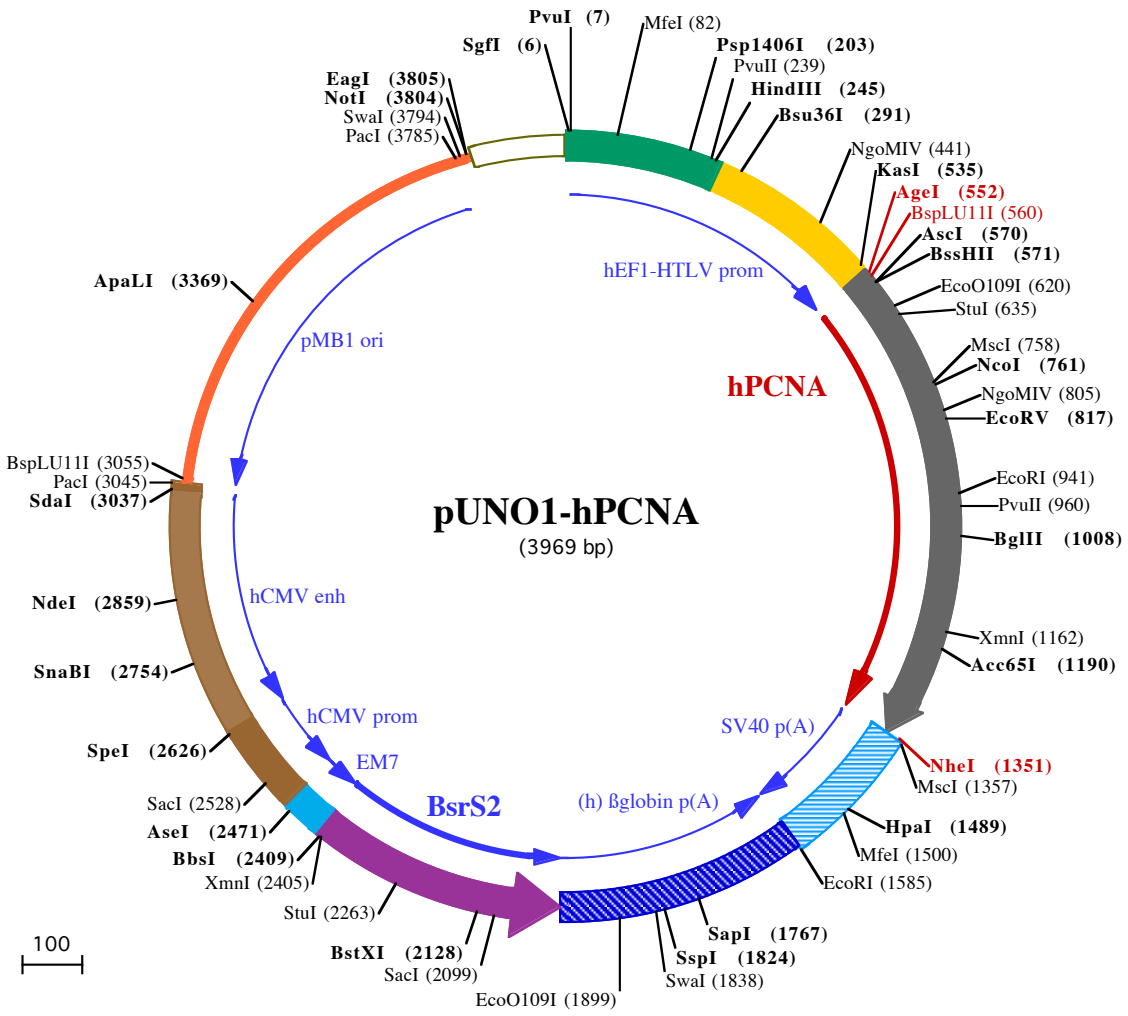
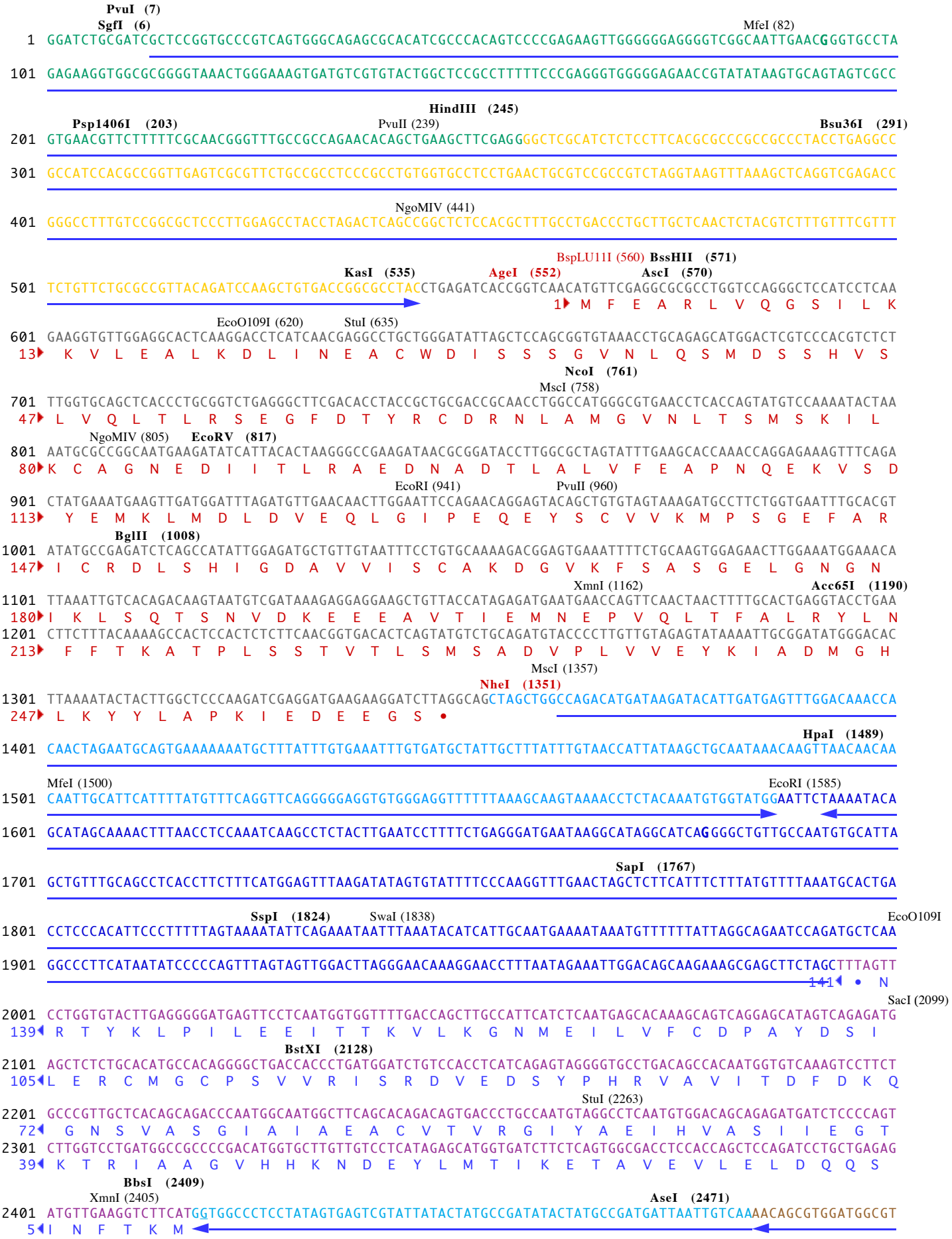
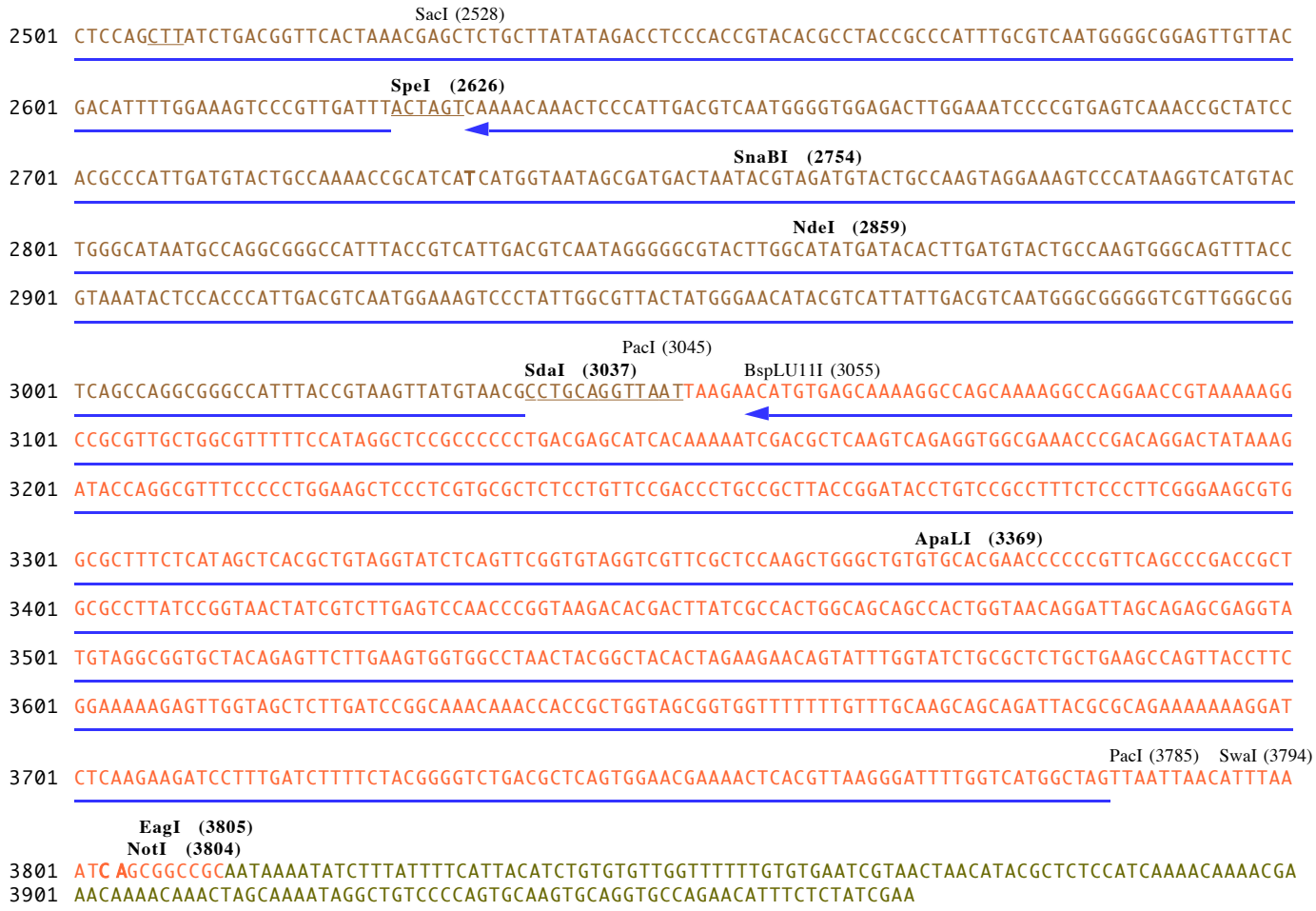

pUNO1-hPCNA
(3969 bp)
PvuI (7)
MfeI (82)
SgfI (6)
Psp1406I (203)
PvuII (239)
HindIII (245)
Bsu36I (291)
EagI (3805)
NotI (3804)
SwaI (3794)
PacI (3785)
NgoMIV (441)
KasI (535)
AgeI (552)
BspLU11I (560)
AscI (570)
BssHII (571)
EcoO109I (620)
StuI (635)
MscI (758)
NcoI (761)
NgoMIV (805)
EcoRV (817)
EcoRI (941)
PvuII (960)
BglII (1008)
XmnI (1162)
Acc65I (1190)
NheI (1351)
MscI (1357)
HpaI (1489)
MfeI (1500)
EcoRI (1585)
SapI (1767)
SspI (1824)
SwaI (1838)
EcoO109I (1899)
BstXI (2128)
SacI (2099)
StuI (2263)
XmnI (2405)
BbsI (2409)
AseI (2471)
SacI (2528)
SpeI (2626)
SnaBI (2754)
NdeI (2859)
BspLU11I (3055)
PacI (3045)
SdaI (3037)
ApaLI (3369)
hEF1-HTLV prom
hPCNA
SV40 p(A)
(h) ßglobin p(A)
BsrS2
EM7
hCMV prom
hCMV enh
pMB1 ori
100


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
BspLU11I (560)
BssHII (571)
KasI (535)
AgeI (552)
AscI (570)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTCAACATGTTCGAGGCGCGCCTGGTCCAGGGCTCCATCCTCAA
1 M F E A R L V Q G S I L K
EcoO109I (620)
StuI (635)
601 GAAGGTGTTGGAGGCACTCAAGGACCTCATCAACGAGGCCTGCTGGGATATTAGCTCCAGCGGTGTAAACCTGCAGAGCATGGACTCGTCCCACGTCTCT
13 K V L E A L K D L I N E A C W D I S S S G V N L Q S M D S S H V S
NcoI (761)
MscI (758)
701 TTGGTGCAGCTCACCCTGCGGTCTGAGGGCTTCGACACCTACCGCTGCGACCGCAACCTGGCCATGGGCGTGAACCTCACCAGTATGTCCAAAATACTAA
47 L V Q L T L R S E G F D T Y R C D R N L A M G V N L T S M S K I L
NgoMIV (805)
EcoRV (817)
801 AATGCGCCGGCAATGAAGATATCATTACACTAAGGGCCGAAGATAACGCGGATACCTTGGCGCTAGTATTTGAAGCACCAAACCAGGAGAAAGTTTCAGA
80 K C A G N E D I I T L R A E D N A D T L A L V F E A P N Q E K V S D
EcoRI (941)
PvuII (960)
901 CTATGAAATGAAGTTGATGGATTTAGATGTTGAACAACTTGGAATTCCAGAACAGGAGTACAGCTGTGTAGTAAAGATGCCTTCTGGTGAATTTGCACGT
113 Y E M K L M D L D V E Q L G I P E Q E Y S C V V K M P S G E F A R
BglII (1008)
1001 ATATGCCGAGATCTCAGCCATATTGGAGATGCTGTTGTAATTTCCTGTGCAAAAGACGGAGTGAAATTTTCTGCAAGTGGAGAACTTGGAAATGGAAACA
147 I C R D L S H I G D A V V I S C A K D G V K F S A S G E L G N G N
XmnI (1162)
Acc65I (1190)
1101 TTAAATTGTCACAGACAAGTAATGTCGATAAAGAGGAGGAAGCTGTTACCATAGAGATGAATGAACCAGTTCAACTAACTTTTGCACTGAGGTACCTGAA
180 I K L S Q T S N V D K E E E A V T I E M N E P V Q L T F A L R Y L N
1201 CTTCTTTACAAAAGCCACTCCACTCTCTTCAACGGTGACACTCAGTATGTCTGCAGATGTACCCCTTGTTGTAGAGTATAAAATTGCGGATATGGGACAC
213 F F T K A T P L S S T V T L S M S A D V P L V V E Y K I A D M G H
MscI (1357)
NheI (1351)
1301 TTAAAATACTACTTGGCTCCCAAGATCGAGGATGAAGAAGGATCTTAGGCAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCA
247 L K Y Y L A P K I E D E E G S •
HpaI (1489)
1401 CAACTAGAATGCAGTGAAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAA
MfeI (1500)
EcoRI (1585)
1501 CAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACA
1601 GCATAGCAAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTA
SapI (1767)
1701 GCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAGATATAGTGTATTTTCCCAAGGTTTGAACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGA
SspI (1824)
SwaI (1838)
EcoO109I
1801 CCTCCCACATTCCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAA
1901 GGCCCTTCATAATATCCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTT
141 • N
SacI (2099)
2001 CCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATG
139 R T 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
BstXI (2128)
2101 AGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCT
105 L E R 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
StuI (2263)
2201 GCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGT
72 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 I I E G T
2301 CTTGGTCCTGATGGCCGCCCCGACATGGTGCTTGTTGTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAG
39 K T 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
BbsI (2409)
XmnI (2405)
AseI (2471)
2401 ATGTTGAAGGTCTTCATGGTGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAAACAGCGTGGATGGCGT
5 I N F T K M


SacI (2528)
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SpeI (2626)
2601 GACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCC
SnaBI (2754)
2701 ACGCCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTAC
NdeI (2859)
2801 TGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACC
2901 GTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGGTCGTTGGGCGG
PacI (3045)
SdaI (3037)
BspLU11I (3055)
3001 TCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGG
3101 CCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAG
3201 ATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTG
ApaLI (3369)
3301 GCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCT
3401 GCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTA
3501 TGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTC
3601 GGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGAT
PacI (3785)
SwaI (3794)
3701 CTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAA
EagI (3805)
NotI (3804)
3801 ATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGA
3901 AACAAAACAAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA