

pUNO1-SpikeV5-dfur

Expression vector encoding the SARS-CoV-2 Brazilian variant (P.1 lineage) Spike (delta furin) gene

Catalog code: p1-spike-v5-df

<https://www.invivogen.com/brazil-p1-spike-expression-vectors>

For research use only

Version 21E07-ED

PRODUCT INFORMATION

Contents

- 20 µg of lyophilized pUNO1-SpikeV5-dfur (plasmid DNA)
- 2 x 1 ml of Blasticidin (10 mg/ml)

Storage and Stability

- Product is shipped at room temperature.
- Store lyophilized DNA at -20°C.
- Resuspended DNA is stable for 1 year at -20°C.
- Store Blasticidin at 4°C or -20°C. The expiry date is specified on the product label.

Quality control

- Plasmid construct is confirmed by restriction analysis and full-length open reading frame (ORF) sequencing.
- After purification by ion exchange chromatography, predominant supercoiled conformation is verified by electrophoresis.

PLASMID FEATURES

Brazilian Variant SARS-CoV-2 Spike cassette

- EF-1 α /HTLV hybrid promoter is a composite promoter comprised of the Elongation Factor-1 α (EF-1 α) core promoter¹ and the 5' untranslated region of the Human T-Cell Leukemia Virus (HTLV). EF-1 α utilizes a type 2 promoter that encodes a "house-keeping" gene. It is expressed at high levels in all cell cycles and lower levels during the G0 phase. Additionally, since the promoter is not tissue-specific it is highly expressed in all cell types. The R segment and part of the U5 sequence (R-U5') of the HTLV Type 1 Long Terminal Repeat² has been coupled to the EF-1 α promoter to enhance stability of DNA and RNA. This modification not only increases steady state transcription, but also significantly increases translation efficiency.

• Codon-optimized Spike ORF

pUNO1-SpikeV5-dfur contains the Spike (S) coding sequence from the Brazilian (BRA) variant (P.1 lineage). This variant is characterized by a number of deletions (del) and mutations within the Spike coding sequence (see below)³. The furin cleavage site in pUNO1-SpikeV5-dfur has been inactivated (dfur) by the inclusion of two mutations (R683/5A). Furthermore, to improve expression of the S protein in cell lines, the gene is codon-optimized and the last 19 amino acids, which contain an ER-retention motif (KxHxx), have been removed^{4,5}.

pUNO1-SpikeV5-dfur includes the following sequence features:

- **S1 domain:** L18F, T20N, P26S, D138Y, R190S, D614G, H655Y
- **RBD:** K417T, E484K, N501Y
- **S1/S2 boundary:** R683A, R685A
- **S2 domain:** T1072I, V1176F

Spike (S) is a structural glycoprotein expressed on the surface of SARS-CoV-2. It mediates membrane fusion and viral entry into target cells upon binding to the host receptor ACE2 and the proteolytic activity of host proteases such as furin and TMPRSS2⁶.

For more information visit: <https://www.invivogen.com/sars2-spike>

- SV40 pAn is the Simian Virus 40 late polyadenylation (pAn) signal and it enables efficient cleavage and polyadenylation reactions resulting in high levels of steady-state mRNA⁷

Antibiotic selection cassette

- hCMV (human cytomegalovirus) enhancer & promoter drive the expression of the blasticidin resistance gene (*bsr*) in mammalian cells.
- EM7 is a bacterial promoter that enables the constitutive expression of the blasticidin resistance gene (*bsr*) in *E. coli*.
- *bsr* (blasticidin resistance gene) encodes a deaminase from *Bacillus cereus* that confers resistance to the antibiotic blasticidin. The expression of the *bsr* gene is driven by the CMV promoter/enhancer and the bacterial EM7 promoter. Therefore, Blasticidin can be used to select stable clones in mammalian cells and *E. coli* transformants.
- Human β-Globin pAn is a strong polyadenylation (pAn) signal placed downstream of *bsr*. The use of β-globin pAn minimizes interference and possible recombination events with the SV40 pAn signal⁸.

General features of pUNO1-SpikeV5-dfur

- pMB1 ori is a minimal *E. coli* origin of replication.

APPLICATIONS

Stable gene expression in mammalian cells.

pUNO1 plasmids are designed for both transient and stable transfection in mammalian cell lines by selection with Blasticidin. Furthermore, they facilitate high levels of expression of the gene of interest.

Antibody screening by flow cytometry

pUNO1-SpikeV5-dfur has been specifically designed for mammalian cell expression of the SARS-CoV-2 S protein. Notably, due to the inactivated furin cleavage site, when this plasmid is expressed by a host cell (e.g. 293T cells) there is high surface expression of the full-length S protein^{4,9}. Ideal for SARS-CoV-2 S-specific antibody screening by flow cytometry (*in-house data*).

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 water.
- Store the resuspended plasmid at -20°C.

• Plasmid amplification and cloning

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

• Blasticidin usage

Blasticidin should be used at 25-100 µg/ml in bacteria and 1-30 µg/ml in mammalian cells. Blasticidin is supplied as a 10 mg/ml colorless solution in HEPES buffer.

REFERENCES

1. Kim D. et al., 1990. Use of the human elongation factor 1 α promoter as a versatile and efficient expression system. Gene 91(2):217-23 2. Takebe Y. et al., 1988. SR alpha promoter: 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. 3. Faria, N.R. et al. 2021. Genomics and epidemiology of the P.1 SARS-CoV-2 lineage in Manaus, Brazil. Science. doi:10.1126/science.abh2644. 4. Johnson, M.C. et al. 2020. Optimized Pseudotyping Conditions for the SARS-CoV-2 Spike Glycoprotein. J Virol 94. 5. Ou, X. et al. 2020. Characterization of spike glycoprotein of SARS-CoV-2 on virus entry and its immune cross-reactivity with SARS-CoV. Nat Commun 11, 1620. 6. Hoffmann M. et al., 2020. SARS-CoV-2 cell entry depends on ACE2 and TMPRSS2 and is blocked by a clinically proven protease inhibitor. Cell. 181:1-16. 7. Carswell S. & Alwine J., 1989. Efficiency of utilization of the simian virus 40 late polyadenylation site: effects of upstream sequences. Mol Cell Biol. 9(10):4248-58. 8. Yu J. & Russell J., 2001. Structural and functional analysis of an mRNP complex that mediates the high stability of human β -globin mRNA. Mol Cell Biol. 21(17):5879-88. 9. Walls, A.C. et al. 2020. Structure, Function, and Antigenicity of the SARS-CoV-2 Spike Glycoprotein. Cell.

RELATED PRODUCTS

Product	Description	Cat. Code
Blasticidin ChemiComp GT116	Selection antibiotic Competent <i>E. coli</i>	ant-bl-1 gt116-11
COVID-19 Product Range		
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A549-hACE2-TMPRSS2 Cells	Cell Line	a549-hace2-tpsa
pUNO1-hACE2	Expression vector	puno1-hace2
pUNO1-hTMPRSS2a	Expression vector	puno1-htp2a
Anti-CoV2RBD-c1-hlgG1	Recombinant Antibody	cov2rbdc1-mab1

For a complete list of InvivoGen's COVID-19 related products visit:
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TECHNICAL SUPPORT

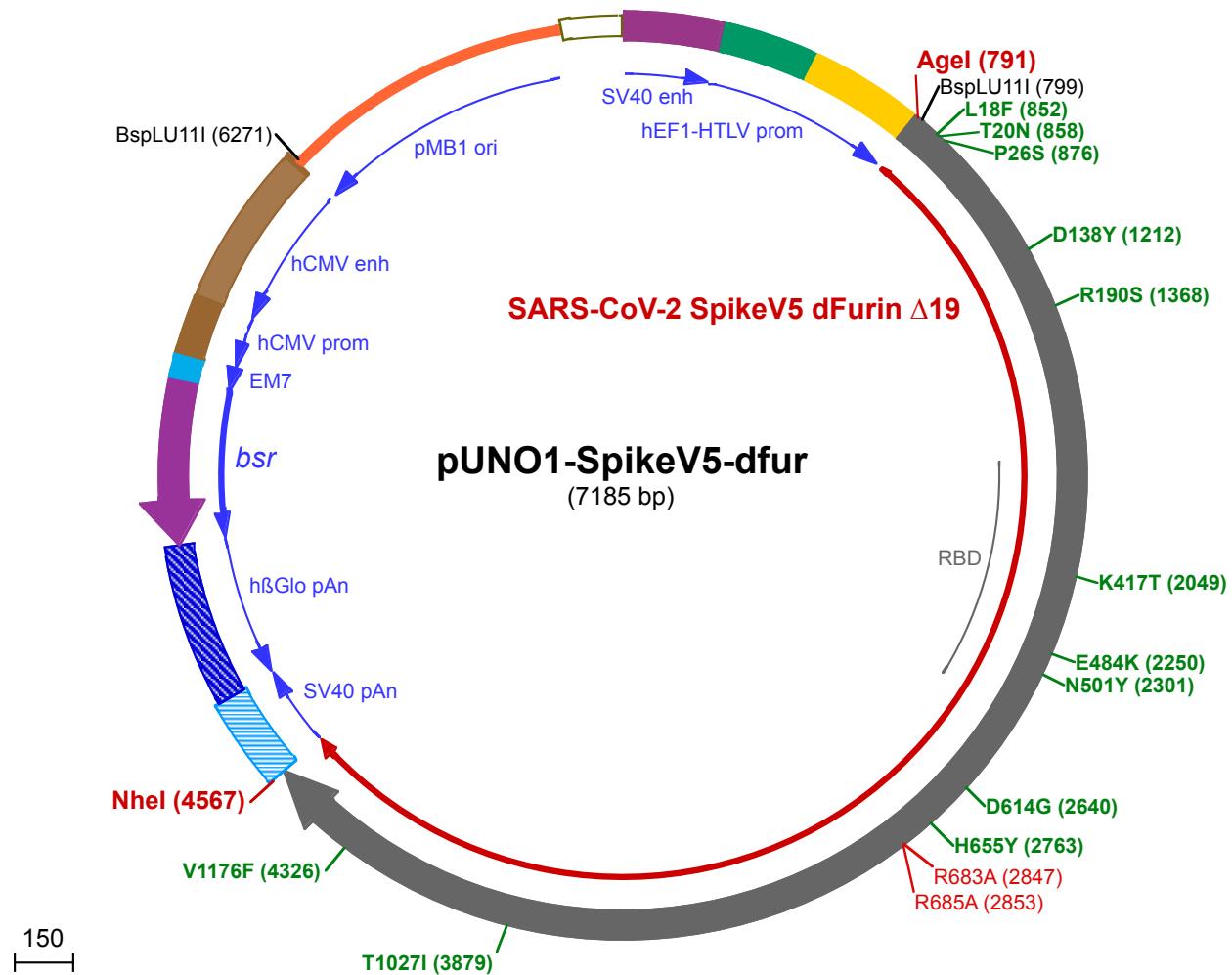
InvivoGen USA (Toll-Free): 888-457-5873

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

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InvivoGen Hong Kong: +852 3622-3480

E-mail: info@invivogen.com



1 GGACCTGCAGGCCGCTGAAATAACCTCTGAAAGAGGAACCTGGTTAGGTACCTCTGAGGCCGAAAGAACAGCTGTGGAATGTGTCAGTTAGGGTGTG
 101 GAAAGTCCCCAGGCTCCCCAGCAGGAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGAAAGTCCCAGGCTCCAGCAGGCAG
 201 AAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGAAAGTCCCAGGCTCCAGCAGGCAG
 301 GAAGTTGGGGGAGGGTGGCAATTGAACGGGTGCCTAGAGAAGGTGGCGGGTAAACTGGAAAGTGATGTCGTACTGGCTCCGCTTTCCC
 401 GAGGGTGGGGGAGAACCGTATATAAGTCAGTAGTCAGCTTTCGCAACGGTTGCGCCAGAACACAGCTGAAGCTCGAGGGCT
 501 GCATCTCTCCTCACCGCCCCCGCCCTACCTGAGGCCCATCCACGCCGGTTGAGTCGCGTCTGCCGCTCCGCTGTGGTGCCTCTGAAC
 601 GTCCGCCGTCTAGTAAGTTAAAGCTCAGTCAGACCGGGCTTGTCCGGCCTCCCTGGAGCCTACCTAGACTCAGCCGCTCTCACGCTTGC
 701 CTGACCCCTGCTTGCCTAAGTCTACGTCTTGTGTTCTGCGCAGTTACAGATCCAAGCTGTGACCGGCCCTACCTGAGATCACCGTCAA

BspLU11 I(799)
AgeI (791)

T20N (858)
L18F (852) **P26S (876)**
 801 CATGTTTGTGTTCTGGTGTGCTTCACTGGTCAAGTCCCAATCGTTAAT**T****I****C****A****C****G****A****C****T****C****C****A****T****C****C****G****A****T****A****C****A****A****T****T****C****T****T****C****A**
 1 M F V P F L V L L P L V S S Q C V N F T N R T Q L P S A Y T N S F T
 901 AGAGGAGTGTACTATCCTGACAAGTGTGTTGGTCAAGTGTCTCCACTCTACTCAGGACCTTTCTGCGCTTCTTAACGTTACATGGTTCATG
 34 R G V Y Y P D K V F R S S V L H S T Q D L F L P F F S N V T W F H
 1001 CAATCCATGTGCTGGGACAAACGGCACCAAACGCTTGACAACCTGTATTGCCATTCAATGATGGGTGTACTTTGCCACAGAGAAATCCAACAT
 67 A I H V S G T N G T K R F D N P V L P F N D G V Y F A S T E K S N I
 1101 CATTGAGGATGGATTTGGACTACTCTGGACTCAAAGACACAGAGCCTGCTGATGTTAACACGCCACAAACGTTGTCAAAAGTGTGCAATT
 100 R I R G W I F G T T L D S K T Q S L L I V N N A T N V V I K V C E F

D138Y (1212)

1201 CAGTTTGCAAT**T****A****T****C****C****T****C****T****G****G****A****G****T****G****T****A****C****T****A****C****A****G****A****T****C****G**
 134 Q F C N Y P F L G V Y Y H K N N K S W M E S E F R V Y S S A N N C

R190S (1368)

1301 CCTCGAGTACGTGAGTCACCCCTTCTGATGGACCTGGAAGGGAAACAGGGAAACTTCAAGAACCTG**A****G****T****A****G****T****T****G****T****T****T****A****A****G****A****C****A****T****G****A****C****G****G****T**
 167 T F E Y V S Q P F L M D L E G K Q G N F K N L S E F V F K N I D G Y
 1401 TTTAAGATCTAGTAAGCATACGCCATCACCTGGTAAGGGATCTTCCCAGGGCTTTCAGCCCTGGAACCTTGGTTACTTGCTTATTGGTATC
 200 F K I Y S K H T P I N L V R D L P Q G F S A L E P L V D L P I G I
 1501 AATATCACCAGATTTCAGACCCCTCTGGCATTGCA**C****G****G****T****T****A****T****T****C****A****G****G****T****G****A****T****T****C****T****C****G****G****T****G****A****T****T****A****T**
 234 N I T R F Q T L L A L H R S Y L T P G D S S S G W T A G A A A Y Y
 1601 TCGGTATCTGCAACCAAGAACGTTCTGCTCAAGTACAACGAAAACGGCACTATTACGGATGCTGTTGATTGCCCCTGGACCCCTGTGAGACTAA
 267 V G Y L Q P R T F L L K Y N E N G T I T D A V D C A L D P L S E T K
 1701 ATGCACCCCTCAAGAGCTTACCGTTGAGAAGGGATTACCAAACCGTAATTTCGGGTCACCCACCGAAAGCATTGTGCGTTCCAAATATCACC
 300 C T L K S F T V E K G I Y Q T S N F R V Q P T E S I V R F P N I T

1801 AATCTGTGCTCCCTTGGCGAAGTGTCAATGCTACAAGGTTGCTCTGTGACGATGGAATAGGAACGCATCTCAATTGTGTCGTGATTACTCCG
 334 N L C P F G E V F N A T R F A S V Y A W N R K R I S N C V A D Y S

1901 TGCTGTACAATTCCGCTTTCTAACCTCAAGTGTATTGGCGTTCACCTACCAAAACTAACGACCTGTGCTTCAACTATGTGATGCCACTCTT
 367 V L Y N S A S F S T F K C Y G V S P T K L N D L C F T N V Y A D S F

K417T (2049)

2001 TGTGATACGAGGCATGAAAGTGAGACAGATTGACCCAGGGCAGACGGC**A****C****A****T****T****G****C****G****A****T****A****C****G****G****A****T****G****T**
 400 R I R G D E V R Q I A P G Q T G T I A D Y N Y K L P D D F T G C V

2101 ATTGCATGAACTCAAACATTGGATTCAAGGTGGTGGCAACTATAACTACCTGTATAGACTGTCAGGAATCCAACCTGAAACCATTGAGCGAG
 434 I A W N S N N L D S K V G G N Y N Y L Y R L F R K S N L K P F E R

E484K (2250)

2201 ATATAAGCACAGAAATCTACCAAGGCTGGAAGTACGCCCTGCAACGGCT**A****A****G****G****T****C****A****C****T****G****T****A****C****G****G****T****C****A****T**
 467 D I S T E I Y Q A G S T P C N G V K G F N C Y F P L Q S Y G F Q P T

N501Y (2301)

2301 AT**A****C****G****G****G****T****G****G****T****T****A****C****C****T****A****T****G****T****C****G****T****A****G****T****T****A****C****G****G****A****T**
 500 Y G V G Y Q P Y R V V V L S F E L L H A P A T V C G P K K S T N L

2401 GTGAAGAACAAATGCGTGAACCTTAACGGACTCACAGGAACGGCGTATTGACGGAGAGTAACAAGAAGTTCTGCCATTCCAGCAGTTGGT
 534 V K N K C V N F N F N G L T G T G V L T E S N K K F L P F Q Q F G

2501 GCGATATTGCCGACACTACCGACGCTGTCCGAGATCCCCAGACATTGGAGATTCTGATATCACACCTGTAGTTCGCGGAGTGAGCGTGA
 567 R D I A D T T D A V R D P Q T L E I L D I T P C S F G G V S V I T P

D614G (2640)

2601 CGGAACCAATACCAGCAATCAGGTTGCCGTCTGTATCAGGGCGTGATTGACCGAGGTACCTGTCGCCATCCACGCTGACCAACTTACACCCACATGG
600► G I N T S N Q V A V I Y O G V N C T E V P V A I H A D Q I T P T W

H655Y (2763)

2701 CGAGTATATTCCACCGGCTCCACGTCTTCAGACACGTGCTGGATGTCTGATCGGTGCAGAATACGTTAACATAAGCTACGAGTGTGATATCCCCATCG
634 R V Y S T G S N V F O T R A G C I I G A E Y V N M S Y E C D I P I

R685A (2853)

R683A (2847)

2801 GTGCTGGAATATGCCCTTATCAAACCAAACCTCTCTAGGGCGGCAGCTAGTGATCCCAGTATCATTGCCTACACAATGAGCCTCG
667▶G A G I C A S Y Q T Q T N S P R A A A S V A S Q S I I A Y T M S L G
2901 TCTGACAAATTCTCTCCCTACACCAACAACTCCATTCTATCCCTACTTCAGAACATCTGACAACTCAATTCTCCCTATCTATCACAAA

2901 TGCTGAGAAATTCTGTGCCAACAGCAACAACTCCATGGTACCTCCTAACTTACAAATCAGTGACAACTGAAATTCTGCCGTATCTGACCAAA
 700 A E N S V A Y S N N S I A I P T N F T I S V T T E I L P V S M T K
 3001 ACAAGCGTTGACTGCACCATGTACATCTGTGGGATTCTACCGAATGTAGCAATCTCCTCTGCAATACGGATCATTCTGCACTCAGCTGAATCTGCC

734▶ T S V D C T M Y I C G D S T E C S N L L L Q Y G S F C T Q L N R A
 3101 TCACAGGTATTGAGCTTGAGCAGGACAAGAATACGCAGGAAGTGTGCCCCAGGTGAAGCAAATCTACAAAACCCATAAAAGACTTTGGCGGATT
 767▶ T G I A V E F O D K N T O F V E A O V K O I Y K T P P I K D E G G F

3201 CAATTCTCACAGATCCTGCCGATCCCTCAAAACCTCCAAGCGTAGCTTATCGAGGATCTGCTCTTACAACAGGTAAACCTCGCAGATGCCGGTTTC
800▶ N F S Q I L P D P S K P S K R S F I E D L L F N K V T L A D A G F

3301 ATCAAGCAGTATGGCGATTGTCGGGAGACATGCCGCTCGGGACCTGATCTGTGACAGAAGTTAACATGGACTGACCGTGTGCCCTCCCTGACCG
 834 ▶ I K Q Y G D C L G D I A A R D L I C A Q K F N G L T V L P P L T
 3401 ACGAGATGATAGCCAAATACACTAGCGCCCTGCTGGCCGGCACCATCACTCTGGGTGGACATTGGAGCTGGCCTGCCCTTCAGATTCCCTTTGCTAT

867 D E M I A Q Y T S A L L A G T I T S G W T F G A G A L Q I P F A M
3501 GCAGATGGCTTACCGCTTAACGGCATGGTGACACAAAACGTTCTGTATGAAAACCAGAAACTCATGCCAACCGATTCAACAGTGCTATCGGTAAG
888 S M A X R E N G C Y T O N V A L Y E N G K I L A N G E N S A L G K

900 Q M A Y R F N G I G V I Q N V L Y E N Q K L I A N Q F N S A I G K
3601 ATACAGGATAGCCTGTATCCACTGCCAGCGATTGGGAAATTGCAGGATGTAGTGAACCAGAATGCCAGGACTTAACACCCCTGGTAAACAGCTCT
934 I Q D S L S S T A S A L G K L Q D V V N Q N A Q A L N T L V K Q L

3701 CTCAAATTTGGTGCCTAGCTGTAATGACATACTGAGCCGGTGGACAAGGTGGAGGCTGAAGTGCAGATTGATAGGCTGATAACTGGCG
967 S S N F G A I S S V L N D I L S R L D K V E A E V Q I D R L I T G R
T1027I(3879)

3801 CCTTCAGTCTCTCAGACCTATGTGACCCAGCAGCTATCCGCCTGCTGAATTGCGCATCCGTAACCTGGCAGCATTAAAATGTCGGAGTGTGTG
1000▶ L Q S L Q T Y V T Q Q L I R A E I R A S A N L A A M S E C V
 3801 CTCTGCTGACTCTAAAGAAGCTGCACTTTGCCGAGCCGATCTGACCTGATCTGTTTCTGCTAATCTGCGACCCGATCTGCTCTGCTGTTCTGCACTT

3901 CTGGGTCACTAAGAGAGTGGACTTTGCGGAAGGGATCACCTGATGTCCTTCCTAGCTGCACCCATGGTGTGGCTTCTGCACTGACTT
1034 P L G Q S K R V D F C G K G Y H L M S F P Q S A P H G V V F L H V T
4001 ATGCCCCAGCTCAGGAAAAGAACCTTCACTACAGCCCCAGCCATCTGCCACGATGGGAAGGCCACTTCCAGGGAAGGCCTATTGTCGTCATGGTAC

1067 Y V P A Q E K N F T T A P A I C H D G K A H F P R E G V F V S N G T
4101 TCATTGGTTCGTCAGAGAAATTCTACGAGCCCCAGATTATAACCACTGACAATACATTGTATCCGGCAATTGTGATGGTTATCGGGATTGTG
1100 H W F V T O R N E X F P Q L I T T D N T E V S C N C D V V I C L V

1100 P H W F V I Q R N F T E P Q I I I D N I F V S G N C D V V I G I V
4201 A A T A A T C T G T T A C G A T C C T T G C A G C C A G A G C T G G A C T C C T T C A A G G A G G A G C T T G A C A A A T A T T T A A G A A T C A C A C A T C A C C T G A C G T C G A C C T C G
1134 P N N T V Y D P L Q P E L D S F K E E L D K Y F K N H T S P D V D L

V1176F (4326)
4301 GAGATATTCAGGAATCAATGCTTCCTTGTCAATTACAGAAGGAGATAGACAGGCTGAATGAGGTTGCCAACCTCAACGAGTCTGTGATCGATCT
1167▶G D I S G I N A S F V N I O K E I D R L N E V A K N L N E S L I D L

4401 GCAGGAGTTGGCAAGTACGAACAGTATCAAATGCCATGGTACATTGGCTGGTTATTGCTGGCAGTAGCTATCGTCATGGTACAATTATG
 1200 Q E L G K Y E Q Y I K W P W Y I W L G F I A G L I A I V M V T I M
NheI (45G7)

NheI (4567)

4501 TTGTTGATGACATCTGCTGTAGTGTCTGAAGGGCTGCTCATGCCAGCTGTTCTAAAGCTAGCTGGCCAGACATGATAAGATACATTGAT
 1234► L C C M T S C C S C L K G C C S C G S C C •
 4601 GAGTTGGACAACCACAACTAGAATGCAGTGAAAAAAATGCTTATTGTAACCAATTATAAGCTGCAATA

4701 AACAGTTAACACAAATTGATTCTTTATGTTTCAGGGGAGGTGTGGAGGTTTAAAGCAAGTAAAACCTCTACAAATGTGGTAT

4801 GGAATTCTAAATACAGCATAGCAAAACTTAACTCTCAAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGCTG

4901 TTGCCAATGTGCAATTAGCTGTTGCAGCCTCACCTTCTTCATGGAGTTAAAGATATACTGTATTTCCAAAGGTTGAACTAGCTTCACTTCTTAT

5001 GTTTAAATGACTGACCTCCCACATTCCCTTTAGTAAAAATTCAGAAAATAATTAAATACATCATGGAAATGAAATAAATGTTTTATTAGGC

5101 GAATCCAGATGTCAGGGCCCTTCAATAATCCCCAGTTAGTAGTTGGACTTAGGGAAACAAAGGAACCTTAATAGAAAATTGGACAGCAAGAAAGCGA

5281 GCTTCTAAGCTTAACTTCCTGTTACTGAGGGGGATGAGTCTCAATGGTTGGTTTGACCACTTCATCTCAATGAGCAGAACAACTCAAGG
141 N R T Y K I P L I E F I T K V I K G N M F I I V E C D P

1114 A Y D S I L E R C M G C P S V R I S R D V E D S Y P H R V A V I

774 T D F D K Q G N S V A S G I A I A E A C V T V R G I Y A E I H V A S
5501 AGATGATCTCCCCAGTCTGGCTCTGATGCCGCCCCGACATGGTCTTGTCTCATAGACATGGTGTCTCAGTGGCAGCTCCACAGCTC
444 L I E C T K T P I A A C V H H K N D E Y I M T I K E T A V E V I E

5601 CAGATCTGCTGAGAGATCTGAAGTCTTCATGATGGCCCTCTATACTAGTGAATCGCTATTATACTATGCCGATACTATGCCGATGATTAAATGTCAAA

5601 CAGATCTTGCCTGAGAGA GTTGAAGGCTCTCATGATGGCCCTCTATACTAGTGAGTCGTATATACTATGCCGATATACTATGCCGATGATAATTGTCAAA

5701 ACACGTGGATGGCGTCTCCAGTTATCTGACGGTCACTAAACGAGCTTGCTTATATAGACCTCCCACCGTACACGCCCTACCGCCCATTGCGTCAAT
5801 GGGCGGAGTTACGACATTTGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCATTGACGTCAATGGGTGGAGACTTGAAATCCCCGTG
5901 AGTCAAACCGCTATCCACGCCATTGATGACTGCCAAAACCGCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTC
6001 CCATAAGGTATGTACTGGGCATAATGCCAGGCGGCCATTACCGTATTGACGTCAATAGGGCGTACTTGGCATATGATACACTTGATGTACTGCC
6101 AAGTGGCAGTTACCGTAAATACCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGAACATACGTATTGACGTCAATGGC
6201 GGGGTCGTTGGCGGTCAAGCCAGGCGGCCATTACCGTAAGTTATGTAACGCCCTGAGGTTAATTAAAGAACATGTGAGCAAAGGCCAGCAAAGGCC
6301 AGGAACCGTAAAAGGCCGCGTTGCGCTGGCGTTTCCATTAGGCTCCCTCGCCTCTCTGTTCCGACCTGCCCTTACCGATACTGTCCGCTTTCT
6401 CGACAGGACTATAAGATAACCAGCGTTCCCTGGAGCTCCCTCGCCTCTCTGTTCCGACCTGCCCTTACCGATACTGTCCGCTTTCT
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6801 GAAGCCAGTTACCTCGAAAAAGAGTTGGTAGCTTGTACCGCAAACAAACCACCGCTGGTAGCGTGGTTTTGTTGCAAGCAGCAGATTACG
6901 CGCAGAAAAAAAGGATCTCAAGAAGATCCTTGATCTTCTACGGGTGACGCTCAGTGGAAACAAACTACGTTAAGGGATTTGGCATGGCTA
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7101 CATCAAAACAAAAGAAACAAACAAACTAGCAAAATAGGCTGCCCCAGTGCAGTGCAAGTGCAGGTGCCAGAACATTCTATCGAA

BspLU11I (6271)