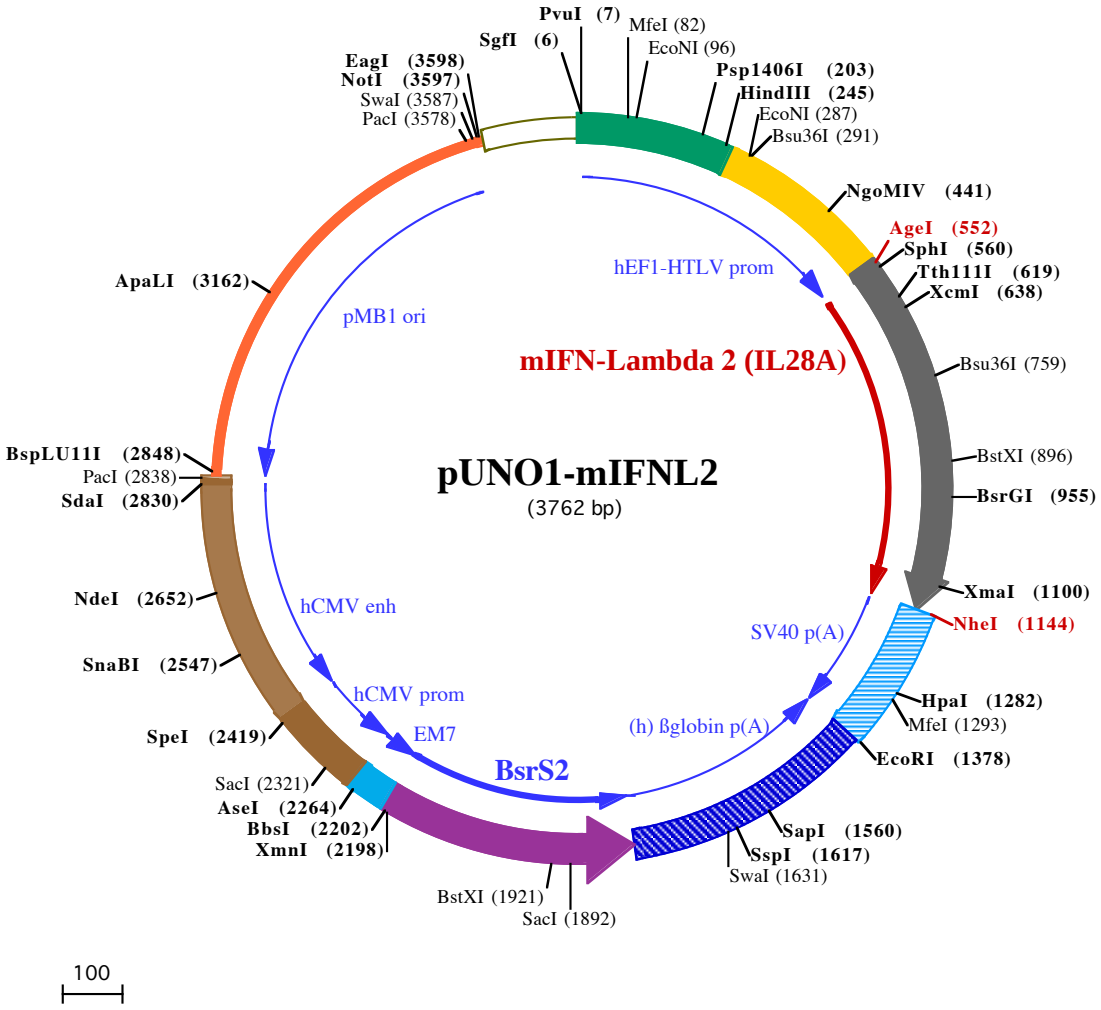
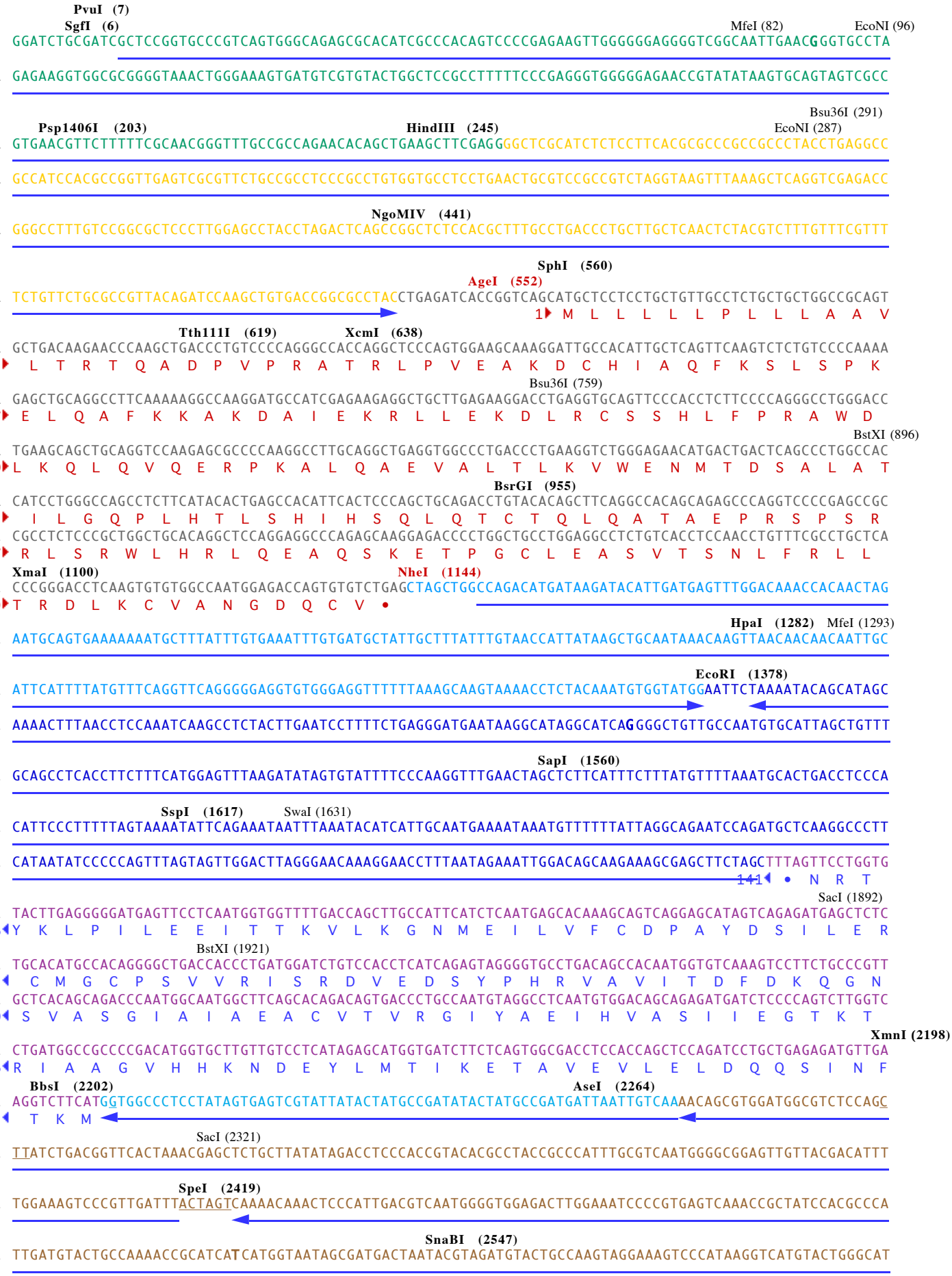

pUNO1-mIFNL2
(3762 bp)
mIFN-Lambda 2 (IL28A)
BsrS2
hEF1-HTLV prom
pMB1 ori
hCMV enh
hCMV prom
EM7
SV40 p(A)
(h) ßglobin p(A)
PvuI (7)
MfeI (82)
EcoNI (96)
Psp1406I (203)
HindIII (245)
EcoNI (287)
Bsu36I (291)
SgfI (6)
EagI (3598)
NotI (3597)
SwaI (3587)
PacI (3578)
NgoMIV (441)
AgeI (552)
SphI (560)
Tth111I (619)
XcmI (638)
Bsu36I (759)
BstXI (896)
BsrGI (955)
XmaI (1100)
NheI (1144)
HpaI (1282)
MfeI (1293)
EcoRI (1378)
SapI (1560)
SspI (1617)
SwaI (1631)
BstXI (1921)
SacI (1892)
SacI (2321)
AseI (2264)
BbsI (2202)
XmnI (2198)
SpeI (2419)
SnaBI (2547)
NdeI (2652)
BspLU11I (2848)
PacI (2838)
SdaI (2830)
ApaLI (3162)
100


PvuI (7)
SgfI (6)
MfeI (82)
EcoNI (96)
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101 GAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC
Bsu36I (291)
Psp1406I (203)
HindIII (245)
EcoNI (287)
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAACTCTACGTCTTTGTTTCGTTT
SphI (560)
AgeI (552)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTCAGCATGCTCCTCCTGCTGTTGCCTCTGCTGCTGGCCGCAGT
1 M L L L L L P L L L A A V
Tth111I (619)
XcmI (638)
601 GCTGACAAGAACCCAAGCTGACCCTGTCCCCAGGGCCACCAGGCTCCCAGTGGAAGCAAAGGATTGCCACATTGCTCAGTTCAAGTCTCTGTCCCCAAAA
13 L T R T Q A D P V P R A T R L P V E A K D C H I A Q F K S L S P K
Bsu36I (759)
701 GAGCTGCAGGCCTTCAAAAAGGCCAAGGATGCCATCGAGAAGAGGCTGCTTGAGAAGGACCTGAGGTGCAGTTCCCACCTCTTCCCCAGGGCCTGGGACC
47 E L Q A F K K A K D A I E K R L L E K D L R C S S H L F P R A W D
BstXI (896)
801 TGAAGCAGCTGCAGGTCCAAGAGCGCCCCAAGGCCTTGCAGGCTGAGGTGGCCCTGACCCTGAAGGTCTGGGAGAACATGACTGACTCAGCCCTGGCCAC
80 L K Q L Q V Q E R P K A L Q A E V A L T L K V W E N M T D S A L A T
BsrGI (955)
901 CATCCTGGGCCAGCCTCTTCATACACTGAGCCACATTCACTCCCAGCTGCAGACCTGTACACAGCTTCAGGCCACAGCAGAGCCCAGGTCCCCGAGCCGC
113 I L G Q P L H T L S H I H S Q L Q T C T Q L Q A T A E P R S P S R
1001 CGCCTCTCCCGCTGGCTGCACAGGCTCCAGGAGGCCCAGAGCAAGGAGACCCCTGGCTGCCTGGAGGCCTCTGTCACCTCCAACCTGTTTCGCCTGCTCA
147 R L S R W L H R L Q E A Q S K E T P G C L E A S V T S N L F R L L
XmaI (1100)
NheI (1144)
1101 CCCGGGACCTCAAGTGTGTGGCCAATGGAGACCAGTGTGTCTGAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAG
180 T R D L K C V A N G D Q C V •
HpaI (1282)
MfeI (1293)
1201 AATGCAGTGAAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGC
EcoRI (1378)
1301 ATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGC
1401 AAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTT
SapI (1560)
1501 GCAGCCTCACCTTCTTTCATGGAGTTTAAGATATAGTGTATTTTCCCAAGGTTTGAACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCA
SspI (1617)
SwaI (1631)
1601 CATTCCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTT
1701 CATAATATCCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTG
141 • N R T
SacI (1892)
1801 TACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTC
136 Y K L P I L E E I T T K V L K G N M E I L V F C D P A Y D S I L E R
BstXI (1921)
1901 TGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCCGTT
103 C M G C P S V V R I S R D V E D S Y P H R V A V I T D F D K Q G N
2001 GCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTC
70 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 I I E G T K T
XmnI (2198)
2101 CTGATGGCCGCCCCGACATGGTGCTTGTTGTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGA
36 R I A A G V H H K N D E Y L M T I K E T A V E V L E L D Q Q S I N F
BbsI (2202)
AseI (2264)
2201 AGGTCTTCATGGTGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAAACAGCGTGGATGGCGTCTCCAGC
3 T K M
SacI (2321)
2301 TTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTT
SpeI (2419)
2401 TGGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCCA
SnaBI (2547)
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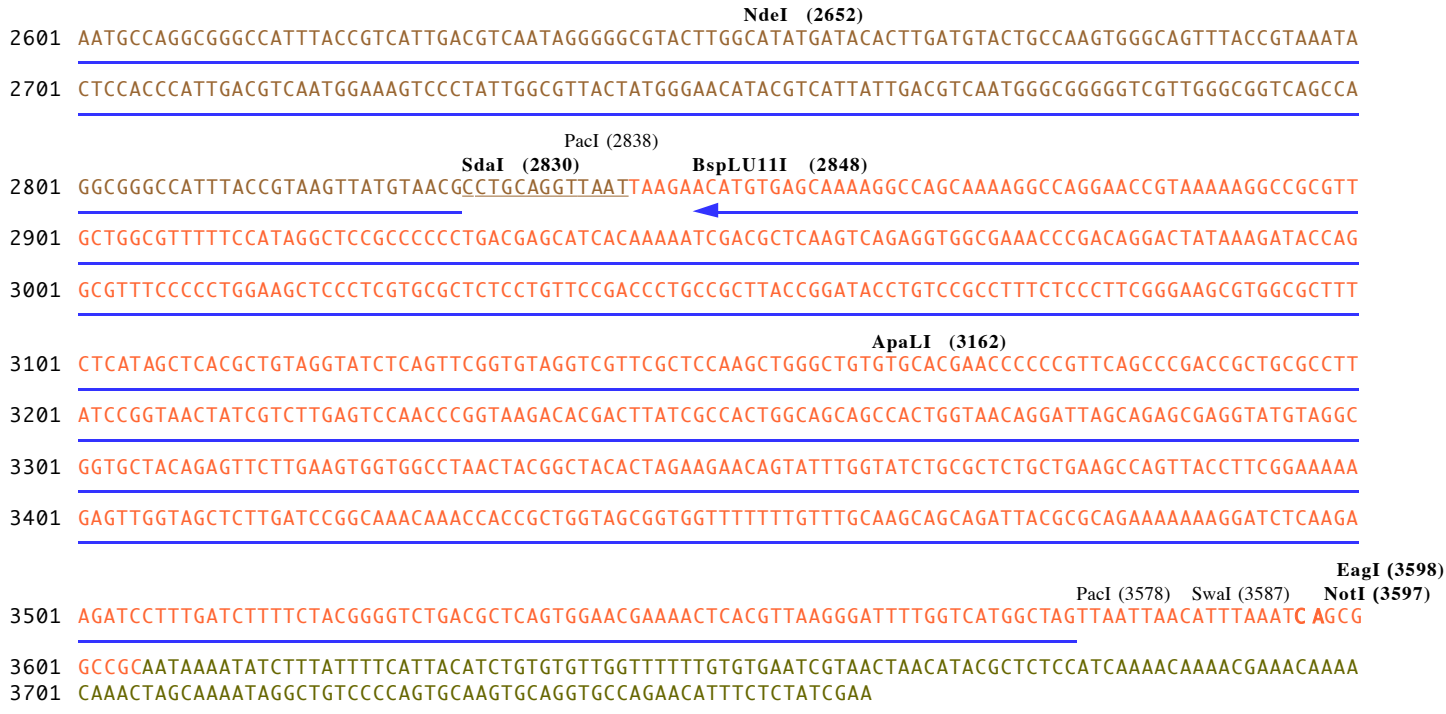
NdeI (2652)
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2701 CTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGGTCGTTGGGCGGTCAGCCA
PacI (2838)
SdaI (2830)
BspLU11I (2848)
2801 GGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTT
2901 GCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAG
3001 GCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTT
ApaLI (3162)
3101 CTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTT
3201 ATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGC
3301 GGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAA
3401 GAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGA
EagI (3598)
PacI (3578) SwaI (3587) NotI (3597)
3501 AGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCG
3601 GCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAA
3701 CAAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA