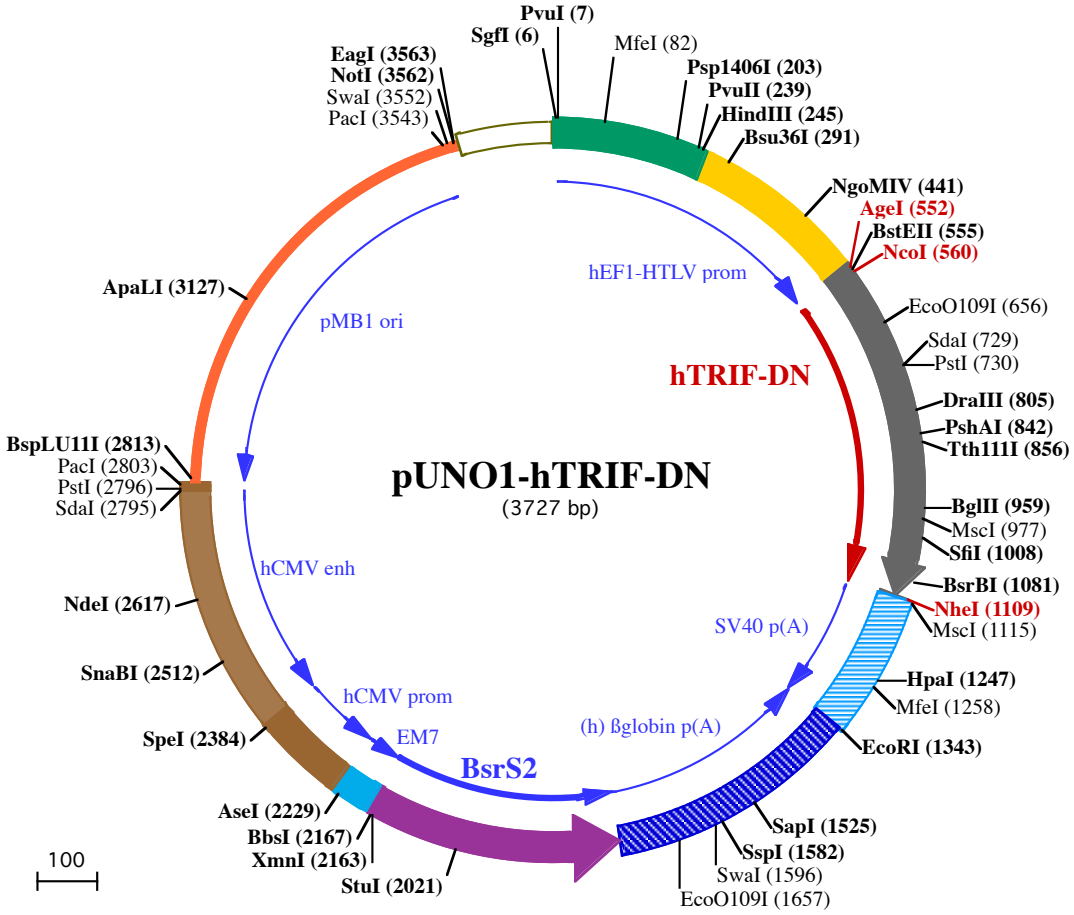
pUNO1-hTRIF-DN
(3727 bp)
hTRIF-DN
hEF1-HTLV prom
pMB1 ori
hCMV enh
hCMV prom
EM7
BsrS2
(h) ßglobin p(A)
SV40 p(A)
PvuI (7)
SgfI (6)
MfeI (82)
Psp1406I (203)
PvuII (239)
HindIII (245)
Bsu36I (291)
NgoMIV (441)
AgeI (552)
BstEII (555)
NcoI (560)
EcoO109I (656)
SdaI (729)
PstI (730)
DraIII (805)
PshAI (842)
Tth111I (856)
BglII (959)
MscI (977)
SfiI (1008)
BsrBI (1081)
NheI (1109)
MscI (1115)
HpaI (1247)
MfeI (1258)
EcoRI (1343)
SapI (1525)
SspI (1582)
SwaI (1596)
EcoO109I (1657)
StuI (2021)
XmnI (2163)
BbsI (2167)
AseI (2229)
SpeI (2384)
SnaBI (2512)
NdeI (2617)
BspLU11I (2813)
PacI (2803)
PstI (2796)
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EagI (3563)
NotI (3562)
SwaI (3552)
PacI (3543)
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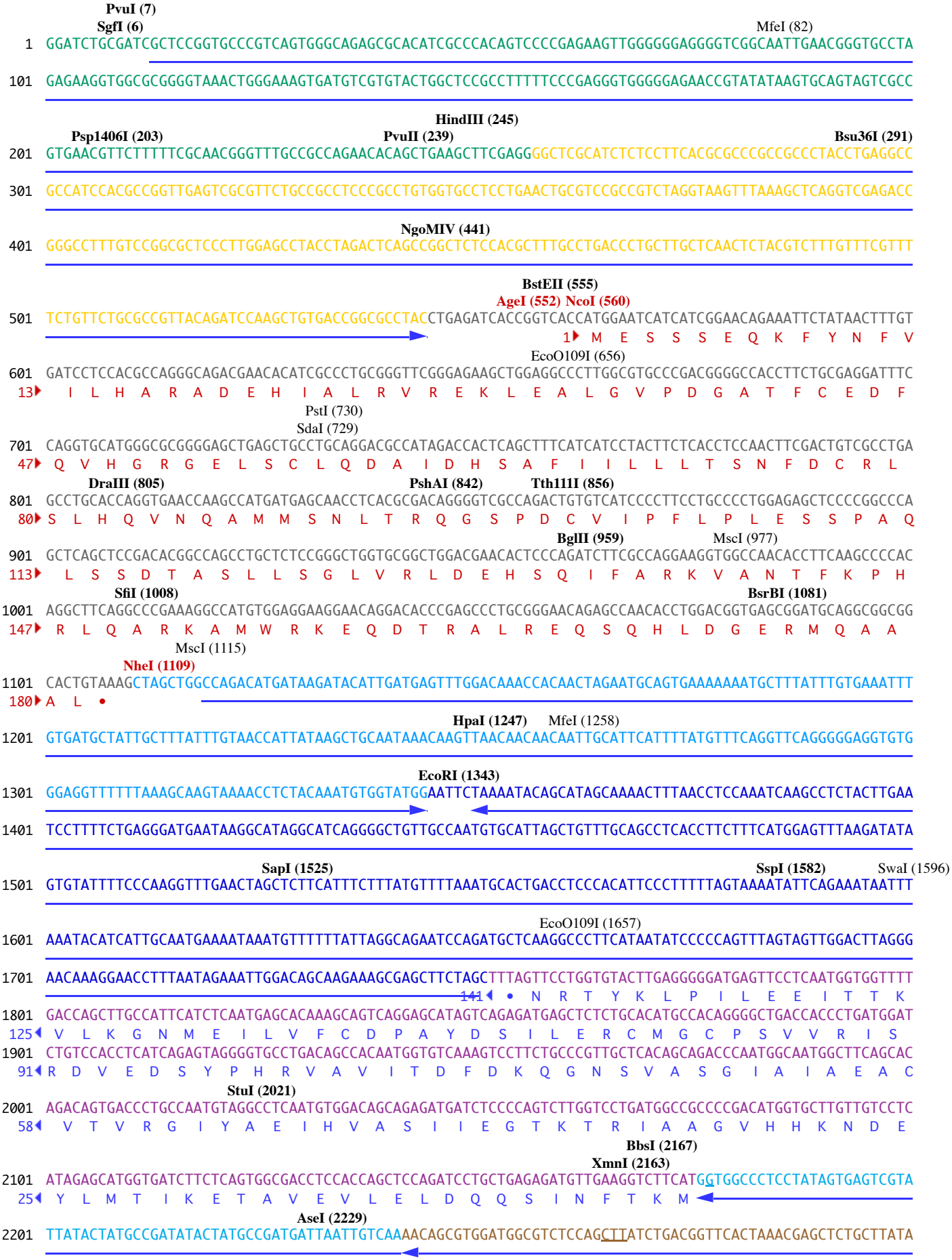
PvuI (7)
SgfI (6)
MfeI (82)
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC
HindIII (245)
Psp1406I (203)
PvuII (239)
Bsu36I (291)
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAACTCTACGTCTTTGTTTCGTTT
BstEII (555)
AgeI (552) NcoI (560)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTCACCATGGAATCATCATCGGAACAGAAATTCTATAACTTTGT
1 M E S S S E Q K F Y N F V
EcoO109I (656)
601 GATCCTCCACGCCAGGGCAGACGAACACATCGCCCTGCGGGTTCGGGAGAAGCTGGAGGCCCTTGGCGTGCCCGACGGGGCCACCTTCTGCGAGGATTTC
13 I L H A R A D E H I A L R V R E K L E A L G V P D G A T F C E D F
PstI (730)
SdaI (729)
701 CAGGTGCATGGGCGCGGGGAGCTGAGCTGCCTGCAGGACGCCATAGACCACTCAGCTTTCATCATCCTACTTCTCACCTCCAACTTCGACTGTCGCCTGA
47 Q V H G R G E L S C L Q D A I D H S A F I I L L L T S N F D C R L
DraIII (805)
PshAI (842)
Tth111I (856)
801 GCCTGCACCAGGTGAACCAAGCCATGATGAGCAACCTCACGCGACAGGGGTCGCCAGACTGTGTCATCCCCTTCCTGCCCCTGGAGAGCTCCCCGGCCCA
80 S L H Q V N Q A M M S N L T R Q G S P D C V I P F L P L E S S P A Q
BglII (959)
MscI (977)
901 GCTCAGCTCCGACACGGCCAGCCTGCTCTCCGGGCTGGTGCGGCTGGACGAACACTCCCAGATCTTCGCCAGGAAGGTGGCCAACACCTTCAAGCCCCAC
113 L S S D T A S L L S G L V R L D E H S Q I F A R K V A N T F K P H
SfiI (1008)
BsrBI (1081)
1001 AGGCTTCAGGCCCGAAAGGCCATGTGGAGGAAGGAACAGGACACCCGAGCCCTGCGGGAACAGAGCCAACACCTGGACGGTGAGCGGATGCAGGCGGCGG
147 R L Q A R K A M W R K E Q D T R A L R E Q S Q H L D G E R M Q A A
MscI (1115)
NheI (1109)
1101 CACTGTAAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAAAAAAATGCTTTATTTGTGAAATTT
180 A L •
HpaI (1247)
MfeI (1258)
1201 GTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTG
EcoRI (1343)
1301 GGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAAACTTTAACCTCCAAATCAAGCCTCTACTTGAA
1401 TCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAGATATA
SapI (1525)
SspI (1582)
SwaI (1596)
1501 GTGTATTTTCCCAAGGTTTGAACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCCTTTTTAGTAAAATATTCAGAAATAATTT
EcoO109I (1657)
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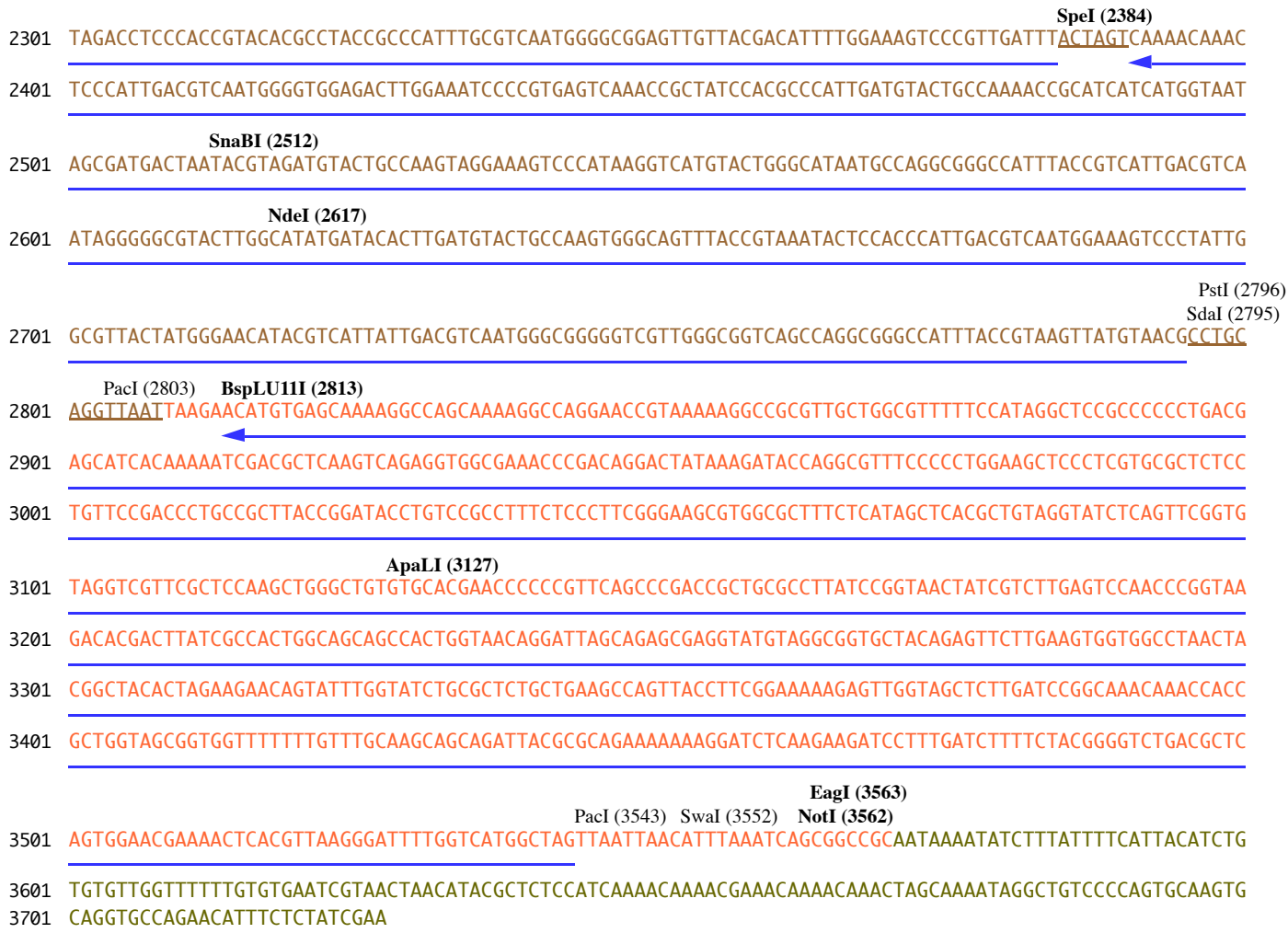
1701 AACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTT
141 • N R T Y K L P I L E E I T T K
1801 GACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGAT
125 V L K G N M E I L V F C D P A Y D S I L E R C M G C P S V V R I S
1901 CTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCAC
91 R D V E D S Y P H R V A V I T D F D K Q G N S V A S G I A I A E A C
StuI (2021)
2001 AGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCCTGATGGCCGCCCCGACATGGTGCTTGTTGTCCTC
58 V T V R G I Y A E I H V A S I I E G T K T R I A A G V H H K N D E
BbsI (2167)
XmnI (2163)
2101 ATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCCTATAGTGAGTCGTA
25 Y L M T I K E T A V E V L E L D Q Q S I N F T K M
AseI (2229)
2201 TTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATA


SpeI (2384)
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2401 TCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCCATTGATGTACTGCCAAAACCGCATCATCATGGTAAT
SnaBI (2512)
2501 AGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCA
NdeI (2617)
2601 ATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTG
PstI (2796)
SdaI (2795)
2701 GCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGC
PacI (2803)
BspLU11I (2813)
2801 AGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACG
2901 AGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCC
3001 TGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTG
ApaLI (3127)
3101 TAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAA
3201 GACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTA
3301 CGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACC
3401 GCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTC
EagI (3563)
PacI (3543)
SwaI (3552)
NotI (3562)
3501 AGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTG
3601 TGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTG
3701 CAGGTGCCAGAACATTTCTCTATCGAA