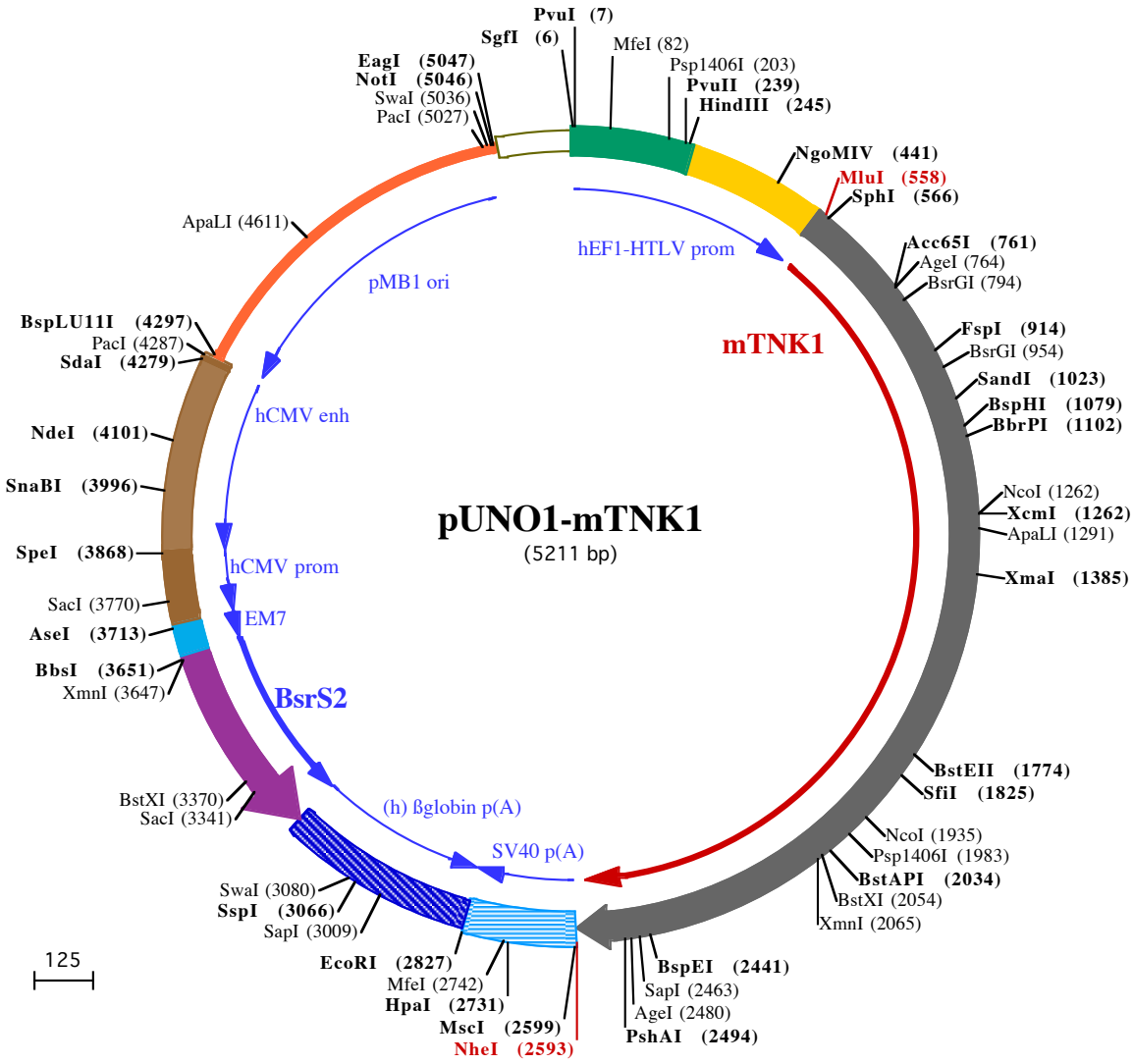
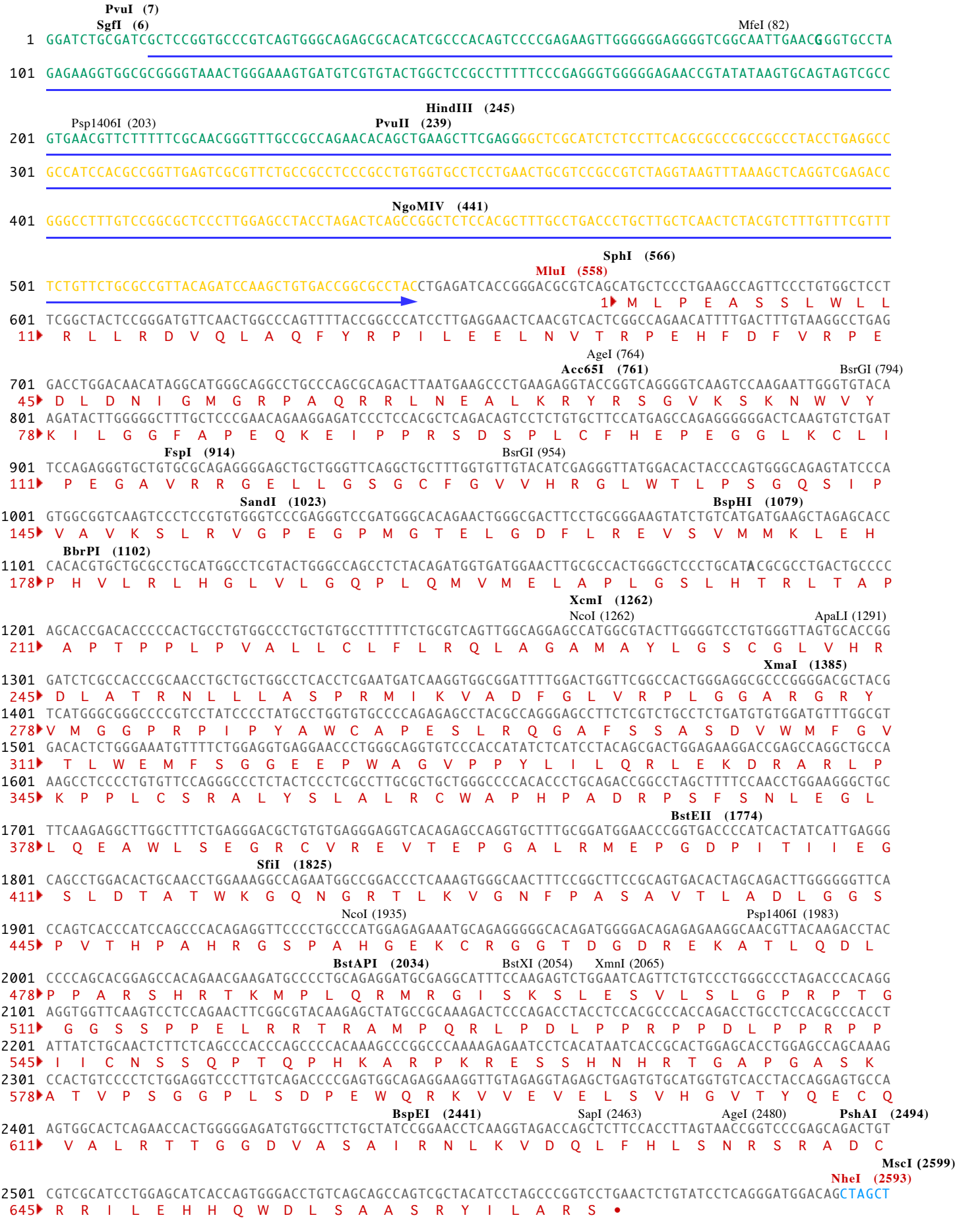
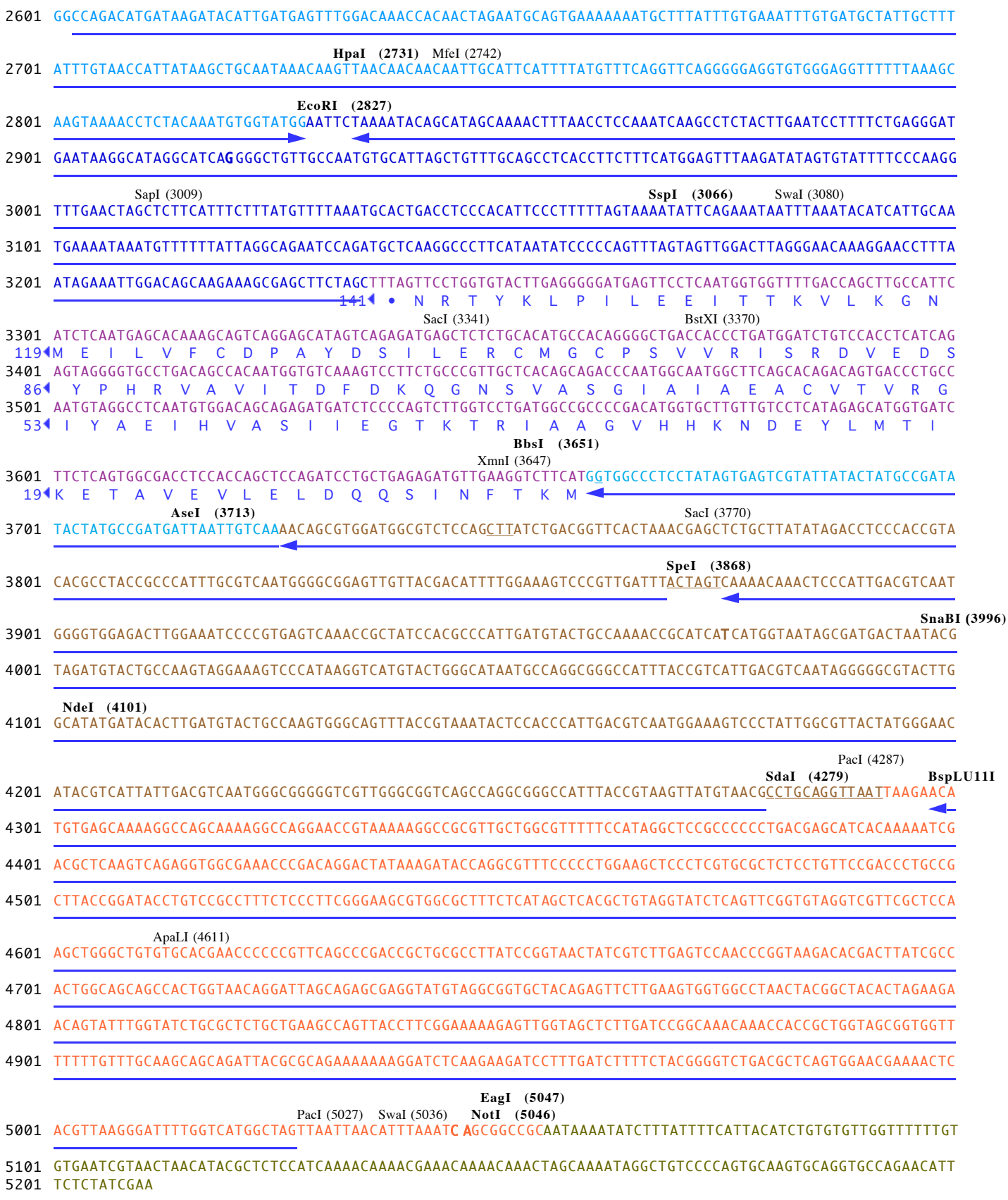

pUNO1-mTNK1
(5211 bp)
mTNK1
BsrS2
hEF1-HTLV prom
pMB1 ori
hCMV enh
hCMV prom
EM7
(h) ßglobin p(A)
SV40 p(A)
PvuI (7)
SgfI (6)
MfeI (82)
Psp1406I (203)
PvuII (239)
HindIII (245)
NgoMIV (441)
MluI (558)
SphI (566)
Acc65I (761)
AgeI (764)
BsrGI (794)
FspI (914)
BsrGI (954)
SandI (1023)
BspHI (1079)
BbrPI (1102)
NcoI (1262)
XcmI (1262)
ApaLI (1291)
XmaI (1385)
BstEII (1774)
SfiI (1825)
NcoI (1935)
Psp1406I (1983)
BstAPI (2034)
BstXI (2054)
XmnI (2065)
BspEI (2441)
SapI (2463)
AgeI (2480)
PshAI (2494)
NheI (2593)
MscI (2599)
HpaI (2731)
MfeI (2742)
EcoRI (2827)
SapI (3009)
SspI (3066)
SwaI (3080)
SacI (3341)
BstXI (3370)
XmnI (3647)
BbsI (3651)
AseI (3713)
SacI (3770)
SpeI (3868)
SnaBI (3996)
NdeI (4101)
SdaI (4279)
PacI (4287)
BspLU11I (4297)
ApaLI (4611)
EagI (5047)
NotI (5046)
SwaI (5036)
PacI (5027)
125


PvuI (7)
SgfI (6)
MfeI (82)
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC
HindIII (245)
Psp1406I (203)
PvuII (239)
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAACTCTACGTCTTTGTTTCGTTT
SphI (566)
MluI (558)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGGACGCGTCAGCATGCTCCCTGAAGCCAGTTCCCTGTGGCTCCT
1 M L P E A S S L W L L
601 TCGGCTACTCCGGGATGTTCAACTGGCCCAGTTTTACCGGCCCATCCTTGAGGAACTCAACGTCACTCGGCCAGAACATTTTGACTTTGTAAGGCCTGAG
11 R L L R D V Q L A Q F Y R P I L E E L N V T R P E H F D F V R P E
AgeI (764)
Acc65I (761)
BsrGI (794)
701 GACCTGGACAACATAGGCATGGGCAGGCCTGCCCAGCGCAGACTTAATGAAGCCCTGAAGAGGTACCGGTCAGGGGTCAAGTCCAAGAATTGGGTGTACA
45 D L D N I G M G R P A Q R R L N E A L K R Y R S G V K S K N W V Y
801 AGATACTTGGGGGCTTTGCTCCCGAACAGAAGGAGATCCCTCCACGCTCAGACAGTCCTCTGTGCTTCCATGAGCCAGAGGGGGGACTCAAGTGTCTGAT
78 K I L G G F A P E Q K E I P P R S D S P L C F H E P E G G L K C L I
FspI (914)
BsrGI (954)
901 TCCAGAGGGTGCTGTGCGCAGAGGGGAGCTGCTGGGTTCAGGCTGCTTTGGTGTTGTACATCGAGGGTTATGGACACTACCCAGTGGGCAGAGTATCCCA
111 P E G A V R R G E L L G S G C F G V V H R G L W T L P S G Q S I P
SandI (1023)
BspHI (1079)
1001 GTGGCGGTCAAGTCCCTCCGTGTGGGTCCCGAGGGTCCGATGGGCACAGAACTGGGCGACTTCCTGCGGGAAGTATCTGTCATGATGAAGCTAGAGCACC
145 V A V K S L R V G P E G P M G T E L G D F L R E V S V M M K L E H
BbrPI (1102)
1101 CACACGTGCTGCGCCTGCATGGCCTCGTACTGGGCCAGCCTCTACAGATGGTGATGGAACTTGCGCCACTGGGCTCCCTGCATACGCGCCTGACTGCCCC
178 P H V L R L H G L V L G Q P L Q M V M E L A P L G S L H T R L T A P
XcmI (1262)
NcoI (1262)
ApaLI (1291)
1201 AGCACCGACACCCCCACTGCCTGTGGCCCTGCTGTGCCTTTTTCTGCGTCAGTTGGCAGGAGCCATGGCGTACTTGGGGTCCTGTGGGTTAGTGCACCGG
211 A P T P P L P V A L L C L F L R Q L A G A M A Y L G S C G L V H R
XmaI (1385)
1301 GATCTCGCCACCCGCAACCTGCTGCTGGCCTCACCTCGAATGATCAAGGTGGCGGATTTTGGACTGGTTCGGCCACTGGGAGGCGCCCGGGGACGCTACG
245 D L A T R N L L L A S P R M I K V A D F G L V R P L G G A R G R Y
1401 TCATGGGCGGGCCCCGTCCTATCCCCTATGCCTGGTGTGCCCCAGAGAGCCTACGCCAGGGAGCCTTCTCGTCTGCCTCTGATGTGTGGATGTTTGGCGT
278 V M G G P R P I P Y A W C A P E S L R Q G A F S S A S D V W M F G V
1501 GACACTCTGGGAAATGTTTTCTGGAGGTGAGGAACCCTGGGCAGGTGTCCCACCATATCTCATCCTACAGCGACTGGAGAAGGACCGAGCCAGGCTGCCA
311 T L W E M F S G G E E P W A G V P P Y L I L Q R L E K D R A R L P
1601 AAGCCTCCCCTGTGTTCCAGGGCCCTCTACTCCCTCGCCTTGCGCTGCTGGGCCCCACACCCTGCAGACCGGCCTAGCTTTTCCAACCTGGAAGGGCTGC
345 K P P L C S R A L Y S L A L R C W A P H P A D R P S F S N L E G L
BstEII (1774)
1701 TTCAAGAGGCTTGGCTTTCTGAGGGACGCTGTGTGAGGGAGGTCACAGAGCCAGGTGCTTTGCGGATGGAACCCGGTGACCCCATCACTATCATTGAGGG
378 L Q E A W L S E G R C V R E V T E P G A L R M E P G D P I T I I E G
SfiI (1825)
1801 CAGCCTGGACACTGCAACCTGGAAAGGCCAGAATGGCCGGACCCTCAAAGTGGGCAACTTTCCGGCTTCCGCAGTGACACTAGCAGACTTGGGGGGTTCA
411 S L D T A T W K G Q N G R T L K V G N F P A S A V T L A D L G G S
NcoI (1935)
Psp1406I (1983)
1901 CCAGTCACCCATCCAGCCCACAGAGGTTCCCCTGCCCATGGAGAGAAATGCAGAGGGGGCACAGATGGGGACAGAGAGAAGGCAACGTTACAAGACCTAC
445 P V T H P A H R G S P A H G E K C R G G T D G D R E K A T L Q D L
BstAPI (2034)
BstXI (2054)
XmnI (2065)
2001 CCCCAGCACGGAGCCACAGAACGAAGATGCCCCTGCAGAGGATGCGAGGCATTTCCAAGAGTCTGGAATCAGTTCTGTCCCTGGGCCCTAGACCCACAGG
478 P P A R S H R T K M P L Q R M R G I S K S L E S V L S L G P R P T G
2101 AGGTGGTTCAAGTCCTCCAGAACTTCGGCGTACAAGAGCTATGCCGCAAAGACTCCCAGACCTACCTCCACGCCCACCAGACCTGCCTCCACGCCCACCT
511 G G S S P P E L R R T R A M P Q R L P D L P P R P P D L P P R P P
2201 ATTATCTGCAACTCTTCTCAGCCCACCCAGCCCCACAAAGCCCGGCCCAAAAGAGAATCCTCACATAATCACCGCACTGGAGCACCTGGAGCCAGCAAAG
545 I I C N S S Q P T Q P H K A R P K R E S S H N H R T G A P G A S K
2301 CCACTGTCCCCTCTGGAGGTCCCTTGTCAGACCCCGAGTGGCAGAGGAAGGTTGTAGAGGTAGAGCTGAGTGTGCATGGTGTCACCTACCAGGAGTGCCA
578 A T V P S G G P L S D P E W Q R K V V E V E L S V H G V T Y Q E C Q
BspEI (2441)
SapI (2463)
AgeI (2480)
PshAI (2494)
2401 AGTGGCACTCAGAACCACTGGGGGAGATGTGGCTTCTGCTATCCGGAACCTCAAGGTAGACCAGCTCTTCCACCTTAGTAACCGGTCCCGAGCAGACTGT
611 V A L R T T G G D V A S A I R N L K V D Q L F H L S N R S R A D C
MscI (2599)
NheI (2593)
2501 CGTCGCATCCTGGAGCATCACCAGTGGGACCTGTCAGCAGCCAGTCGCTACATCCTAGCCCGGTCCTGAACTCTGTATCCTCAGGGATGGACAGCTAGCT
645 R R I L E H H Q W D L S A A S R Y I L A R S •


HpaI (2731)
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BbsI (3651)
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SacI (3770)
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