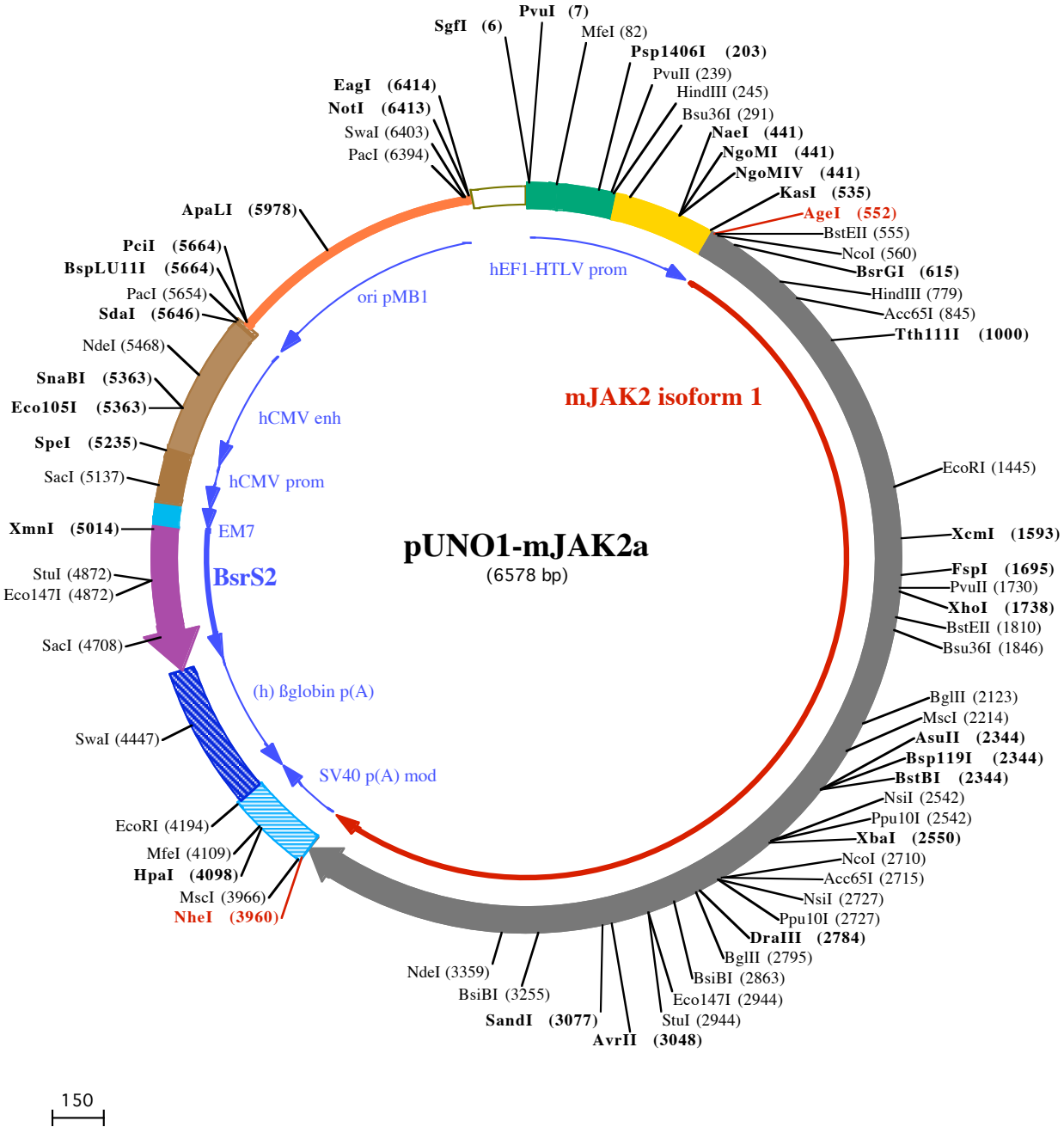
pUNO1-mJAK2a
(6578 bp)
mJAK2 isoform 1
hEF1-HTLV prom
ori pMB1
hCMV enh
hCMV prom
EM7
BsrS2
(h) ßglobin p(A)
SV40 p(A) mod
SgfI (6)
PvuI (7)
MfeI (82)
Psp1406I (203)
PvuII (239)
HindIII (245)
Bsu36I (291)
NaeI (441)
NgoMI (441)
NgoMIV (441)
KasI (535)
AgeI (552)
BstEII (555)
NcoI (560)
BsrGI (615)
HindIII (779)
Acc65I (845)
Tth111I (1000)
EcoRI (1445)
XcmI (1593)
FspI (1695)
PvuII (1730)
XhoI (1738)
BstEII (1810)
Bsu36I (1846)
BglII (2123)
MscI (2214)
AsuII (2344)
Bsp119I (2344)
BstBI (2344)
NsiI (2542)
Ppu10I (2542)
XbaI (2550)
NcoI (2710)
Acc65I (2715)
NsiI (2727)
Ppu10I (2727)
DraIII (2784)
BglII (2795)
BsiBI (2863)
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StuI (2944)
AvrII (3048)
SandI (3077)
BsiBI (3255)
NdeI (3359)
NheI (3960)
MscI (3966)
HpaI (4098)
MfeI (4109)
EcoRI (4194)
SwaI (4447)
SacI (4708)
Eco147I (4872)
StuI (4872)
XmnI (5014)
SacI (5137)
SpeI (5235)
Eco105I (5363)
SnaBI (5363)
NdeI (5468)
SdaI (5646)
PacI (5654)
BspLU11I (5664)
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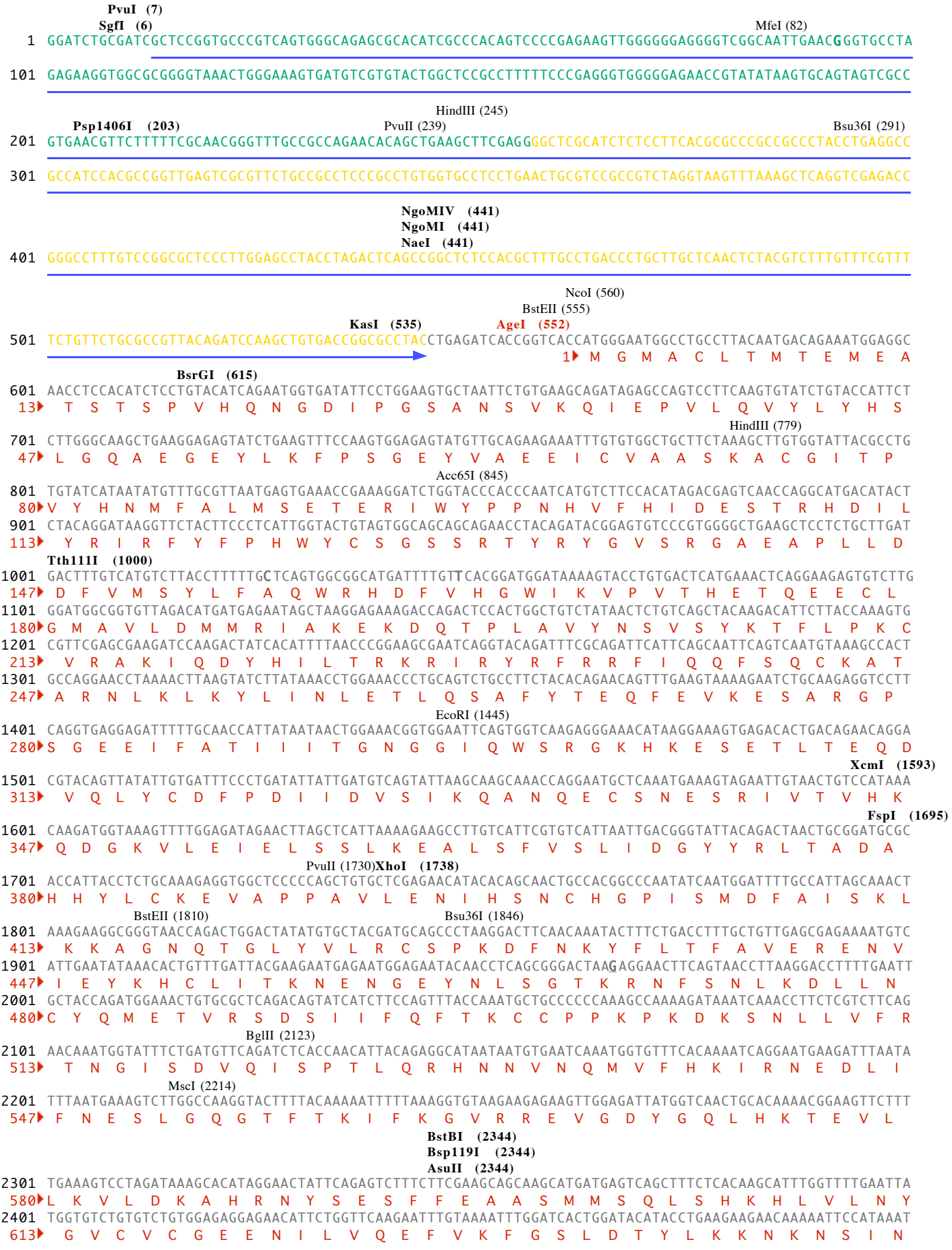
PacI (6394)
SwaI (6403)
NotI (6413)
EagI (6414)
150

InvivoGen


PvuI (7)
SgfI (6)
MfeI (82)
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC
HindIII (245)
Psp1406I (203)
PvuII (239)
Bsu36I (291)
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
NgoMIV (441)
NgoMI (441)
NaeI (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAACTCTACGTCTTTGTTTCGTTT
NcoI (560)
BstEII (555)
KasI (535)
AgeI (552)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTCACCATGGGAATGGCCTGCCTTACAATGACAGAAATGGAGGC
1 M G M A C L T M T E M E A
BsrGI (615)
601 AACCTCCACATCTCCTGTACATCAGAATGGTGATATTCCTGGAAGTGCTAATTCTGTGAAGCAGATAGAGCCAGTCCTTCAAGTGTATCTGTACCATTCT
13 T S T S P V H Q N G D I P G S A N S V K Q I E P V L Q V Y L Y H S
HindIII (779)
701 CTTGGGCAAGCTGAAGGAGAGTATCTGAAGTTTCCAAGTGGAGAGTATGTTGCAGAAGAAATTTGTGTGGCTGCTTCTAAAGCTTGTGGTATTACGCCTG
47 L G Q A E G E Y L K F P S G E Y V A E E I C V A A S K A C G I T P
Acc65I (845)
801 TGTATCATAATATGTTTGCGTTAATGAGTGAAACCGAAAGGATCTGGTACCCACCCAATCATGTCTTCCACATAGACGAGTCAACCAGGCATGACATACT
80 V Y H N M F A L M S E T E R I W Y P P N H V F H I D E S T R H D I L
901 CTACAGGATAAGGTTCTACTTCCCTCATTGGTACTGTAGTGGCAGCAGCAGAACCTACAGATACGGAGTGTCCCGTGGGGCTGAAGCTCCTCTGCTTGAT
113 Y R I R F Y F P H W Y C S G S S R T Y R Y G V S R G A E A P L L D
Tth111I (1000)
1001 GACTTTGTCATGTCTTACCTTTTTGCTCAGTGGCGGCATGATTTTGTTCACGGATGGATAAAAGTACCTGTGACTCATGAAACTCAGGAAGAGTGTCTTG
147 D F V M S Y L F A Q W R H D F V H G W I K V P V T H E T Q E E C L
1101 GGATGGCGGTGTTAGACATGATGAGAATAGCTAAGGAGAAAGACCAGACTCCACTGGCTGTCTATAACTCTGTCAGCTACAAGACATTCTTACCAAAGTG
180 G M A V L D M M R I A K E K D Q T P L A V Y N S V S Y K T F L P K C
1201 CGTTCGAGCGAAGATCCAAGACTATCACATTTTAACCCGGAAGCGAATCAGGTACAGATTTCGCAGATTCATTCAGCAATTCAGTCAATGTAAAGCCACT
213 V R A K I Q D Y H I L T R K R I R Y R F R R F I Q Q F S Q C K A T
1301 GCCAGGAACCTAAAACTTAAGTATCTTATAAACCTGGAAACCCTGCAGTCTGCCTTCTACACAGAACAGTTTGAAGTAAAAGAATCTGCAAGAGGTCCTT
247 A R N L K L K Y L I N L E T L Q S A F Y T E Q F E V K E S A R G P
EcoRI (1445)
1401 CAGGTGAGGAGATTTTTGCAACCATTATAATAACTGGAAACGGTGGAATTCAGTGGTCAAGAGGGAAACATAAGGAAAGTGAGACACTGACAGAACAGGA
280 S G E E I F A T I I I T G N G G I Q W S R G K H K E S E T L T E Q D
XcmI (1593)
1501 CGTACAGTTATATTGTGATTTCCCTGATATTATTGATGTCAGTATTAAGCAAGCAAACCAGGAATGCTCAAATGAAAGTAGAATTGTAACTGTCCATAAA
313 V Q L Y C D F P D I I D V S I K Q A N Q E C S N E S R I V T V H K
FspI (1695)
1601 CAAGATGGTAAAGTTTTGGAGATAGAACTTAGCTCATTAAAAGAAGCCTTGTCATTCGTGTCATTAATTGACGGGTATTACAGACTAACTGCGGATGCGC
347 Q D G K V L E I E L S S L K E A L S F V S L I D G Y Y R L T A D A
PvuII (1730)XhoI (1738)
1701 ACCATTACCTCTGCAAAGAGGTGGCTCCCCCAGCTGTGCTCGAGAACATACACAGCAACTGCCACGGCCCAATATCAATGGATTTTGCCATTAGCAAACT
380 H H Y L C K E V A P P A V L E N I H S N C H G P I S M D F A I S K L
BstEII (1810)
Bsu36I (1846)
1801 AAAGAAGGCGGGTAACCAGACTGGACTATATGTGCTACGATGCAGCCCTAAGGACTTCAACAAATACTTTCTGACCTTTGCTGTTGAGCGAGAAAATGTC
413 K K A G N Q T G L Y V L R C S P K D F N K Y F L T F A V E R E N V
1901 ATTGAATATAAACACTGTTTGATTACGAAGAATGAGAATGGAGAATACAACCTCAGCGGGACTAAGAGGAACTTCAGTAACCTTAAGGACCTTTTGAATT
447 I E Y K H C L I T K N E N G E Y N L S G T K R N F S N L K D L L N
2001 GCTACCAGATGGAAACTGTGCGCTCAGACAGTATCATCTTCCAGTTTACCAAATGCTGCCCCCCAAAGCCAAAAGATAAATCAAACCTTCTCGTCTTCAG
480 C Y Q M E T V R S D S I I F Q F T K C C P P K P K D K S N L L V F R
BglII (2123)
2101 AACAAATGGTATTTCTGATGTTCAGATCTCACCAACATTACAGAGGCATAATAATGTGAATCAAATGGTGTTTCACAAAATCAGGAATGAAGATTTAATA
513 T N G I S D V Q I S P T L Q R H N N V N Q M V F H K I R N E D L I
MscI (2214)
2201 TTTAATGAAAGTCTTGGCCAAGGTACTTTTACAAAAATTTTTAAAGGTGTAAGAAGAGAAGTTGGAGATTATGGTCAACTGCACAAAACGGAAGTTCTTT
547 F N E S L G Q G T F T K I F K G V R R E V G D Y G Q L H K T E V L
BstBI (2344)
Bsp119I (2344)
AsuII (2344)
2301 TGAAAGTCCTAGATAAAGCACATAGGAACTATTCAGAGTCTTTCTTCGAAGCAGCAAGCATGATGAGTCAGCTTTCTCACAAGCATTTGGTTTTGAATTA
580 L K V L D K A H R N Y S E S F F E A A S M M S Q L S H K H L V L N Y
2401 TGGTGTCTGTGTCTGTGGAGAGGAGAACATTCTGGTTCAAGAATTTGTAAAATTTGGATCACTGGATACATACCTGAAGAAGAACAAAAATTCCATAAAT
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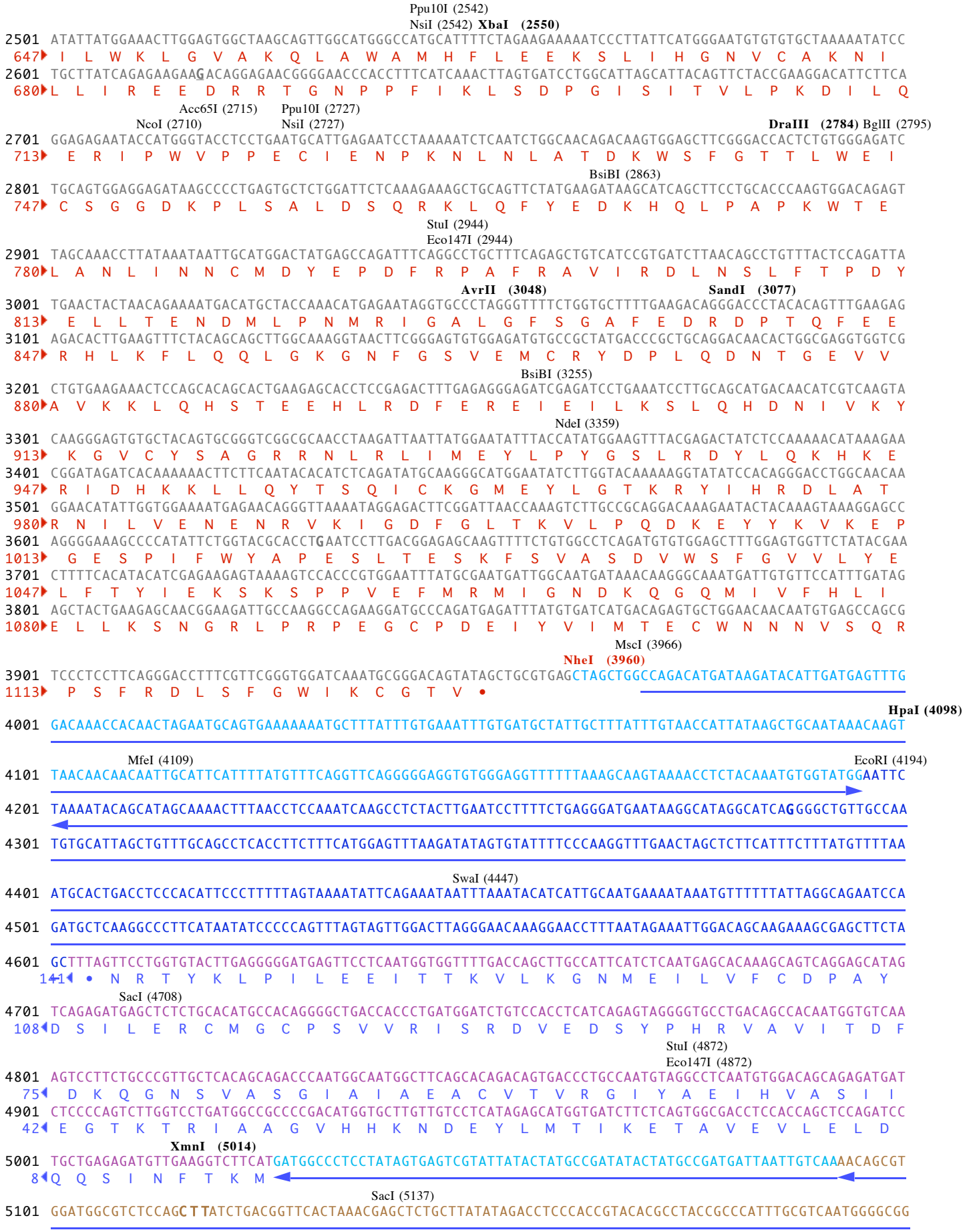
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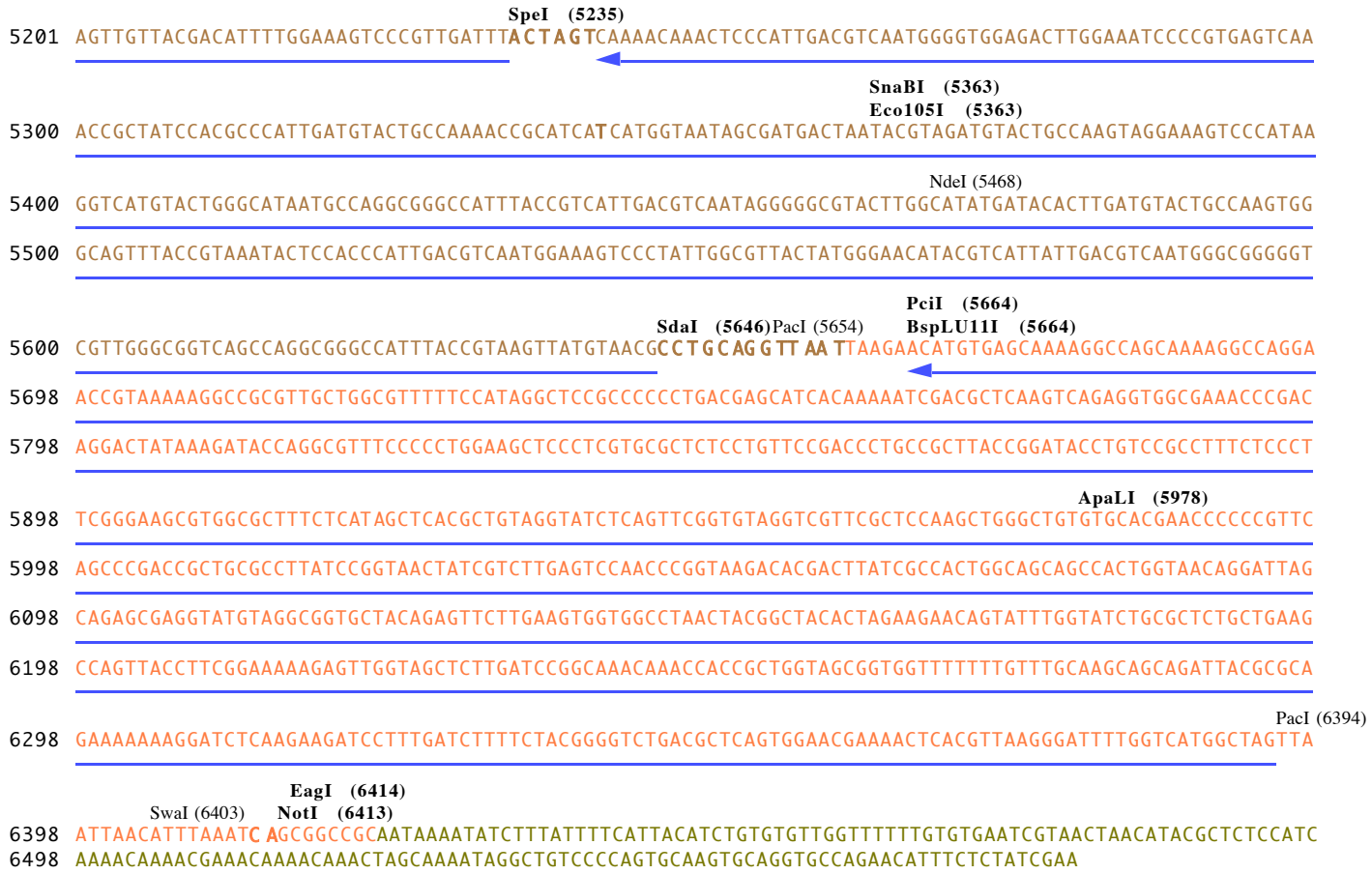
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