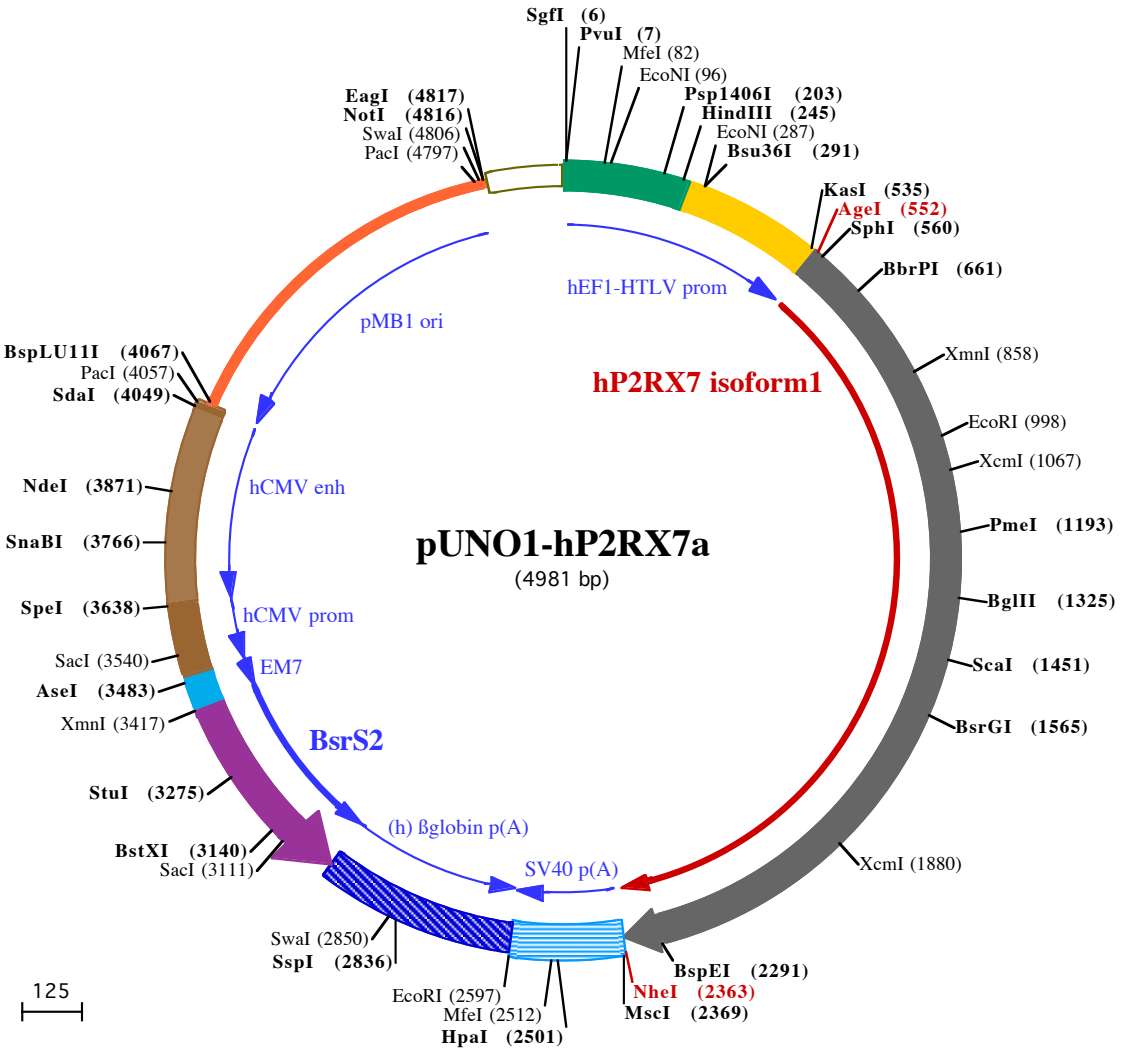
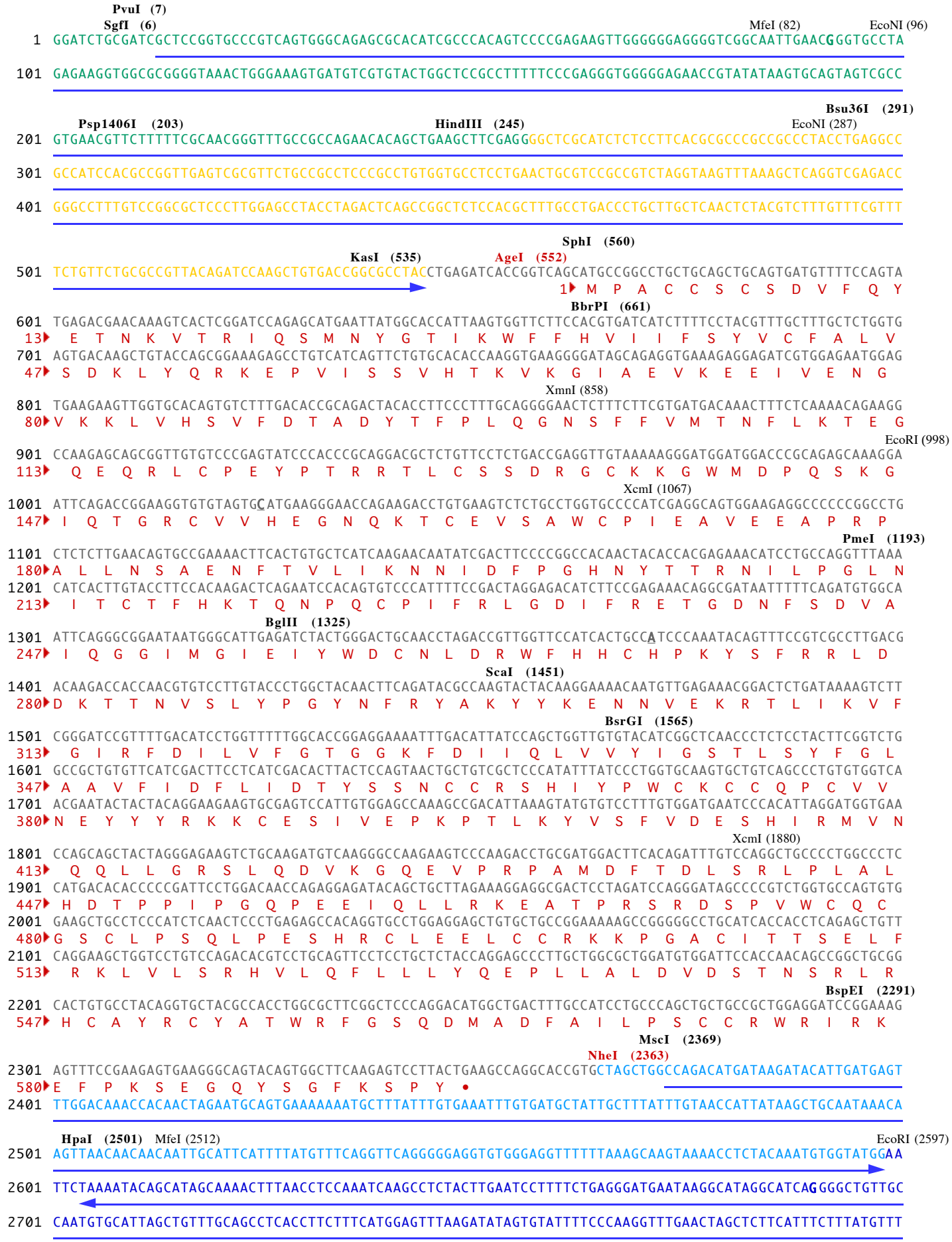
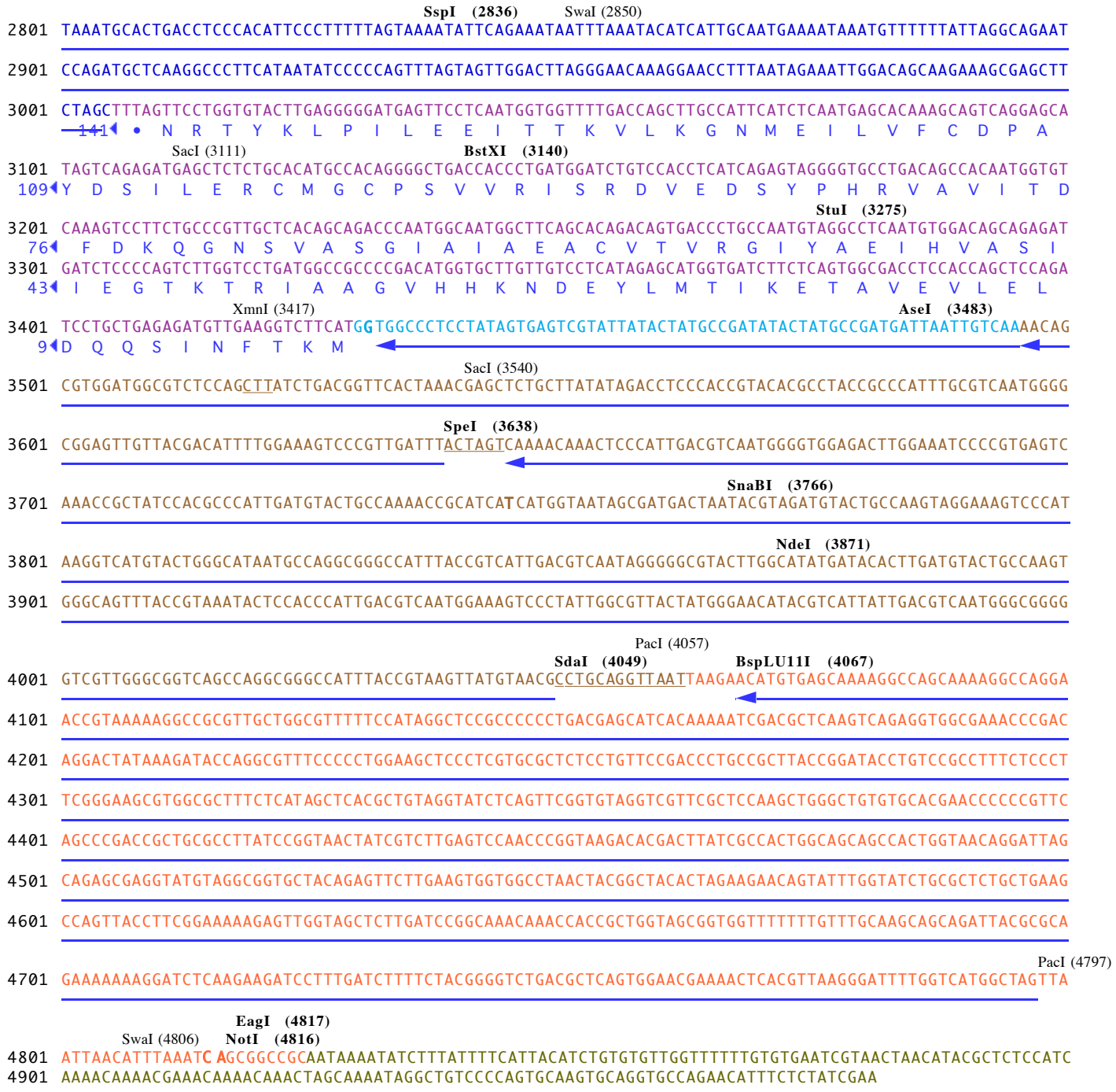

pUNO1-hP2RX7a
(4981 bp)
hP2RX7 isoform1
hEF1-HTLV prom
pMB1 ori
hCMV enh
hCMV prom
EM7
BsrS2
(h) ßglobin p(A)
SV40 p(A)
SgfI (6)
PvuI (7)
MfeI (82)
EcoNI (96)
Psp1406I (203)
HindIII (245)
EcoNI (287)
Bsu36I (291)
KasI (535)
AgeI (552)
SphI (560)
BbrPI (661)
XmnI (858)
EcoRI (998)
XcmI (1067)
PmeI (1193)
BglII (1325)
ScaI (1451)
BsrGI (1565)
XcmI (1880)
BspEI (2291)
NheI (2363)
MscI (2369)
EcoRI (2597)
MfeI (2512)
HpaI (2501)
SwaI (2850)
SspI (2836)
BstXI (3140)
SacI (3111)
StuI (3275)
XmnI (3417)
AseI (3483)
SacI (3540)
SpeI (3638)
SnaBI (3766)
NdeI (3871)
BspLU11I (4067)
PacI (4057)
SdaI (4049)
EagI (4817)
NotI (4816)
SwaI (4806)
PacI (4797)
125


PvuI (7)
SgfI (6)
MfeI (82)
EcoNI (96)
Bsu36I (291)
Psp1406I (203)
HindIII (245)
EcoNI (287)
SphI (560)
KasI (535)
AgeI (552)
BbrPI (661)
XmnI (858)
EcoRI (998)
XcmI (1067)
PmeI (1193)
BglII (1325)
ScaI (1451)
BsrGI (1565)
XcmI (1880)
BspEI (2291)
MscI (2369)
NheI (2363)
HpaI (2501)
MfeI (2512)
EcoRI (2597)


SspI (2836)
SwaI (2850)
2801 TAAATGCACTGACCTCCCACATTCCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAAT
2901 CCAGATGCTCAAGGCCCTTCATAATATCCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTT
3001 CTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCA
141 • N 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
SacI (3111)
BstXI (3140)
3101 TAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGT
109 Y D S I 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
StuI (3275)
3201 CAAAGTCCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGAT
76 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 I
3301 GATCTCCCCAGTCTTGGTCCTGATGGCCGCCCCGACATGGTGCTTGTTGTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGA
43 I E G T 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
XmnI (3417)
AseI (3483)
3401 TCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAAACAG
9 D Q Q S I N F T K M
SacI (3540)
3501 CGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCCATTTGCGTCAATGGGG
SpeI (3638)
3601 CGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTC
SnaBI (3766)
3701 AAACCGCTATCCACGCCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCAT
NdeI (3871)
3801 AAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGT
3901 GGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGG
PacI (4057)
SdaI (4049)
BspLU11I (4067)
4001 GTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGA
4101 ACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGAC
4201 AGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCT
4301 TCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTC
4401 AGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAG
4501 CAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAG
4601 CCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCA
PacI (4797)
4701 GAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTA
EagI (4817)
SwaI (4806)
NotI (4816)
4801 ATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATC
4901 AAAACAAAACGAAACAAAACAAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA