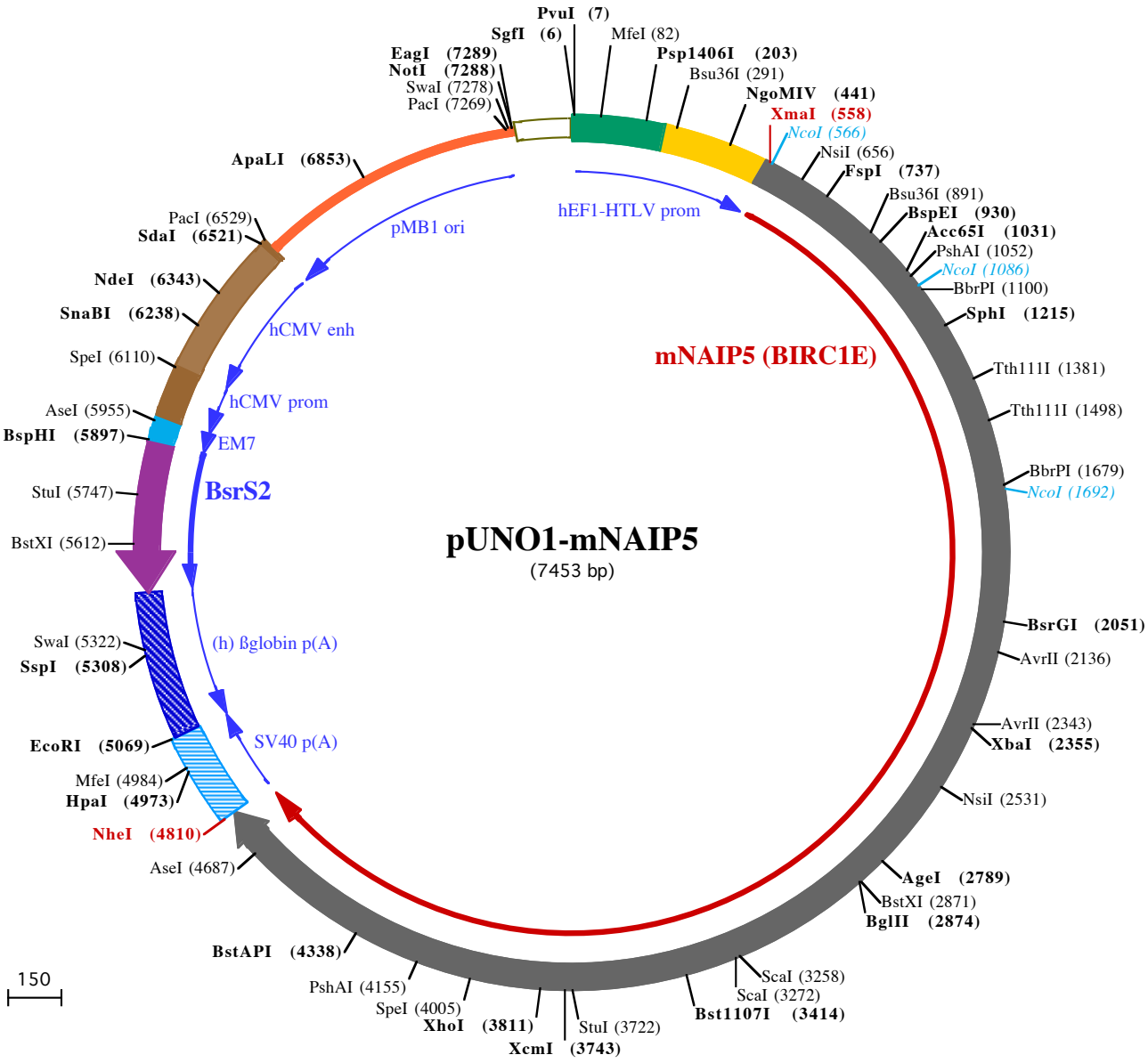
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(7453 bp)
mNAIP5 (BIRC1E)
hEF1-HTLV prom
pMB1 ori
hCMV enh
hCMV prom
EM7
BsrS2
(h) ßglobin p(A)
SV40 p(A)
PvuI (7)
SgfI (6)
MfeI (82)
EagI (7289)
NotI (7288)
Psp1406I (203)
Bsu36I (291)
SwaI (7278)
PacI (7269)
NgoMIV (441)
XmaI (558)
NcoI (566)
NsiI (656)
FspI (737)
Bsu36I (891)
BspEI (930)
Acc65I (1031)
PshAI (1052)
NcoI (1086)
BbrPI (1100)
SphI (1215)
Tth111I (1381)
Tth111I (1498)
BbrPI (1679)
NcoI (1692)
BsrGI (2051)
AvrII (2136)
AvrII (2343)
XbaI (2355)
NsiI (2531)
AgeI (2789)
BstXI (2871)
BglII (2874)
ScaI (3258)
ScaI (3272)
Bst1107I (3414)
StuI (3722)
XcmI (3743)
XhoI (3811)
SpeI (4005)
PshAI (4155)
BstAPI (4338)
AseI (4687)
NheI (4810)
HpaI (4973)
MfeI (4984)
EcoRI (5069)
SspI (5308)
SwaI (5322)
BstXI (5612)
StuI (5747)
BspHI (5897)
AseI (5955)
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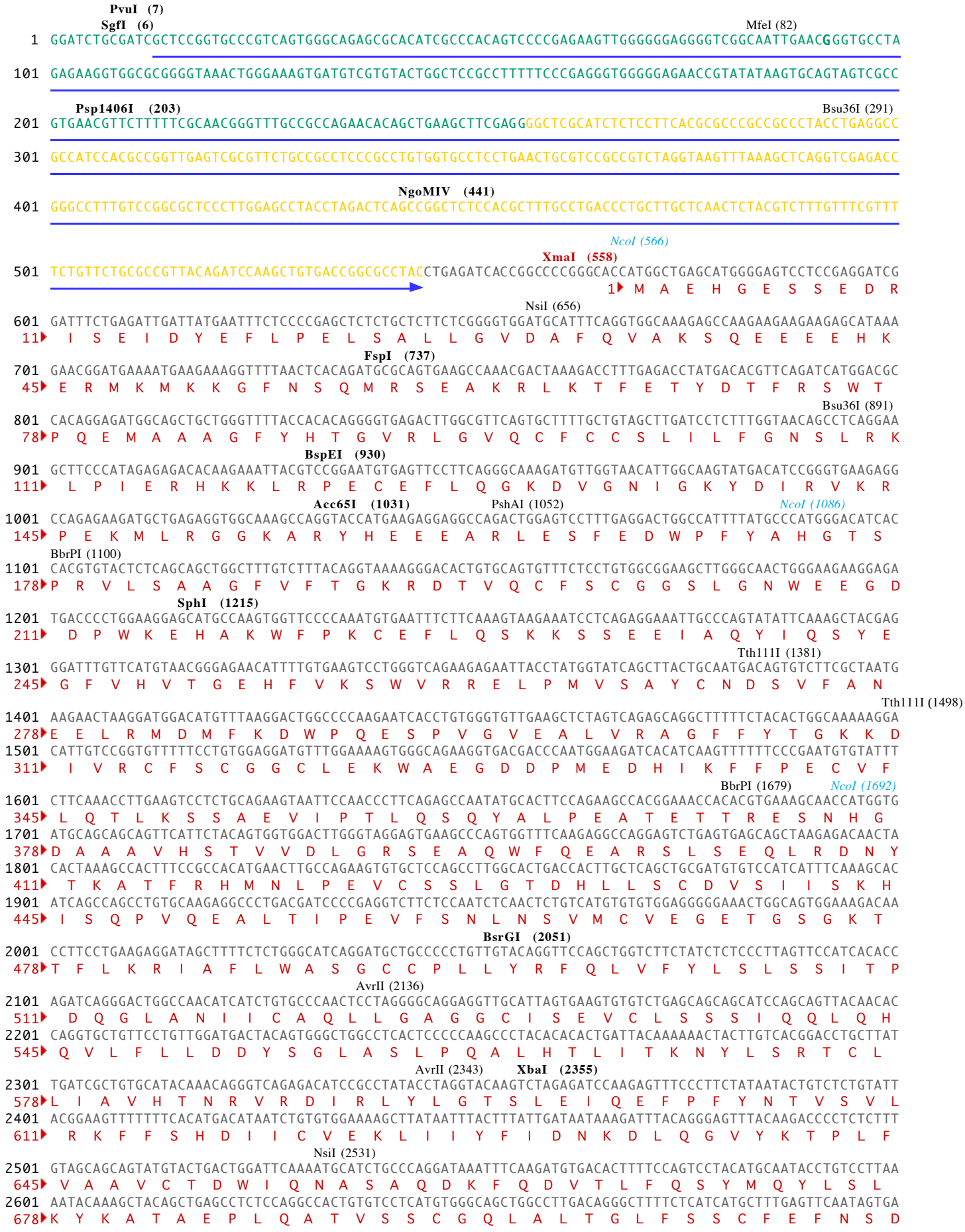
SdaI (6521)
PacI (6529)
ApaLI (6853)
150


PvuI (7)
SgfI (6)
MfeI (82)
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC
Psp1406I (203)
Bsu36I (291)
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAACTCTACGTCTTTGTTTCGTTT
NcoI (566)
XmaI (558)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGCCCCGGGCACCATGGCTGAGCATGGGGAGTCCTCCGAGGATCG
1 M A E H G E S S E D R
NsiI (656)
601 GATTTCTGAGATTGATTATGAATTTCTCCCCGAGCTCTCTGCTCTTCTCGGGGTGGATGCATTTCAGGTGGCAAAGAGCCAAGAAGAAGAAGAGCATAAA
11 I S E I D Y E F L P E L S A L L G V D A F Q V A K S Q E E E E H K
FspI (737)
701 GAACGGATGAAAATGAAGAAAGGTTTTAACTCACAGATGCGCAGTGAAGCCAAACGACTAAAGACCTTTGAGACCTATGACACGTTCAGATCATGGACGC
45 E R M K M K K G F N S Q M R S E A K R L K T F E T Y D T F R S W T
Bsu36I (891)
801 CACAGGAGATGGCAGCTGCTGGGTTTTACCACACAGGGGTGAGACTTGGCGTTCAGTGCTTTTGCTGTAGCTTGATCCTCTTTGGTAACAGCCTCAGGAA
78 P Q E M A A A G F Y H T G V R L G V Q C F C C S L I L F G N S L R K
BspEI (930)
901 GCTTCCCATAGAGAGACACAAGAAATTACGTCCGGAATGTGAGTTCCTTCAGGGCAAAGATGTTGGTAACATTGGCAAGTATGACATCCGGGTGAAGAGG
111 L P I E R H K K L R P E C E F L Q G K D V G N I G K Y D I R V K R
Acc65I (1031)
PshAI (1052)
NcoI (1086)
1001 CCAGAGAAGATGCTGAGAGGTGGCAAAGCCAGGTACCATGAAGAGGAGGCCAGACTGGAGTCCTTTGAGGACTGGCCATTTTATGCCCATGGGACATCAC
145 P E K M L R G G K A R Y H E E E A R L E S F E D W P F Y A H G T S
BbrPI (1100)
1101 CACGTGTACTCTCAGCAGCTGGCTTTGTCTTTACAGGTAAAAGGGACACTGTGCAGTGTTTCTCCTGTGGCGGAAGCTTGGGCAACTGGGAAGAAGGAGA
178 P R V L S A A G F V F T G K R D T V Q C F S C G G S L G N W E E G D
SphI (1215)
1201 TGACCCCTGGAAGGAGCATGCCAAGTGGTTCCCCAAATGTGAATTTCTTCAAAGTAAGAAATCCTCAGAGGAAATTGCCCAGTATATTCAAAGCTACGAG
211 D P W K E H A K W F P K C E F L Q S K K S S E E I A Q Y I Q S Y E
Tth111I (1381)
1301 GGATTTGTTCATGTAACGGGAGAACATTTTGTGAAGTCCTGGGTCAGAAGAGAATTACCTATGGTATCAGCTTACTGCAATGACAGTGTCTTCGCTAATG
245 G F V H V T G E H F V K S W V R R E L P M V S A Y C N D S V F A N
Tth111I (1498)
1401 AAGAACTAAGGATGGACATGTTTAAGGACTGGCCCCAAGAATCACCTGTGGGTGTTGAAGCTCTAGTCAGAGCAGGCTTTTTCTACACTGGCAAAAAGGA
278 E E L R M D M F K D W P Q E S P V G V E A L V R A G F F Y T G K K D
1501 CATTGTCCGGTGTTTTTCCTGTGGAGGATGTTTGGAAAAGTGGGCAGAAGGTGACGACCCAATGGAAGATCACATCAAGTTTTTTCCCGAATGTGTATTT
311 I V R C F S C G G C L E K W A E G D D P M E D H I K F F P E C V F
BbrPI (1679)
NcoI (1692)
1601 CTTCAAACCTTGAAGTCCTCTGCAGAAGTAATTCCAACCCTTCAGAGCCAATATGCACTTCCAGAAGCCACGGAAACCACACGTGAAAGCAACCATGGTG
345 L Q T L K S S A E V I P T L Q S Q Y A L P E A T E T T R E S N H G
1701 ATGCAGCAGCAGTTCATTCTACAGTGGTGGACTTGGGTAGGAGTGAAGCCCAGTGGTTTCAAGAGGCCAGGAGTCTGAGTGAGCAGCTAAGAGACAACTA
378 D A A A V H S T V V D L G R S E A Q W F Q E A R S L S E Q L R D N Y
1801 CACTAAAGCCACTTTCCGCCACATGAACTTGCCAGAAGTGTGCTCCAGCCTTGGCACTGACCACTTGCTCAGCTGCGATGTGTCCATCATTTCAAAGCAC
411 T K A T F R H M N L P E V C S S L G T D H L L S C D V S I I S K H
1901 ATCAGCCAGCCTGTGCAAGAGGCCCTGACGATCCCCGAGGTCTTCTCCAATCTCAACTCTGTCATGTGTGTGGAGGGGGAAACTGGCAGTGGAAAGACAA
445 I S Q P V Q E A L T I P E V F S N L N S V M C V E G E T G S G K T
BsrGI (2051)
2001 CCTTCCTGAAGAGGATAGCTTTTCTCTGGGCATCAGGATGCTGCCCCCTGTTGTACAGGTTCCAGCTGGTCTTCTATCTCTCCCTTAGTTCCATCACACC
478 T F L K R I A F L W A S G C C P L L Y R F Q L V F Y L S L S S I T P
AvrII (2136)
2101 AGATCAGGGACTGGCCAACATCATCTGTGCCCAACTCCTAGGGGCAGGAGGTTGCATTAGTGAAGTGTGTCTGAGCAGCAGCATCCAGCAGTTACAACAC
511 D Q G L A N I I C A Q L L G A G G C I S E V C L S S S I Q Q L Q H
2201 CAGGTGCTGTTCCTGTTGGATGACTACAGTGGGCTGGCCTCACTCCCCCAAGCCCTACACACACTGATTACAAAAAACTACTTGTCACGGACCTGCTTAT
545 Q V L F L L D D Y S G L A S L P Q A L H T L I T K N Y L S R T C L
AvrII (2343)
XbaI (2355)
2301 TGATCGCTGTGCATACAAACAGGGTCAGAGACATCCGCCTATACCTAGGTACAAGTCTAGAGATCCAAGAGTTTCCCTTCTATAATACTGTCTCTGTATT
578 L I A V H T N R V R D I R L Y L G T S L E I Q E F P F Y N T V S V L
2401 ACGGAAGTTTTTTTCACATGACATAATCTGTGTGGAAAAGCTTATAATTTACTTTATTGATAATAAAGATTTACAGGGAGTTTACAAGACCCCTCTCTTT
611 R K F F S H D I I C V E K L I I Y F I D N K D L Q G V Y K T P L F
NsiI (2531)
2501 GTAGCAGCAGTATGTACTGACTGGATTCAAAATGCATCTGCCCAGGATAAATTTCAAGATGTGACACTTTTCCAGTCCTACATGCAATACCTGTCCTTAA
645 V A A V C T D W I Q N A S A Q D K F Q D V T L F Q S Y M Q Y L S L
2601 AATACAAAGCTACAGCTGAGCCTCTCCAGGCCACTGTGTCCTCATGTGGGCAGCTGGCCTTGACAGGGCTTTTCTCATCATGCTTTGAGTTCAATAGTGA
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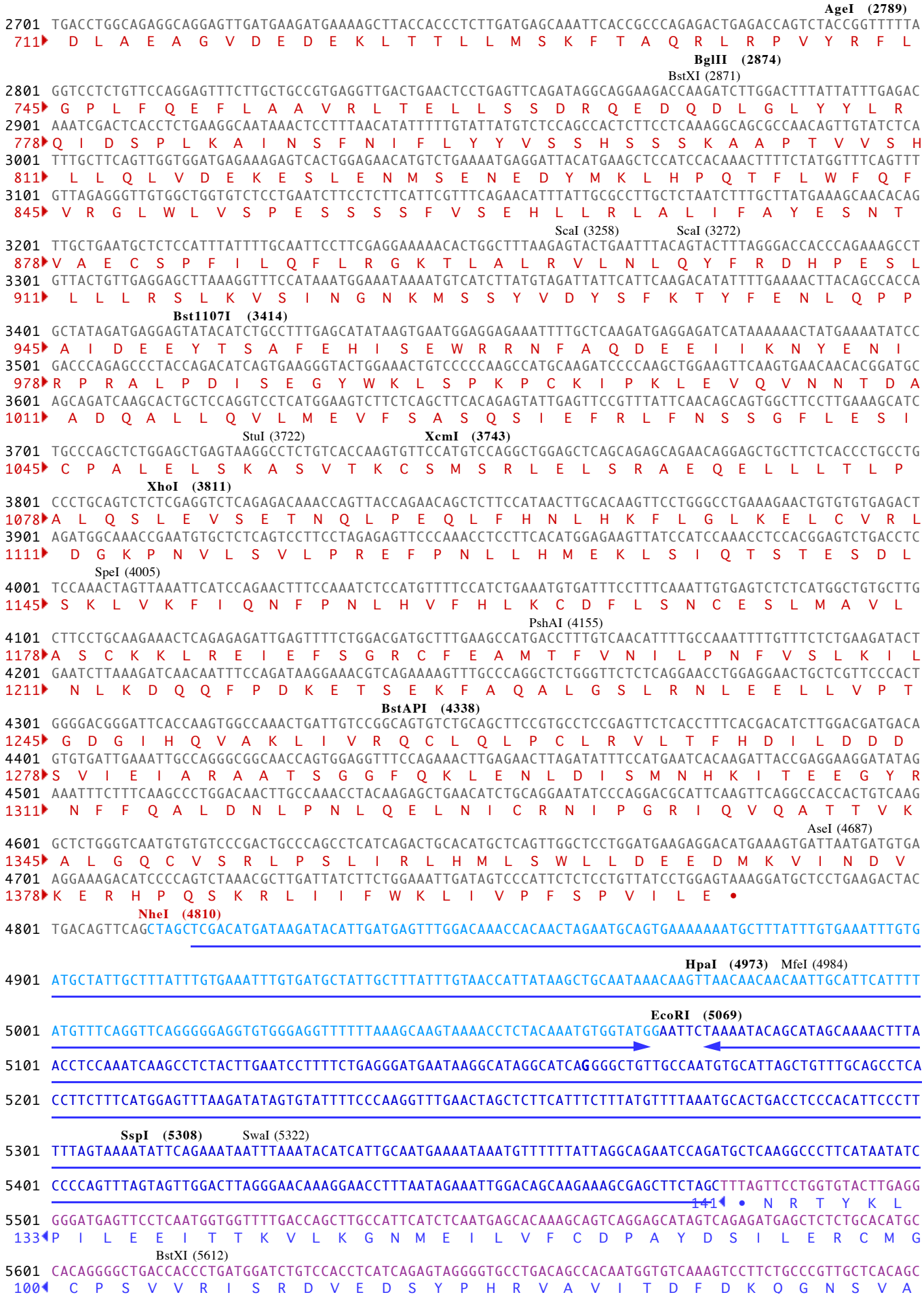
AgeI (2789)
BglII (2874)
BstXI (2871)
ScaI (3258)
ScaI (3272)
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StuI (3722)
XcmI (3743)
XhoI (3811)
SpeI (4005)
PshAI (4155)
BstAPI (4338)
AseI (4687)
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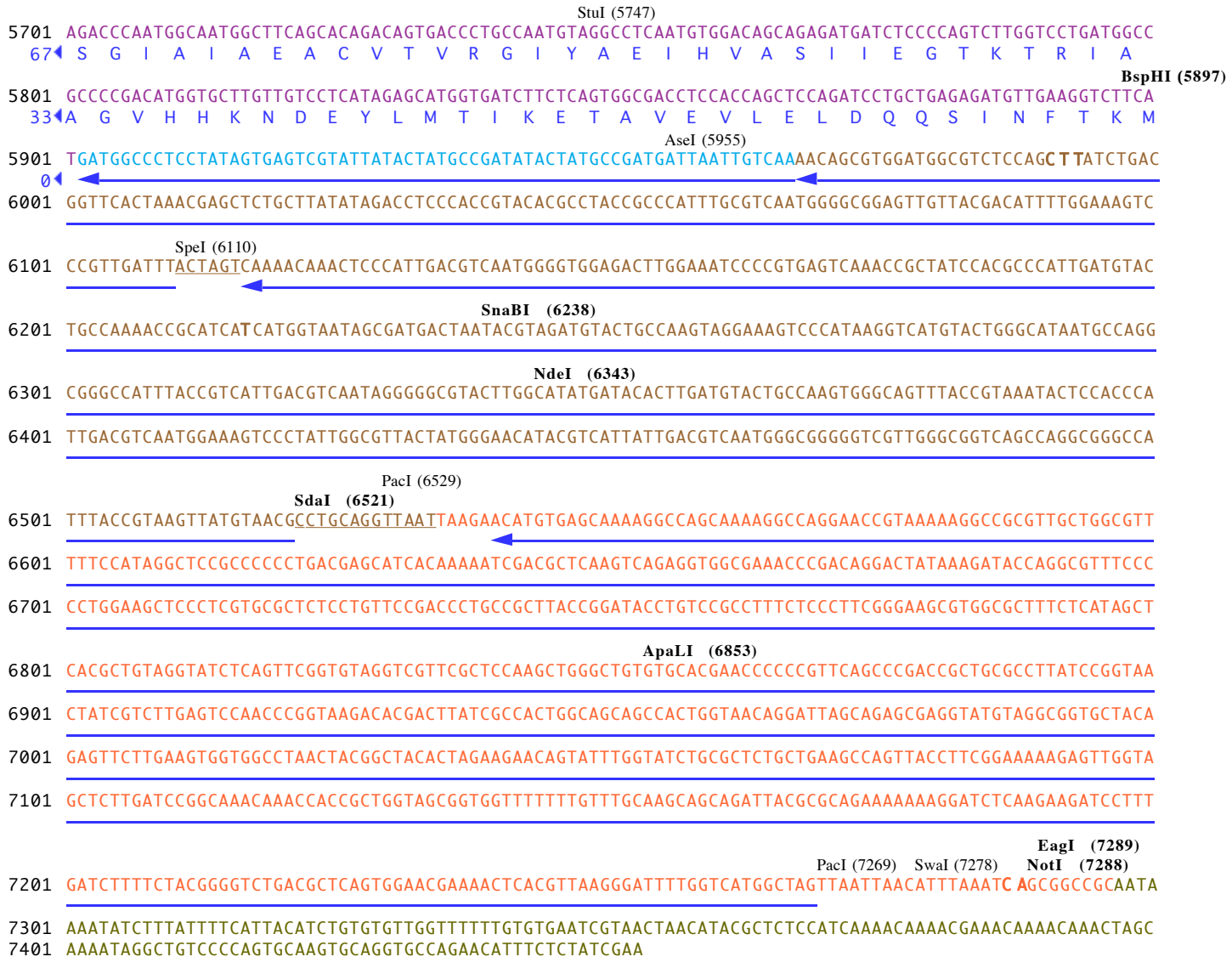
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67 S G I A I A E A C V T V R G I Y A E I H V A S I I E G T K T R I A
BspHI (5897)
5801 GCCCCGACATGGTGCTTGTTGTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCA
33 A G V H H K N D E Y L M T I K E T A V E V L E L D Q Q S I N F T K M
AseI (5955)
5901 TGATGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAAACAGCGTGGATGGCGTCTCCAGCTTTATCTGAC
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6001 GGTTCACTAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTC
SpeI (6110)
6101 CCGTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCCATTGATGTAC
SnaBI (6238)
6201 TGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTACTGGGCATAATGCCAGG
NdeI (6343)
6301 CGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCA
6401 TTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCA
PacI (6529)
SdaI (6521)
6501 TTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTT
6601 TTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCC
6701 CCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCT
ApaLI (6853)
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6901 CTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACA
7001 GAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTA
7101 GCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTT
EagI (7289)
PacI (7269) SwaI (7278) NotI (7288)
7201 GATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATA
7301 AAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAAACTAGC
7401 AAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA