

pFUSE-SEAP-hIgG4-Fc

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

Catalog # pfuse-hg4sp

For research use only

Version # 08H29-SV

PRODUCT INFORMATION

Content:

- 20 µg of pFUSE-SEAP-hIgG4-Fc plasmid provided as lyophilized DNA
- 4 pouches of *E. coli* Fast-Media® Zeo (2 TB and 2 Agar)

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 *E. coli* Fast-Media® Zeo at room temperature. Fast-Media® pouches are stable 18 months when stored properly.

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-hIgG2-Fc 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 utilizing InvivoGen's SEAP Reporter Assay Kit (rep-sap) or QUANTI-Blue™ (rep-qb1 or repqb2).

PLASMID FEATURES

• **hEF1-HTLV prom** is a composite promoter comprising the Elongation Factor-1 α (EF-1 α) 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-1 α promoter exhibits a strong activity and yields long lasting expression of a transgene *in vivo*. The R-U5' has been coupled to the EF-1 α 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.

• **hIgG4 Fc (human):** The Fc region of human IgG4 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 *Streptallosteichus 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.

Selection of bacteria with *E. coli* Fast-Media®

Fast-Media® is a fast and convenient way to prepare liquid and solid media for bacterial culture by using only a microwave. Fast-Media® is a TB (liquid) or LB (solid) based medium that already contains the antibiotic. Fast-Media® Zeo is available separately: #fas-zn-l (liquid), #fas-zn-s (agar).

Method:

- 1- Pour the contents of a Fast-Media® pouch into a clean borosilicate glass bottle or flask.
- 2- Add 200 ml of distilled water to the flask
- 3- Heat in a microwave on MEDIUM power setting (about 400Watts), until bubbles start appearing (approximately 3 minutes). **Do not heat a closed container. Do not autoclave Fast-Media®.**
- 4- Swirl gently to mix the preparation. **Be careful, the bottle and media are hot, use heatproof pads or gloves and care when handling.**
- 5- Reheat the media for 30 seconds and gently swirl again. Repeat as necessary to completely dissolve the powder into solution. But be careful to avoid overboiling and volume loss.
- 6- Let agar medium cool to 45°C before pouring plates. Let liquid media cool to 37°C before seeding bacteria.

Note: Do not reheat solidified Fast-Media® as the antibiotic will be permanently destroyed by the procedure.

References:

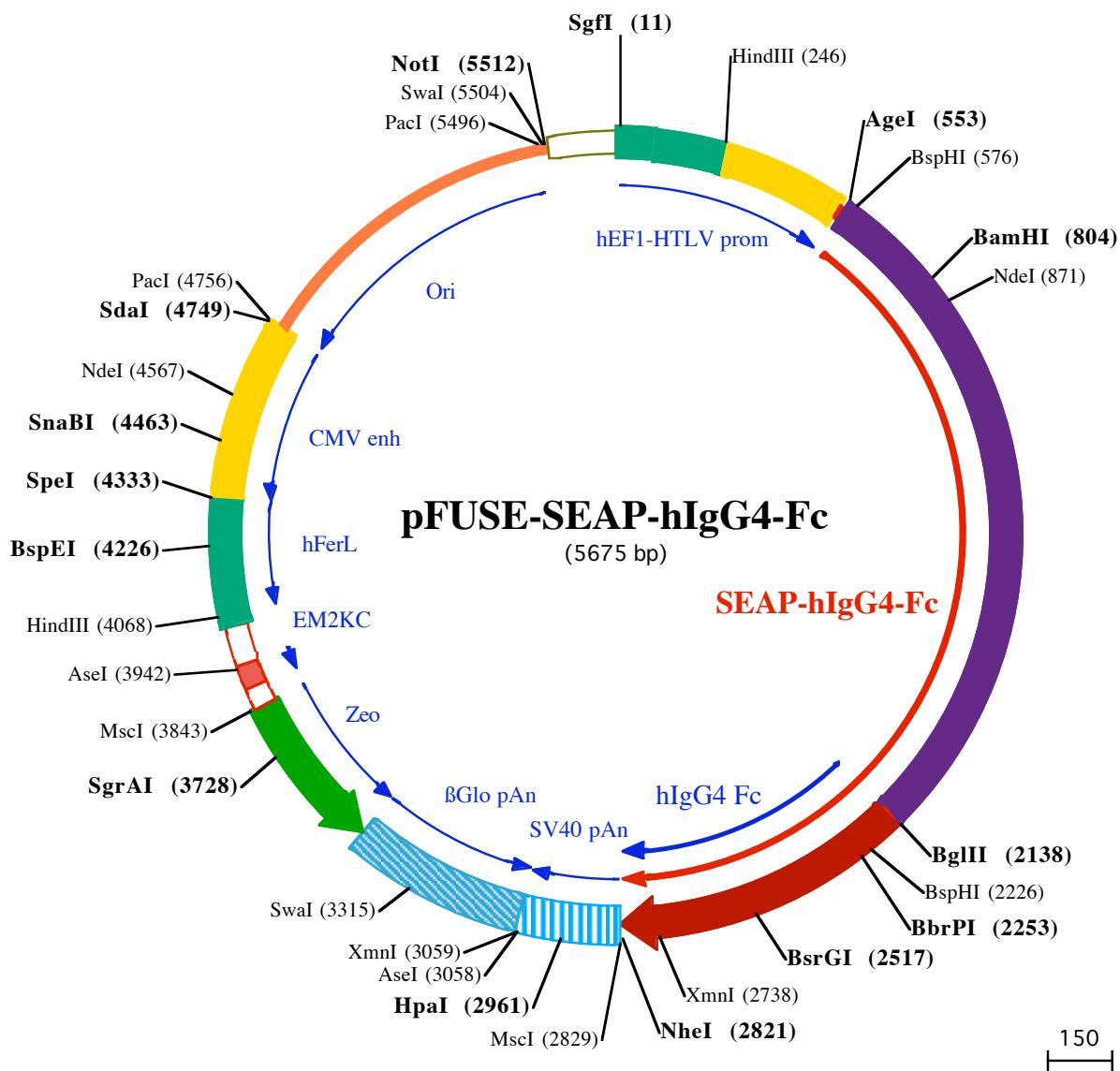
1. Kim, D.W. et al. (1990). Gene 2: 217-223.
2. Takebe, Y. et al. (1988). Mol. Cell Biol. 1: 466-472.
3. Carswell, S., and Alwine, J.C. (1989). Mol. Cell Biol. 10: 4248-4258.
4. Yu J & Russell JE. (2001). Mol Cell Biol, 21(17):5879-88.

TECHNICAL SUPPORT

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Sgfl (11)

1 GGATCTGCATGCCGGTCCCCGTCAAGTGGCAGAGCGCACATGCCACAGTCCCAGAAGTTGGGGGAGGGTGGGCAATTGAACGGGTGCTA

101 GAGAAAGGTGGCGGGTAAACTGGAAAGTGATTCGTACTGGCTCGCTTTCCGAGGGTGGGGAGAACCGTATAAGTCAGTAGTCGCC

HindIII (246)

201 GTGAACGTTCTTCGCAACGGTTGCCAGAACACAGCTGAAGCTCGAGGGCTGCATCTCTTACCGGCCGCCCTACCTGAGGCC

301 GCCATCCAGCCGGTGAAGTCGCTCTGCCCTCCCGCTGGTGCCTCTGAAGTCCGCTCCCGTAGTAAGTTAACGTCAGGTCAGACC

401 GGGCTTGTCCGGCGCCCTGGAGCCTACCTAGACTCAGCCGCTCTCCACGCTTGCCTGACCTGCTCAACTCTACGCTTGTCTT

AgeI (553)

501 TCTGTTCTGCCTTACAGATCCAAGCTGACCGGGCCTACCTGAGATACCGGTTAGCTGAGGAGGACATCATGATTCTGGGCCCTGCATGCT
→ 1►Met I eLeu Gl y ProCysMet Le

601 GCTGCTGCTGCTGCTGGGCTGAGGCTACAGCTCTCCCTGGCATCATCCAGTTGAGGAGGAACCCGGACTTCTGGAACCGCGAGGCCAG
8► uLeuLeuLeuLeuLeuGl yLeuArgLeuGl nLeuSerLeuGl l eLei eP r oVal Gl uGl uAsnPr oAspHeTrpAsnArgGl uAl aAl aGl u

701 GCGCTGGGTGCCGCCAGAACGCTGCAGCCTCACAGCAGCCCAAGAACCTCATCTCTGGCGATGGGGTGTCTACGGTACAGCTG
42► Al aLeuGl yAl aAl aLysLeuGl nProAl aGl nThr Al aAl aLysAsnLeu l eLePheLeuGl yAspGl yMet Gl yVal Ser Thr Val Thr Al aA

BamHI (804)

801 CCAGGATCTAAAAGGGCAGAAGAAGGACAAACTGGGCTGAGATACTGGCTATGGACCGCTCCCATATGGCTCTGTCCAAAGACATACAATGT
75► l aArgl l eLeuGl yGl nLysLysAspLysLeuGl yProGl uI l eProLeuAl aMetAspArgPheProTyrVal l aLeuSer LysThr TyrAsnVa

901 AGACAAACATGTGCCAGACAGTGGAGCACAGCCAGGCCAACCTGTGGGGCTAACGGGCAACTTCCAGACATTGGCTTGAGTCAGCCGCCCTT
108► l AspLysHi sVal ProAspSer Gl yAl aThr Al aThr Al aTy rLeuCysGl yVal LysGl yAsnPheGl nThr l eGl yLeuSer Al aAl aAl aArgPhe

1001 AACAGTGAAACAGCACGCGCAACAGGCTACCTCCGTGATGAACTGGGCAAGAACGAGGAGTCAGTGGAGTGGTAACCCACACGAGTGC
142► AsnGl nCysAsnThr Th r ArgGl yAsnGl uVal l i eSer Val MetAsnArgAl aLysLysAl aGl yLysSer Val Gl yVal Val Thr Th r ArgVal G

1101 AGCACGCCGCCGCCGCCAACCTAGCCCACAGGGTAACCGCAACTGGTACCGGACGCCAGCTGGCTCGCTGGCCCGCCAGGGGTGCCAGGA
175► l InHi sAl aSer ProAl aGl yTh r Ty r Al h i s Th r Val AsnArgAsnTrpTyrSerAspAl aAspVal ProAl aSer Al aArgGl nGl uGl yCysGl nAs

1201 CATCGCTACGCAGCTCATCTCCACATGGACATTGATGTGATCTGGGGAGGCCAGAAGTACATTTGCATGGGAAACCCAGACCTGAGTACCA
208► p l eAl aTh r Gl nLeu l eLeuAsnMetAsp l eAspVal l eLeuGl yGl yAl aRgLysTyrMetPheArgMetGl yTh r ProAspProGl uTyrPro

1301 GATGACTACAGCCAAGTGGGACAGGCTGGACGGGAGAATCTGGTGGCAGGAATGGCTGGCAGGGTCCCGTATGTGGAACCGCAGT
242► AspAspTyrSer Gl nGl yGl yTh r ArgLeuAspGl yLysAsnLeuVa l Gl nGl uTrpLeuAl aLysArgGl nGl yAl aArgTyrVal TrpAsnArgTh r G

1401 AGCTCATGCAGGCTCCCTGGACCCTGCTGTGACCCATCTCATGGGTCTTTGAGCCTGGAGACATGAAATACGAGATCCACCGAGACTCCACACTGGA
275► l uLeuMetGl nAl aSer LeuAspProSer Val Th r Hi sLeuMetGl yLeuPheGl uProGl yAspMetLysTyrGl u l eHi sArgAspSer Th r LeuAs

1501 CCCCTCCCTGATGGAGTACAGAGGCTGCCCTGGCCCTGCTGAGCAGGAACCCCCCGCTCTCTCTCTGGAGGGTGGTCGATCGACCAAGGT
308► pProSer LeuMetGl uMetTh r Gl uAl aAl aLeuArgLeuSerArgAspProArgGl yPheLeuPheValGl uGl yArgl l eAspHi sGl y

1601 CATACGAAAGCAGGGTACCGGGACTGACTGAGACGATCATGTTGACGACGCCATTGAGGGCGGGCCAGCTCACCGAGGAGGACACGCTGA
342► Hi sGl uSer ArgAl aTyr ArgAl aLeuThr Gl uTh r l i eMetPheAspAspAl l i eGl uArgAl aGl yGl nLeuThr Ser Gl uGl uAspThr LeuS

1701 GGCCTGCACTGGGCCACCACTCCACGCTCTCTGGAGGCTACCCCTGCGAGGGAGCTCATCTGGGGCCCTGGCAAGGCCGGAGAC
375► er LeuVal Th r Al aAspHi sHi sVal PheSer PheGl yGl yTyrProLeuArgGl ySer Ser l i ePheGl yLeuAl aProGl yLysAl aArgAspAr

1801 GAAGGCCCTACCGGCTCTTACCGGAAACGGCTCAGGTATGTGCTCAAGGACGGGCCGGCGATGTTACCGAGAGCAGGGAGCCCCGGAG
408► gLysAl aTyrTh r Val LeuLeuTyrGl yAsnGl yProGl yTyrVal LeuLysAspGl yAl aArgProAspVal Th r Gl uSer Gl ySer ProGl u

1901 TATCGGCAGCAGTCAGCAGTGGCCCTGGACGAAGAGACCCACGCAGGGCAGGACGTGGCGGTGTTCGCGCCGGCCCGAGCCACCTGGTACGGG
442► TyrArgGl nGl nSer Al aVal ProAspGl uGl uTh r Hi sAl aGl yGl uAspVal Al aVal PheAl aArgGl yProGl nAl aHi sLeuVal Hi sGl yV

2001 TGAGGAGCAGACCTTACGGCACGCTCATGGCCGGCTGGAGGCCACCCCTGGACGAGGACCTACACGGCTGGCACCTGGGCCCCCGCCGGACCCGAGC
475► al Gl nGl uGl nThr Phel l eAl aHi sVal MetAl aPheAl aAl aCysLeuGl uProTyrTh r Al aCysAspLeuAl aProProAl aGl yTh r Th r AspAl

BglII (2138)

2101 CGCGCACCCGGGGGGTCCAGCTGGATAGATCTCCCCATGCCCATATGCCAGACCTGAGTTCTGGGGGACCATCAGTCTTCTG
508► aAl aHi sProGl yArgSer ArgSer LysArgLeuAspArgSer ProProCysProSer CysProAl aProGl uPheLeuGl yGl yProSer Val PheLeu
1► ProProCysProSer CysProAl aProGl uPheLeuGl yGl yProSer Val PheLeu

BspHI (2226)

2201 TTCCCCAAAACCAAGGACACTCTCATGATCTCCGGACCCCTGAGGTACCTGGCTGGGGAGCTGAGCCAGGAAGACCCGGAGGTCAGTCA
542► PheProProLysProLysAspThr LeuMet l eSer ArgThr ProGl uVal Th r CysVal Val Val AspVal Ser Gl nGl uAspProGl uVal Gl nPheA
20► PheProProLysProLysAspThr LeuMet l eSer ArgThr ProGl uVal Th r CysVal Val Val AspVal Ser Gl nGl uAspProGl uVal Gl nPheA

2301 ACTGGTACGTGGATGGCTGGAGGTGCATAATGCCAACAGAACAGCCGGGGAGGAGCAGTTCAACAGCACGTCACCGTGTGGTCAGC
575► snTrpTyrValAspGl yVal Gl uVal Hi sAsnAl aLysThr LysProArgGl uGl uPheAsnSer Th r ArgVal Val Ser Val LeuThr Val Le
53► snTrpTyrValAspGl yVal Gl uVal Hi sAsnAl aLysThr LysProArgGl uGl uPheAsnSer Th r ArgVal Val Ser Val LeuThr Val Le

2401 GCACCAAGGACTGGCTAACGGAGATACAAGTCAAGGGTCTCAAACAGGCCCTCCGTCTCCATCGAGAAAACCATCTCAAAGCCAAGGGCAG
608► uHi sGl nAspTrpLeuAsnGl yLysGl uTyrLysCysLysVal SerAsnLysGl yLeuProSer Ser l i eGl uLysThr l i eSer LysAl aLysGl yGl n
86► uHi sGl nAspTrpLeuAsnGl yLysGl uTyrLysCysLysVal SerAsnLysGl yLeuProSer Ser l i eGl uLysThr l i eSer LysAl aLysGl yGl n

BsrGI (2517)

2501 CCCCGAGAGCCACAGGTGACCTGGCCCCATCCAGGAGGAGATGCCAACAGGTCAGCTGACCTGCCGCTAAAGGCTTCTACCCAGC
642► ProArgGl uProGl nVal TyrThr LeuProProSer Gl nGl uGl uMetTh r LysAsnGl nVal Ser LeuThr CysLeuVal LysGl yPheTyrProSer A
120► ProArgGl uProGl nVal TyrThr LeuProProSer Gl nGl uGl uMetTh r LysAsnGl nVal Ser LeuThr CysLeuVal LysGl yPheTyrProSer A
2601 ACATCGCGTGGAGGGAGACCAATGGCAGGGAGACAACACTACAAGACCACGCCCTCCGTGCTGGACTCCGACGCCCTTCTTACAGCAG
675► sp l eAl aVal Gl uTrpGl uSerAsnGl yGl nProGl uAsnAsnTyrLysTh r ProProVal LeuAspSerAspGl ySer PhePheLeuTyrSer Ar
153► sp l eAl aVal Gl uTrpGl uSerAsnGl yGl nProGl uAsnAsnTyrLysTh r ProProVal LeuAspSerAspGl ySer PhePheLeuTyrSer Ar

XmnI (2738)

2701 GCTAACCGTGGACAAGAGCAGGTGGCAGGGAGGAATGCTCTCATGCTCGTATGCAGGGCTCTGACAACACTACACAGAGGCCTCC
708► gLeuThr Val AspLysSer ArgTrpGl nGl uGl yAsnVal PheSer CysSer Val MetTh r Hi sGl uLeuHi sAsnHi sTyrTh r Gl nLysSer LeuSer
186► gLeuThr Val AspLysSer ArgTrpGl nGl uGl yAsnVal PheSer CysSer Val MetTh r Hi sGl uAl uLeuHi sAsnHi sTyrTh r Gl nLysSer LeuSer

MscI (2829)

2801 CTGTCCTGGTAAATGAGTGCAGCTGGCCAGACATGATAAGATACTGATGAGTTGGACAAACCAACTAGAATGCAGTAAAAAATGTTTAT

742► LeuSer ProGl yLys***

220► LeuSer ProGl yLys***

NheI (2821)

2901 TTGTGAAATTGTGATGCTATTGCTTATTGTAACCATTATAAGCTCAATAAACAGTTAACACAATTGATTCTTATGTTTCAGGTTCA

AseI (3058)

3001 GGGGAGGTGGGGAGGTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTAACTCAAACAGCATAGCAAAACTTAACTCCAATC

3101 AAGCCTACTTGAATCCTTCTGAGGGATGAATAAGGCATAGGCATAGGGCTGTTCCAATGTCATTAGCTGTTGAGCCTCACCTCTTCAT
 3201 GGAGTTAAGATATAGTGTATTTCCAAGGTTGAAGTCTTCATTTCTTATGTTAAATGCACTGACCTCCACATTCCCTTTAGTAAAAT

Swal (3315)

3301 ATT CAG A A A T A T T A A A T A C T C A T T G C A T G A A A A T A A T G T T T T A T A G G C A G A A T C C A G A T G C T C A A G G C C T C A T A A T A T C C C A G T T A G
 3401 TAGTTGGACTTAGGAAACAAGGAACCTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTATCCTCAGTCCTGCTCCCTGCCACAAAGTGC
 3501 ACGCAGTTGCCGCCGGGTGCGCAGGGGAACCTCCGCCAACGGCTGCTGCCGATCTGGTATGGCCGGGGAGGGCTCCGGAAAGTCGTGG
 115◀ aI Cys Asn Glu Al aPro Asp Arg Leu Al aPhe Glu I Arg Gly Trp Pro Glu nGl uGl l eGl uThr Met Al aPro Glu Ser Al aAsp Arg Phe Asn Thr Se
 3601 ACACGACCTCGACCCTCGGTACAGCTCGCCAGGCCACACCCAGGGTGTGTCGGCACACCTGGTCTGGACCGCCTGAT
 82◀ r Val Val Glu User Trp Glu Al aTyr Leu Glu I Asp Leu Glu I Arg Val I Trp Val I Trp Al aLeu Thr Asn Asp Pro Val Val Glu nAsp Glu nVal Al aSer I le

SgrAI (3728)

3701 GAACAGGGTCACGTCGTCGGACACACCGGGAAGTCGTCCTCACGAAGTCCGGAGAACCCAGGCCGGTCTGGCCAGAACCTGACCGCTCCGG
 49◀ Phe Leu Thr Val Asp Asp Arg Val Val Glu yAl aPhe Asp Asp Glu uVal Phe Asp Arg Ser Phe Glu I Leu Arg Asp Thr Trp Phe Glu uVal Al aGl yAl aV
 MscI (3843)

3801 ACGTCGCGCGGGTGAGCACGGACGGCACTGGTCAACTTGGCCATGATGGCTCCTCctgtcaggagagggaaagagaaggtagtacaattgCTAT
 15◀ aI Asp Arg Al aThr Leu Val Pro Val Al aSer Thr Leu Lys Al aMet

AseI (3942)

3901 AGT GAG TTG TATT A T A C T AT G C A G A T A T A C T AT G C C A T G T C A A T G T C A A C T A G G G C T G C A g g t t c a t a g t g c c a c t t t c t g c a c t g c c c a t c

HindIII (4068)

4001 tcctggccaccctttcccaggcatagacagtcaacttcacAAACTCACAGGAGGGAGAACGGCAGAGCTTGAGACAGACCCGGGACCGCCGA
 4101 GCGAGGGGACGTGGCTAGGGGGCTTCTTTATGGTGCAGGGGGCTGGAGGGGGCTGGGGAGGCCATGGGCAATCTGGTGGCAGGGC

BspEI (4226)

4201 GGGGCCGAAGGCCGTGCTGACCATCCGGAGCACATAGGAGTCTCAGCCCCCGCCCAAAGCAAGGGGAAGTCACGCCCTGAGGCCAGCGTGGT

SpeI (4333)

4301 TGAAATGGGGCTGGGGGGTTGGGGCCCTGACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGAGACTGGAAATCCCGTGA
 4401 CTATCCACGCCATTGATGTAAGTCCAAACCGCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCAAAGTAGGAAGTCCCATAAGTC

NdeI (4567)

4501 ATG TACTGGGCATAATGCCAGGGGCCATTACCGTCAATTGACGTCAATAGGGGGCTACTTGGCATATGATACTACATTGATGTA
 4601 TTTACCGTAAATACCCATTGACGTCAATGGAAAGTCCATTGGCGTTACTATGGGAACATACGTATTGACGTCAATGGGGGGGTC

PacI (4756)

SdaI (4749)

4701 GGGCGGTAGCCAGGCAGGGCATTACCGTAAGTTATGTAACGCCCTCGAGGTTAATTAAGAACATGAGCAAAGGCCAGCAAAGGGCAGGAACCGTA
 4801 AAAAGGCCGCGTTGGCTGGCTTTCCATAGGCTCGCCCGGCTGACGAGCATCACAAATCGACGCTCAAGTCAGAGGTGGCAGAACCCGACAGGACT

4901 ATAAAGATAACCAGGGTTCCCTGGAAGCTCCCTGTGCGCTCCTGTTCCGACCCCTGCCGTTACGGGATACCTGTCGCTTCCCTGGGA
 5001 AGCGTGGCCTTCATAGCTACCGCTGAGGTATCTCAGTTGGCTGAGGTGTCGCTCCAGCTGGCTGTGACGAACCCCCGGTCAGCCG
 5101 ACCGCTGCCCTATCCGTAACTATCGTCTGAGTCCAACCGGAAGACACGACTTATGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC
 5201 GAGGTATGAGGGCGTCTACAGAGTTCTGAAGTGGCTTAACACTACGGCTACACTAGAAGAACAGTTGGTATTCGCTGCTGAGCCATT
 5301 ACCTTCGGAAAAAGAGTTGGTAGCTTGTACCGCAAACAAACCCAGCTGGTAGCGGTGGTTTTGCAAGCAGCAGATTACGCGCAGAAAAA

PacI (5496)

5401 AAGGATCTAAGAACGATCTTGATCTTCTACGGGTCTGACGCTCAGTGGAAACGAAACTCACGTTAAGGGATTGGTATGGCTAGTTAAC

Swal (5504) NotI (5512)

5501 ATTTAAATCAGCGGCCAATAAAATCTTATTTCTTACATCTGTTGTTGGTTGGTGAATGTAACATACGCTCTCCATCAAAC
 5601 AAACGAAACAAACAAACTAGCAAATAGGCTGCCAGTGCAAGTGCAGGTGCAAGAACATTCTATCGAA