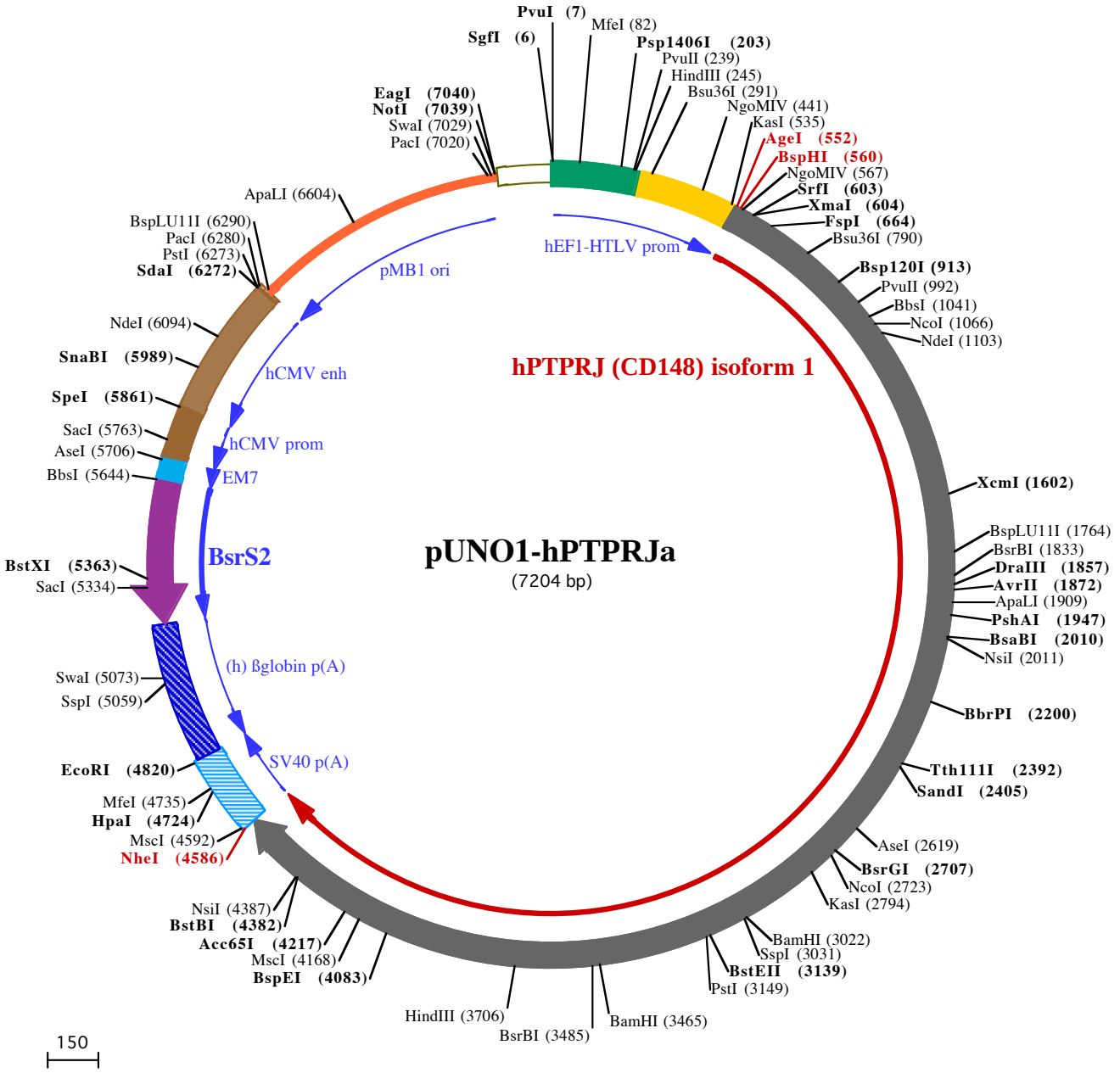
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(7204 bp)
hPTPRJ (CD148) isoform 1
hEF1-HTLV prom
pMB1 ori
hCMV enh
hCMV prom
EM7
BsrS2
(h) ßglobin p(A)
SV40 p(A)
PvuI (7)
SgfI (6)
MfeI (82)
Psp1406I (203)
PvuII (239)
HindIII (245)
Bsu36I (291)
NgoMIV (441)
KasI (535)
AgeI (552)
BspHI (560)
NgoMIV (567)
SrfI (603)
XmaI (604)
FspI (664)
Bsu36I (790)
Bsp120I (913)
PvuII (992)
BbsI (1041)
NcoI (1066)
NdeI (1103)
XcmI (1602)
BspLU11I (1764)
BsrBI (1833)
DraIII (1857)
AvrII (1872)
ApaLI (1909)
PshAI (1947)
BsaBI (2010)
NsiI (2011)
BbrPI (2200)
Tth111I (2392)
SandI (2405)
AseI (2619)
BsrGI (2707)
NcoI (2723)
KasI (2794)
BamHI (3022)
SspI (3031)
BstEII (3139)
PstI (3149)
BamHI (3465)
BsrBI (3485)
HindIII (3706)
NsiI (4387)
BstBI (4382)
Acc65I (4217)
MscI (4168)
BspEI (4083)
MfeI (4735)
HpaI (4724)
MscI (4592)
NheI (4586)
EcoRI (4820)
SwaI (5073)
SspI (5059)
BstXI (5363)
SacI (5334)
BbsI (5644)
AseI (5706)
SacI (5763)
SpeI (5861)
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NdeI (6094)
SdaI (6272)
PstI (6273)
PacI (6280)
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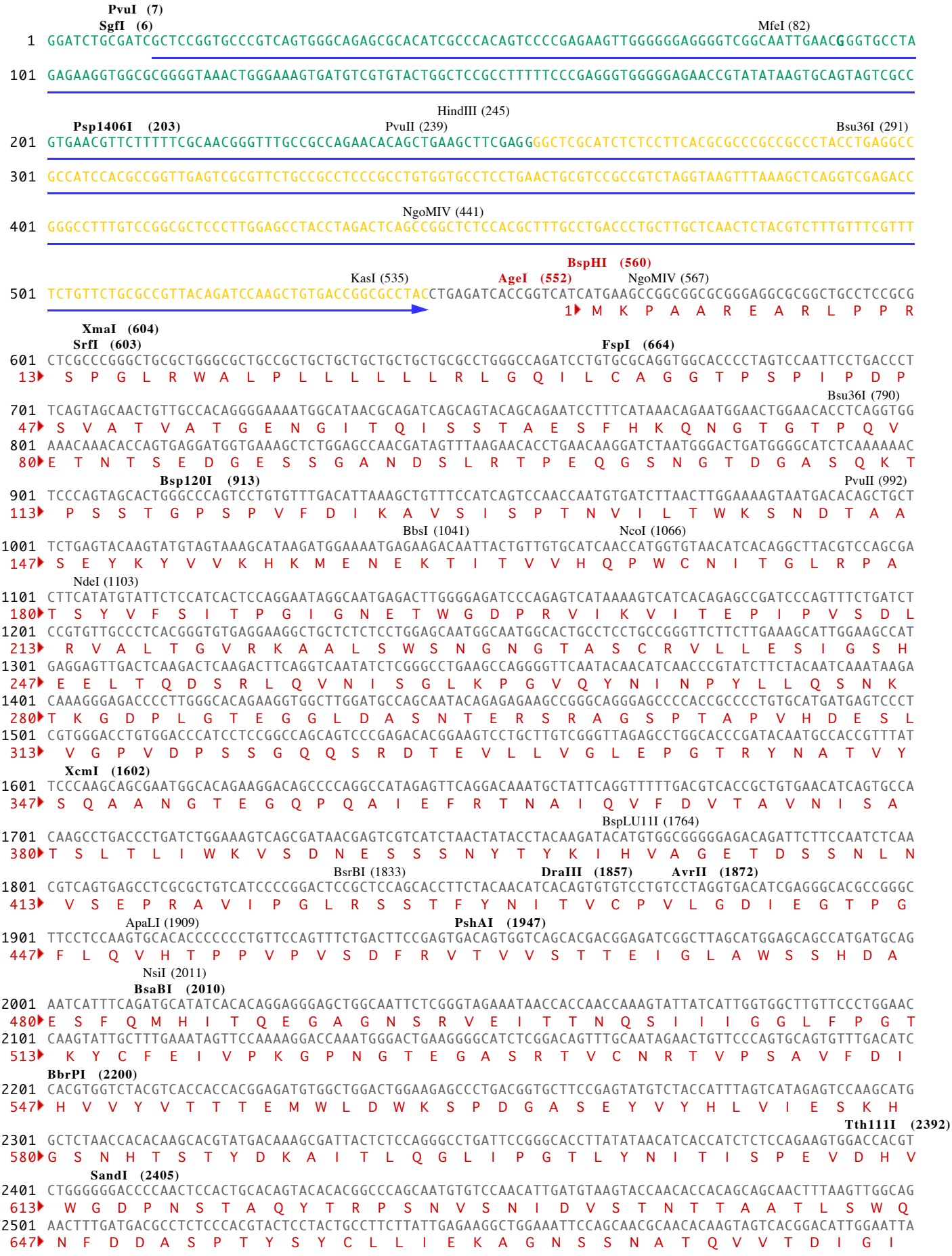
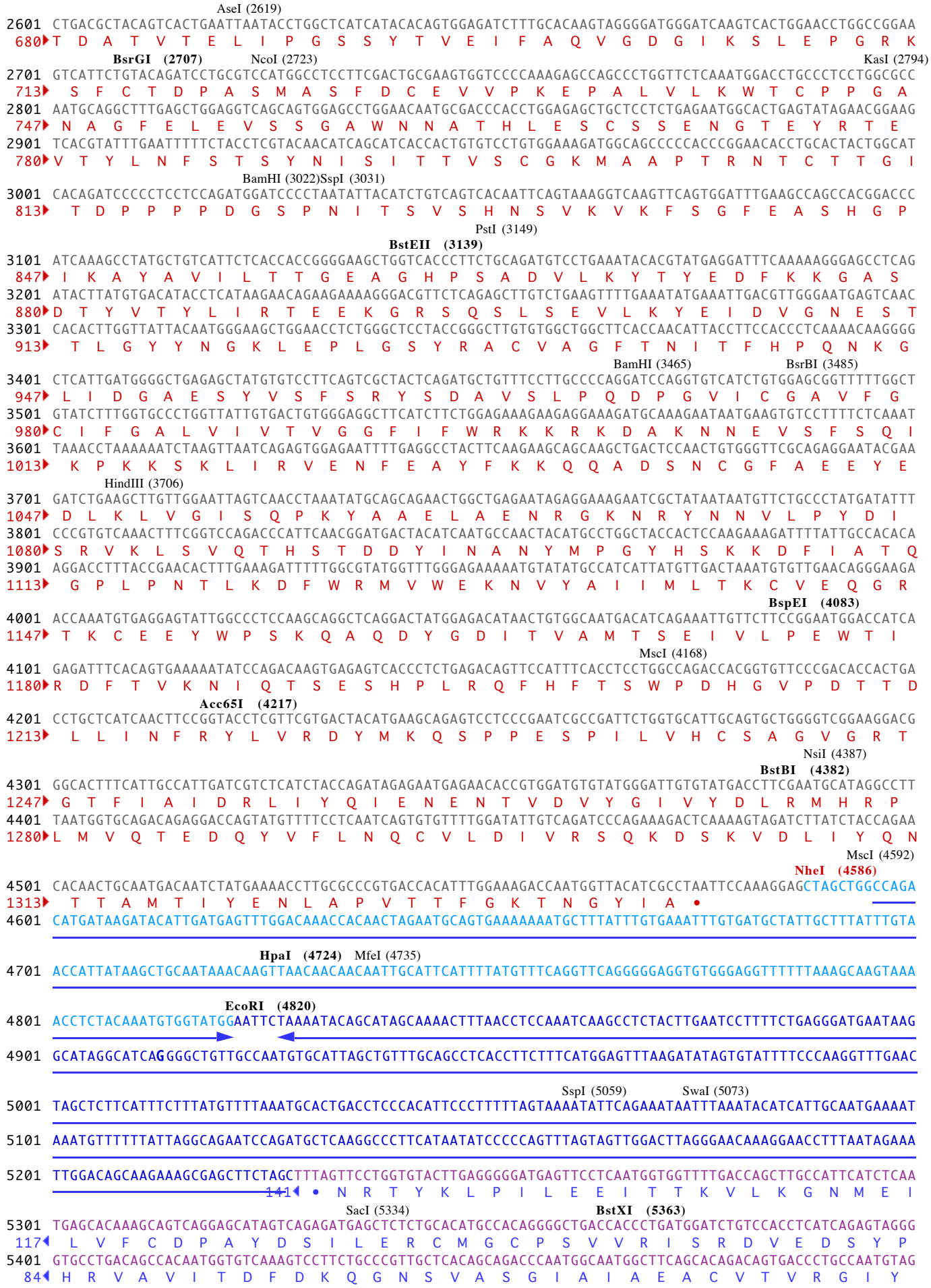
PacI (7020)
NotI (7039)
EagI (7040)
150


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
BspHI (560)
KasI (535)
AgeI (552)
NgoMIV (567)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTCATCATGAAGCCGGCGGCGCGGGAGGCGCGGCTGCCTCCGCG
1 M K P A A R E A R L P P R
XmaI (604)
SrfI (603)
FspI (664)
601 CTCGCCCGGGCTGCGCTGGGCGCTGCCGCTGCTGCTGCTGCTGCTGCGCCTGGGCCAGATCCTGTGCGCAGGTGGCACCCCTAGTCCAATTCCTGACCCT
13 S P G L R W A L P L L L L L L R L G Q I L C A G G T P S P I P D P
Bsu36I (790)
701 TCAGTAGCAACTGTTGCCACAGGGGAAAATGGCATAACGCAGATCAGCAGTACAGCAGAATCCTTTCATAAACAGAATGGAACTGGAACACCTCAGGTGG
47 S V A T V A T G E N G I T Q I S S T A E S F H K Q N G T G T P Q V
801 AAACAAACACCAGTGAGGATGGTGAAAGCTCTGGAGCCAACGATAGTTTAAGAACACCTGAACAAGGATCTAATGGGACTGATGGGGCATCTCAAAAAAC
80 E T N T S E D G E S S G A N D S L R T P E Q G S N G T D G A S Q K T
Bsp120I (913)
PvuII (992)
901 TCCCAGTAGCACTGGGCCCAGTCCTGTGTTTGACATTAAAGCTGTTTCCATCAGTCCAACCAATGTGATCTTAACTTGGAAAAGTAATGACACAGCTGCT
113 P S S T G P S P V F D I K A V S I S P T N V I L T W K S N D T A A
BbsI (1041)
NcoI (1066)
1001 TCTGAGTACAAGTATGTAGTAAAGCATAAGATGGAAAATGAGAAGACAATTACTGTTGTGCATCAACCATGGTGTAACATCACAGGCTTACGTCCAGCGA
147 S E Y K Y V V K H K M E N E K T I T V V H Q P W C N I T G L R P A
NdeI (1103)
1101 CTTCATATGTATTCTCCATCACTCCAGGAATAGGCAATGAGACTTGGGGAGATCCCAGAGTCATAAAAGTCATCACAGAGCCGATCCCAGTTTCTGATCT
180 T S Y V F S I T P G I G N E T W G D P R V I K V I T E P I P V S D L
1201 CCGTGTTGCCCTCACGGGTGTGAGGAAGGCTGCTCTCTCCTGGAGCAATGGCAATGGCACTGCCTCCTGCCGGGTTCTTCTTGAAAGCATTGGAAGCCAT
213 R V A L T G V R K A A L S W S N G N G T A S C R V L L E S I G S H
1301 GAGGAGTTGACTCAAGACTCAAGACTTCAGGTCAATATCTCGGGCCTGAAGCCAGGGGTTCAATACAACATCAACCCGTATCTTCTACAATCAAATAAGA
247 E E L T Q D S R L Q V N I S G L K P G V Q Y N I N P Y L L Q S N K
1401 CAAAGGGAGACCCCTTGGGCACAGAAGGTGGCTTGGATGCCAGCAATACAGAGAGAAGCCGGGCAGGGAGCCCCACCGCCCCTGTGCATGATGAGTCCCT
280 T K G D P L G T E G G L D A S N T E R S R A G S P T A P V H D E S L
1501 CGTGGGACCTGTGGACCCATCCTCCGGCCAGCAGTCCCGAGACACGGAAGTCCTGCTTGTCGGGTTAGAGCCTGGCACCCGATACAATGCCACCGTTTAT
313 V G P V D P S S G Q Q S R D T E V L L V G L E P G T R Y N A T V Y
XcmI (1602)
1601 TCCCAAGCAGCGAATGGCACAGAAGGACAGCCCCAGGCCATAGAGTTCAGGACAAATGCTATTCAGGTTTTTGACGTCACCGCTGTGAACATCAGTGCCA
347 S Q A A N G T E G Q P Q A I E F R T N A I Q V F D V T A V N I S A
BspLU11I (1764)
1701 CAAGCCTGACCCTGATCTGGAAAGTCAGCGATAACGAGTCGTCATCTAACTATACCTACAAGATACATGTGGCGGGGGAGACAGATTCTTCCAATCTCAA
380 T S L T L I W K V S D N E S S S N Y T Y K I H V A G E T D S S N L N
BsrBI (1833)
DraIII (1857)
AvrII (1872)
1801 CGTCAGTGAGCCTCGCGCTGTCATCCCCGGACTCCGCTCCAGCACCTTCTACAACATCACAGTGTGTCCTGTCCTAGGTGACATCGAGGGCACGCCGGGC
413 V S E P R A V I P G L R S S T F Y N I T V C P V L G D I E G T P G
ApaLI (1909)
PshAI (1947)
1901 TTCCTCCAAGTGCACACCCCCCCTGTTCCAGTTTCTGACTTCCGAGTGACAGTGGTCAGCACGACGGAGATCGGCTTAGCATGGAGCAGCCATGATGCAG
447 F L Q V H T P P V P V S D F R V T V V S T T E I G L A W S S H D A
NsiI (2011)
BsaBI (2010)
2001 AATCATTTCAGATGCATATCACACAGGAGGGAGCTGGCAATTCTCGGGTAGAAATAACCACCAACCAAAGTATTATCATTGGTGGCTTGTTCCCTGGAAC
480 E S F Q M H I T Q E G A G N S R V E I T T N Q S I I I G G L F P G T
2101 CAAGTATTGCTTTGAAATAGTTCCAAAAGGACCAAATGGGACTGAAGGGGCATCTCGGACAGTTTGCAATAGAACTGTTCCCAGTGCAGTGTTTGACATC
513 K Y C F E I V P K G P N G T E G A S R T V C N R T V P S A V F D I
BbrPI (2200)
2201 CACGTGGTCTACGTCACCACCACGGAGATGTGGCTGGACTGGAAGAGCCCTGACGGTGCTTCCGAGTATGTCTACCATTTAGTCATAGAGTCCAAGCATG
547 H V V Y V T T T E M W L D W K S P D G A S E Y V Y H L V I E S K H
Tth111I (2392)
2301 GCTCTAACCACACAAGCACGTATGACAAAGCGATTACTCTCCAGGGCCTGATTCCGGGCACCTTATATAACATCACCATCTCTCCAGAAGTGGACCACGT
580 G S N H T S T Y D K A I T L Q G L I P G T L Y N I T I S P E V D H V
SandI (2405)
2401 CTGGGGGGACCCCAACTCCACTGCACAGTACACACGGCCCAGCAATGTGTCCAACATTGATGTAAGTACCAACACCACAGCAGCAACTTTAAGTTGGCAG
613 W G D P N S T A Q Y T R P S N V S N I D V S T N T T A A T L S W Q
2501 AACTTTGATGACGCCTCTCCCACGTACTCCTACTGCCTTCTTATTGAGAAGGCTGGAAATTCCAGCAACGCAACACAAGTAGTCACGGACATTGGAATTA
647 N F D D A S P T Y S Y C L L I E K A G N S S N A T Q V V T D I G I


AseI (2619)
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BamHI (3022)SspI (3031)
PstI (3149)
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MscI (4168)
Acc65I (4217)
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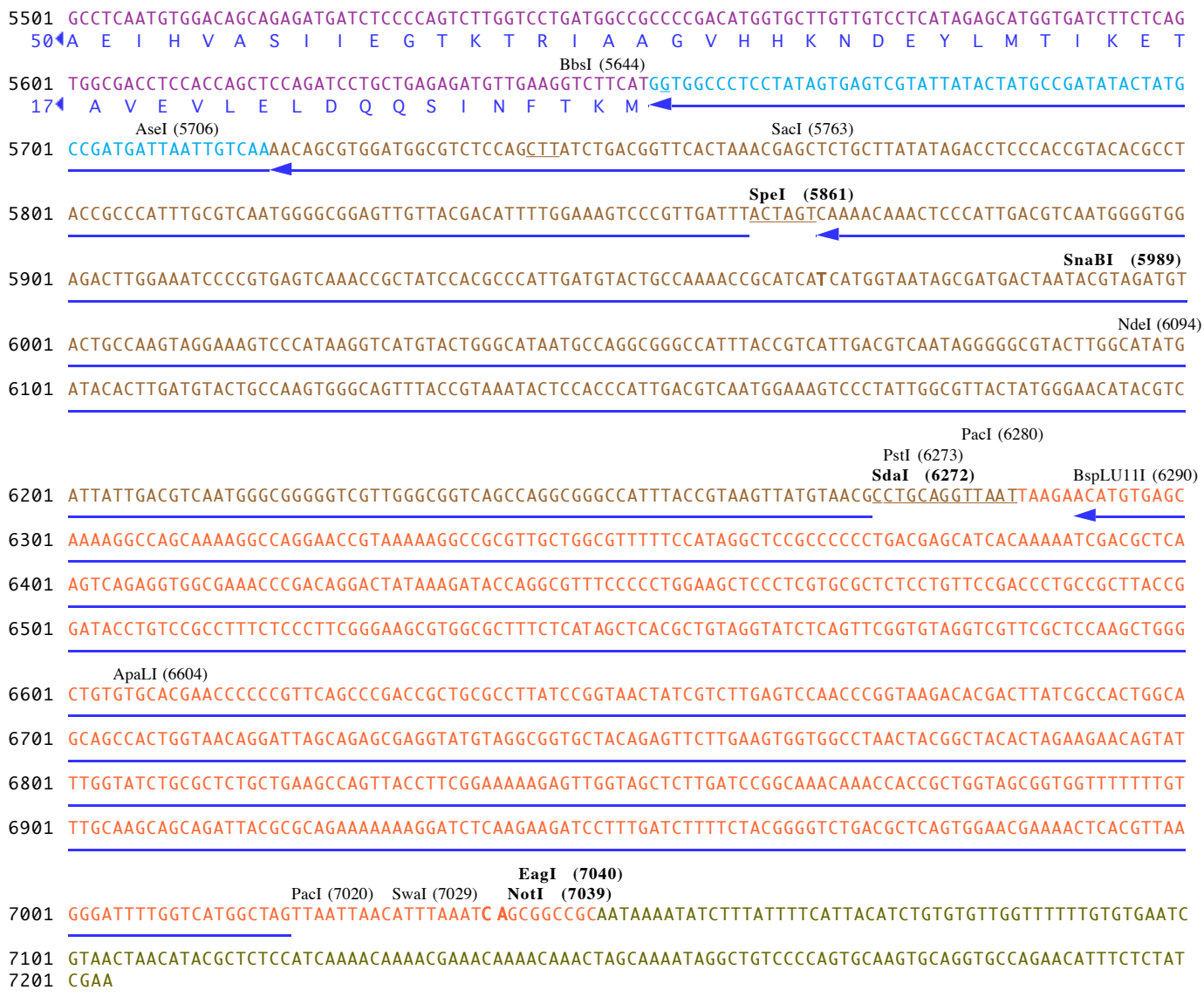
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50 A E I H V A S I I E G T K T R I A A G V H H K N D E Y L M T I K E T
BbsI (5644)
5601 TGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATG
17 A V E V L E L D Q Q S I N F T K M
AseI (5706)
SacI (5763)
5701 CCGATGATTAATTGTCAAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCT
SpeI (5861)
5801 ACCGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAAACTCCCATTGACGTCAATGGGGTGG
SnaBI (5989)
5901 AGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGT
NdeI (6094)
6001 ACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATG
6101 ATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTC
PacI (6280)
PstI (6273)
SdaI (6272)
BspLU11I (6290)
6201 ATTATTGACGTCAATGGGCGGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGC
6301 AAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCA
6401 AGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCG
6501 GATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGG
ApaLI (6604)
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6701 GCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTAT
6801 TTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGT
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EagI (7040)
PacI (7020)
SwaI (7029)
NotI (7039)
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7201 CGAA