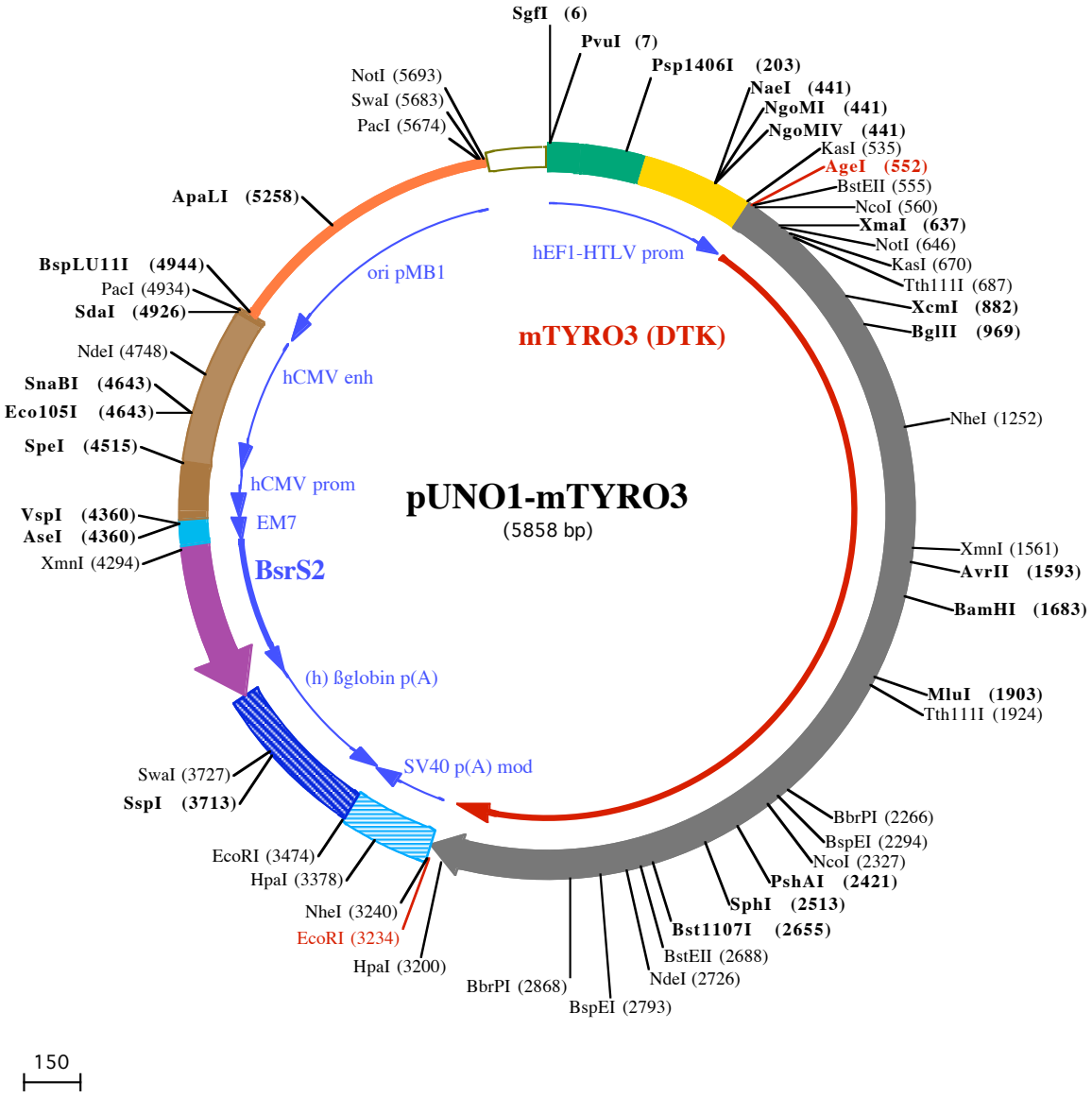
pUNO1-mTYRO3
(5858 bp)
mTYRO3 (DTK)
hEF1-HTLV prom
ori pMB1
hCMV enh
hCMV prom
EM7
BsrS2
(h) ßglobin p(A)
SV40 p(A) mod
SgfI (6)
PvuI (7)
Psp1406I (203)
NaeI (441)
NgoMI (441)
NgoMIV (441)
KasI (535)
AgeI (552)
BstEII (555)
NcoI (560)
XmaI (637)
NotI (646)
KasI (670)
Tth111I (687)
XcmI (882)
BglII (969)
NheI (1252)
XmnI (1561)
AvrII (1593)
BamHI (1683)
MluI (1903)
Tth111I (1924)
BbrPI (2266)
BspEI (2294)
NcoI (2327)
PshAI (2421)
SphI (2513)
Bst1107I (2655)
BstEII (2688)
NdeI (2726)
BspEI (2793)
BbrPI (2868)
HpaI (3200)
EcoRI (3234)
NheI (3240)
HpaI (3378)
EcoRI (3474)
SspI (3713)
SwaI (3727)
XmnI (4294)
AseI (4360)
VspI (4360)
SpeI (4515)
Eco105I (4643)
SnaBI (4643)
NdeI (4748)
SdaI (4926)
PacI (4934)
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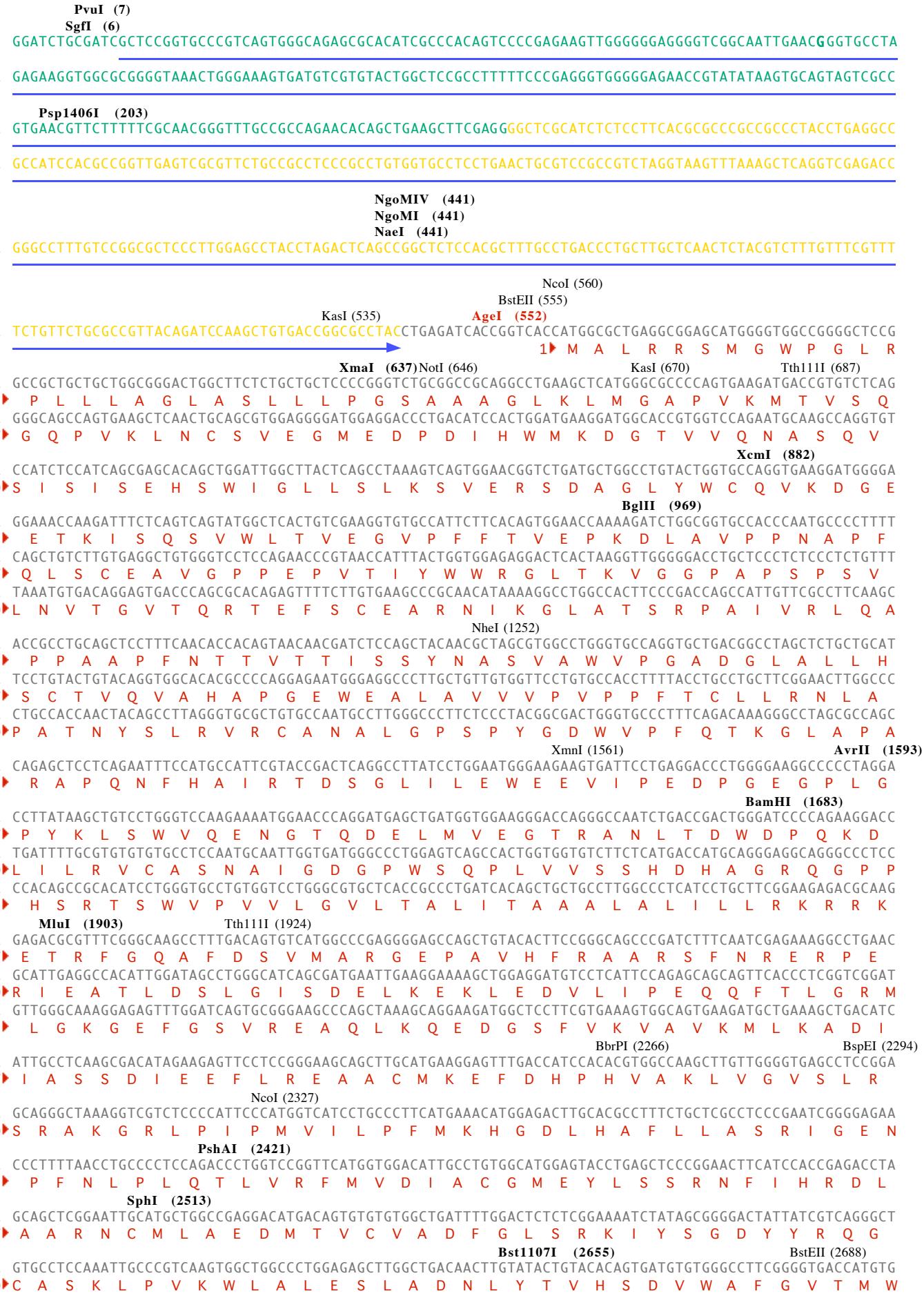
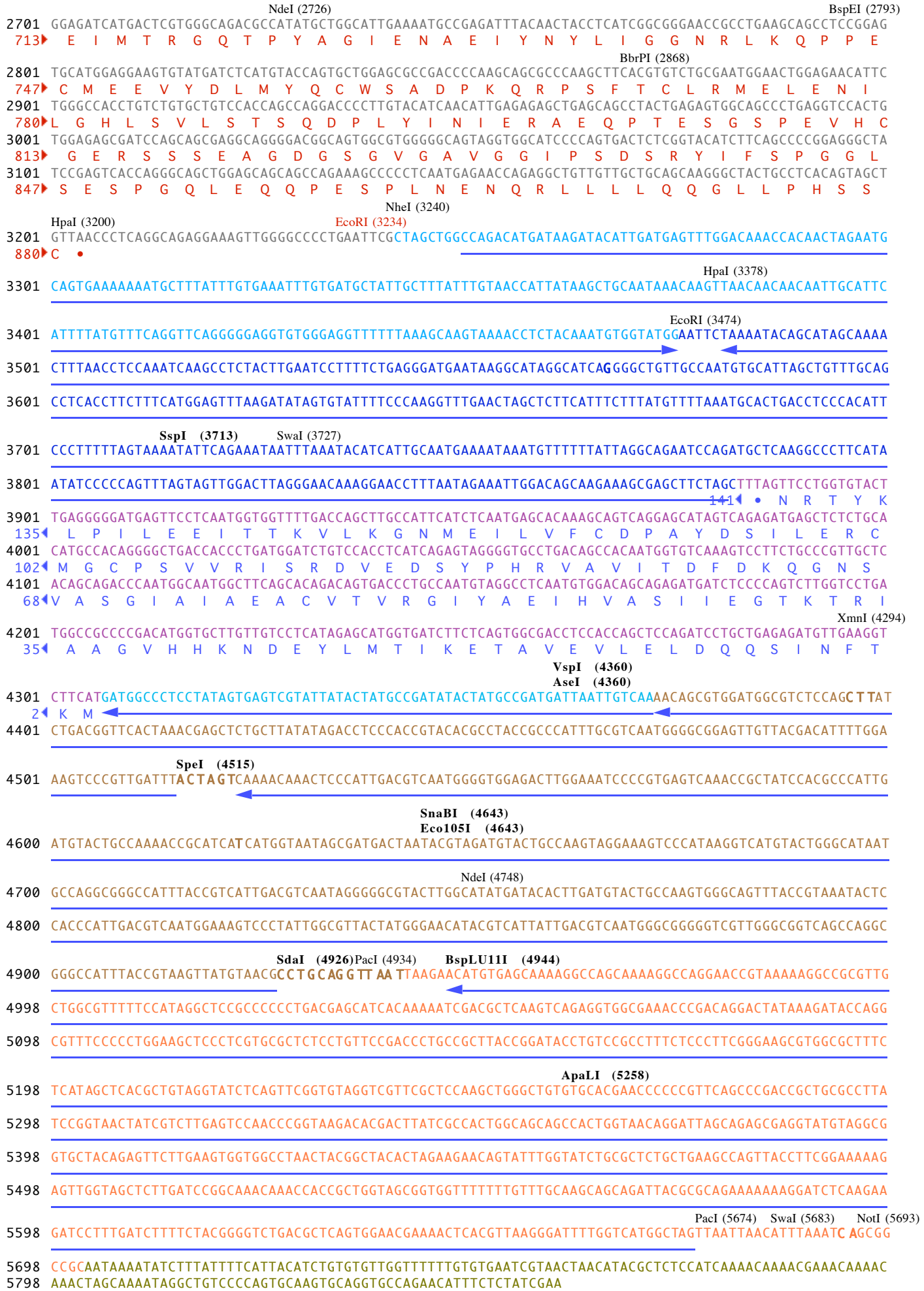
ApaLI (5258)
PacI (5674)
SwaI (5683)
NotI (5693)
150

InvivoGen


PvuI (7)
SgfI (6)
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC
Psp1406I (203)
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
NgoMIV (441)
NgoMI (441)
NaeI (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAACTCTACGTCTTTGTTTCGTTT
NcoI (560)
BstEII (555)
KasI (535)
AgeI (552)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTCACCATGGCGCTGAGGCGGAGCATGGGGTGGCCGGGGCTCCG
1 M A L R R S M G W P G L R
XmaI (637)
NotI (646)
KasI (670)
Tth111I (687)
601 GCCGCTGCTGCTGGCGGGACTGGCTTCTCTGCTGCTCCCCGGGTCTGCGGCCGCAGGCCTGAAGCTCATGGGCGCCCCAGTGAAGATGACCGTGTCTCAG
13 P L L L A G L A S L L L P G S A A A G L K L M G A P V K M T V S Q
701 GGGCAGCCAGTGAAGCTCAACTGCAGCGTGGAGGGGATGGAGGACCCTGACATCCACTGGATGAAGGATGGCACCGTGGTCCAGAATGCAAGCCAGGTGT
47 G Q P V K L N C S V E G M E D P D I H W M K D G T V V Q N A S Q V
XcmI (882)
801 CCATCTCCATCAGCGAGCACAGCTGGATTGGCTTACTCAGCCTAAAGTCAGTGGAACGGTCTGATGCTGGCCTGTACTGGTGCCAGGTGAAGGATGGGGA
80 S I S I S E H S W I G L L S L K S V E R S D A G L Y W C Q V K D G E
BglII (969)
901 GGAAACCAAGATTTCTCAGTCAGTATGGCTCACTGTCGAAGGTGTGCCATTCTTCACAGTGGAACCAAAAGATCTGGCGGTGCCACCCAATGCCCCTTTT
113 E T K I S Q S V W L T V E G V P F F T V E P K D L A V P P N A P F
1001 CAGCTGTCTTGTGAGGCTGTGGGTCCTCCAGAACCCGTAACCATTTACTGGTGGAGAGGACTCACTAAGGTTGGGGGACCTGCTCCCTCTCCCTCTGTTT
147 Q L S C E A V G P P E P V T I Y W W R G L T K V G G P A P S P S V
1101 TAAATGTGACAGGAGTGACCCAGCGCACAGAGTTTTCTTGTGAAGCCCGCAACATAAAAGGCCTGGCCACTTCCCGACCAGCCATTGTTCGCCTTCAAGC
180 L N V T G V T Q R T E F S C E A R N I K G L A T S R P A I V R L Q A
NheI (1252)
1201 ACCGCCTGCAGCTCCTTTCAACACCACAGTAACAACGATCTCCAGCTACAACGCTAGCGTGGCCTGGGTGCCAGGTGCTGACGGCCTAGCTCTGCTGCAT
213 P P A A P F N T T V T T I S S Y N A S V A W V P G A D G L A L L H
1301 TCCTGTACTGTACAGGTGGCACACGCCCCAGGAGAATGGGAGGCCCTTGCTGTTGTGGTTCCTGTGCCACCTTTTACCTGCCTGCTTCGGAACTTGGCCC
247 S C T V Q V A H A P G E W E A L A V V V P V P P F T C L L R N L A
1401 CTGCCACCAACTACAGCCTTAGGGTGCGCTGTGCCAATGCCTTGGGCCCTTCTCCCTACGGCGACTGGGTGCCCTTTCAGACAAAGGGCCTAGCGCCAGC
280 P A T N Y S L R V R C A N A L G P S P Y G D W V P F Q T K G L A P A
XmnI (1561)
AvrII (1593)
1501 CAGAGCTCCTCAGAATTTCCATGCCATTCGTACCGACTCAGGCCTTATCCTGGAATGGGAAGAAGTGATTCCTGAGGACCCTGGGGAAGGCCCCCTAGGA
313 R A P Q N F H A I R T D S G L I L E W E E V I P E D P G E G P L G
BamHI (1683)
1601 CCTTATAAGCTGTCCTGGGTCCAAGAAAATGGAACCCAGGATGAGCTGATGGTGGAAGGGACCAGGGCCAATCTGACCGACTGGGATCCCCAGAAGGACC
347 P Y K L S W V Q E N G T Q D E L M V E G T R A N L T D W D P Q K D
1701 TGATTTTGCGTGTGTGTGCCTCCAATGCAATTGGTGATGGGCCCTGGAGTCAGCCACTGGTGGTGTCTTCTCATGACCATGCAGGGAGGCAGGGCCCTCC
380 L I L R V C A S N A I G D G P W S Q P L V V S S H D H A G R Q G P P
1801 CCACAGCCGCACATCCTGGGTGCCTGTGGTCCTGGGCGTGCTCACCGCCCTGATCACAGCTGCTGCCTTGGCCCTCATCCTGCTTCGGAAGAGACGCAAG
413 H S R T S W V P V V L G V L T A L I T A A A L A L I L L R K R R K
MluI (1903)
Tth111I (1924)
1901 GAGACGCGTTTCGGGCAAGCCTTTGACAGTGTCATGGCCCGAGGGGAGCCAGCTGTACACTTCCGGGCAGCCCGATCTTTCAATCGAGAAAGGCCTGAAC
447 E T R F G Q A F D S V M A R G E P A V H F R A A R S F N R E R P E
2001 GCATTGAGGCCACATTGGATAGCCTGGGCATCAGCGATGAATTGAAGGAAAAGCTGGAGGATGTCCTCATTCCAGAGCAGCAGTTCACCCTCGGTCGGAT
480 R I E A T L D S L G I S D E L K E K L E D V L I P E Q Q F T L G R M
2101 GTTGGGCAAAGGAGAGTTTGGATCAGTGCGGGAAGCCCAGCTAAAGCAGGAAGATGGCTCCTTCGTGAAAGTGGCAGTGAAGATGCTGAAAGCTGACATC
513 L G K G E F G S V R E A Q L K Q E D G S F V K V A V K M L K A D I
BbrPI (2266)
BspEI (2294)
2201 ATTGCCTCAAGCGACATAGAAGAGTTCCTCCGGGAAGCAGCTTGCATGAAGGAGTTTGACCATCCACACGTGGCCAAGCTTGTTGGGGTGAGCCTCCGGA
547 I A S S D I E E F L R E A A C M K E F D H P H V A K L V G V S L R
NcoI (2327)
2301 GCAGGGCTAAAGGTCGTCTCCCCATTCCCATGGTCATCCTGCCCTTCATGAAACATGGAGACTTGCACGCCTTTCTGCTCGCCTCCCGAATCGGGGAGAA
580 S R A K G R L P I P M V I L P F M K H G D L H A F L L A S R I G E N
PshAI (2421)
2401 CCCTTTTAACCTGCCCCTCCAGACCCTGGTCCGGTTCATGGTGGACATTGCCTGTGGCATGGAGTACCTGAGCTCCCGGAACTTCATCCACCGAGACCTA
613 P F N L P L Q T L V R F M V D I A C G M E Y L S S R N F I H R D L
SphI (2513)
2501 GCAGCTCGGAATTGCATGCTGGCCGAGGACATGACAGTGTGTGTGGCTGATTTTGGACTCTCTCGGAAAATCTATAGCGGGGACTATTATCGTCAGGGCT
647 A A R N C M L A E D M T V C V A D F G L S R K I Y S G D Y Y R Q G
Bst1107I (2655)
BstEII (2688)
2601 GTGCCTCCAAATTGCCCGTCAAGTGGCTGGCCCTGGAGAGCTTGGCTGACAACTTGTATACTGTACACAGTGATGTGTGGGCCTTCGGGGTGACCATGTG
680 C A S K L P V K W L A L E S L A D N L Y T V H S D V W A F G V T M W


NdeI (2726)
BspEI (2793)
BbrPI (2868)
NheI (3240)
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EcoRI (3234)
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EcoRI (3474)
SspI (3713)
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