGCAGAA

PacI (5499)

5401 AAAAAGGATCTCAAGAAGATCTTGTATTTCTACGGGCTGACGCTAGTGGAAACAAACTACGTTAAGGGATTTGGTATGGCTAGTTAATT

SwaI (5507) NotI (5515)

5501 AACATTTAAATCAGCGGCCGAATAAAATATCTTATTTCTTACATCTGTGTTGGTTTTGTGAATGTAACACTACGCTCTCCATCAA
 5601 ACAAAACGAAACAAACAAACTAGCAAAATAGGCTGCCCCAGTGCAAGTGCAGGTGCCAGAACATTCTATCGAA