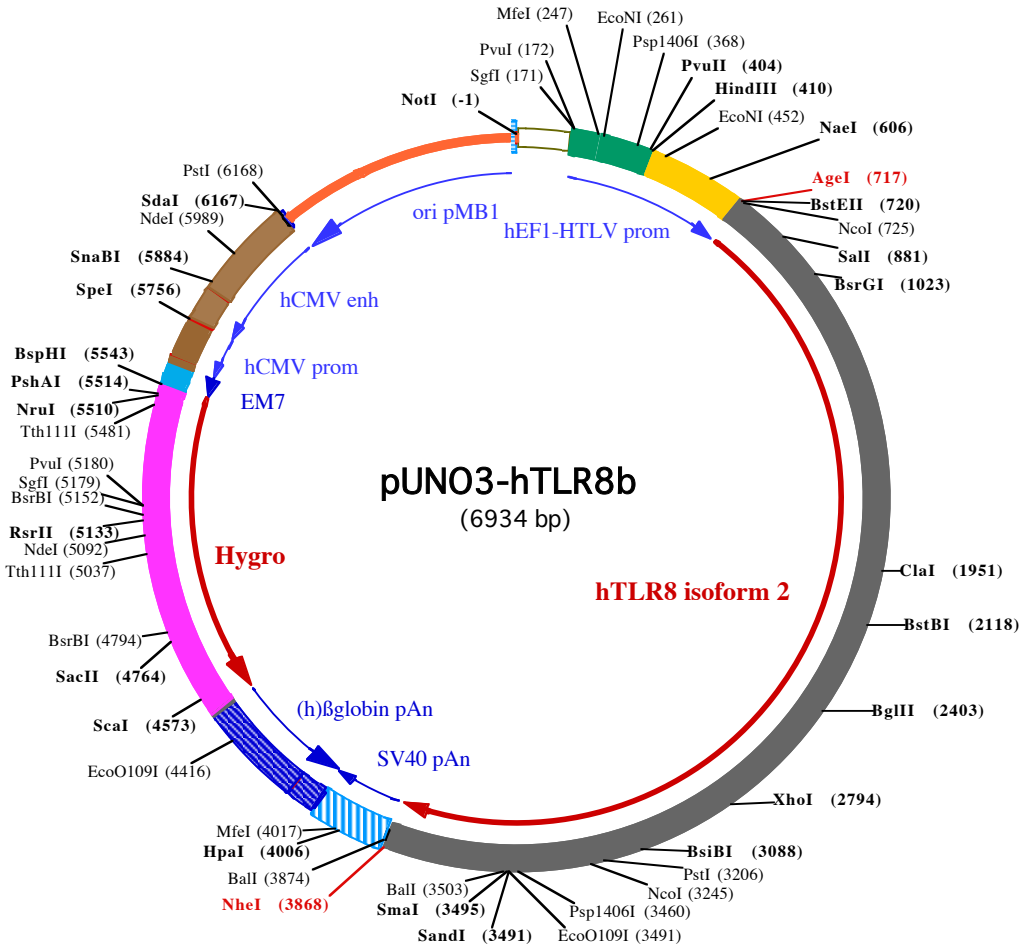
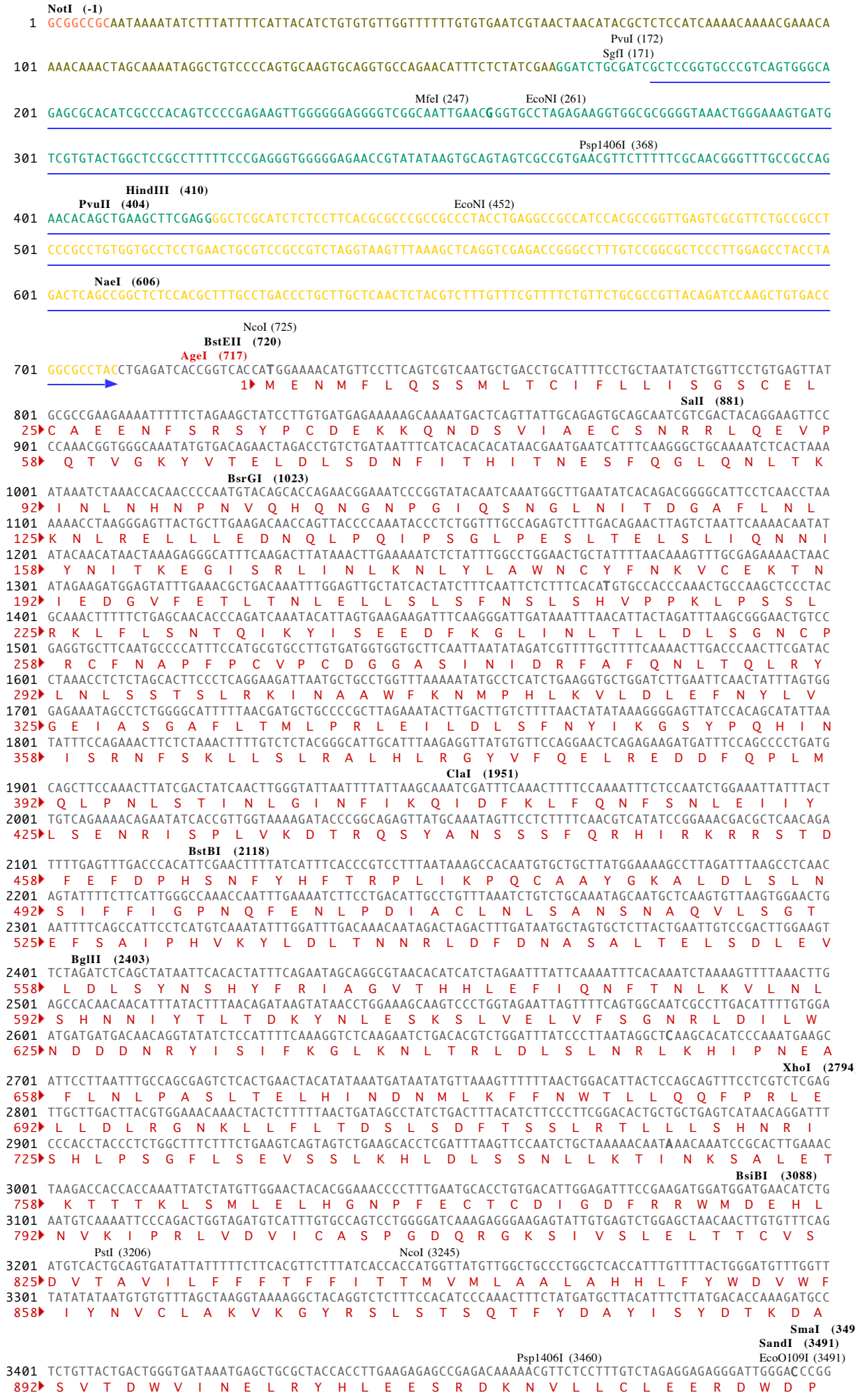

pUNO3-hTLR8b
(6934 bp)
MfeI (247)
EcoNI (261)
Psp1406I (368)
PvuII (404)
HindIII (410)
EcoNI (452)
NaeI (606)
AgeI (717)
BstEII (720)
NcoI (725)
SalI (881)
BsrGI (1023)
ClaI (1951)
BstBI (2118)
BglII (2403)
XhoI (2794)
BsiBI (3088)
PstI (3206)
NcoI (3245)
Psp1406I (3460)
EcoO109I (3491)
SandI (3491)
SmaI (3495)
BalI (3503)
NheI (3868)
BalI (3874)
HpaI (4006)
MfeI (4017)
EcoO109I (4416)
ScaI (4573)
SacII (4764)
BsrBI (4794)
Tth111I (5037)
NdeI (5092)
RsrII (5133)
BsrBI (5152)
SgfI (5179)
PvuI (5180)
Tth111I (5481)
NruI (5510)
PshAI (5514)
BspHI (5543)
SpeI (5756)
SnaBI (5884)
NdeI (5989)
SdaI (6167)
PstI (6168)
NotI (-1)
SgfI (171)
PvuI (172)
ori pMB1
hEF1-HTLV prom
hCMV enh
hCMV prom
EM7
Hygro
hTLR8 isoform 2
(h)ßglobin pAn
SV40 pAn

InvivoGen


NotI (-1)
PvuI (172)
SgfI (171)
MfeI (247)
EcoNI (261)
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HindIII (410)
PvuII (404)
EcoNI (452)
NaeI (606)
NcoI (725)
BstEII (720)
AgeI (717)
SalI (881)
BsrGI (1023)
ClaI (1951)
BstBI (2118)
BglII (2403)
XhoI (2794
BsiBI (3088)
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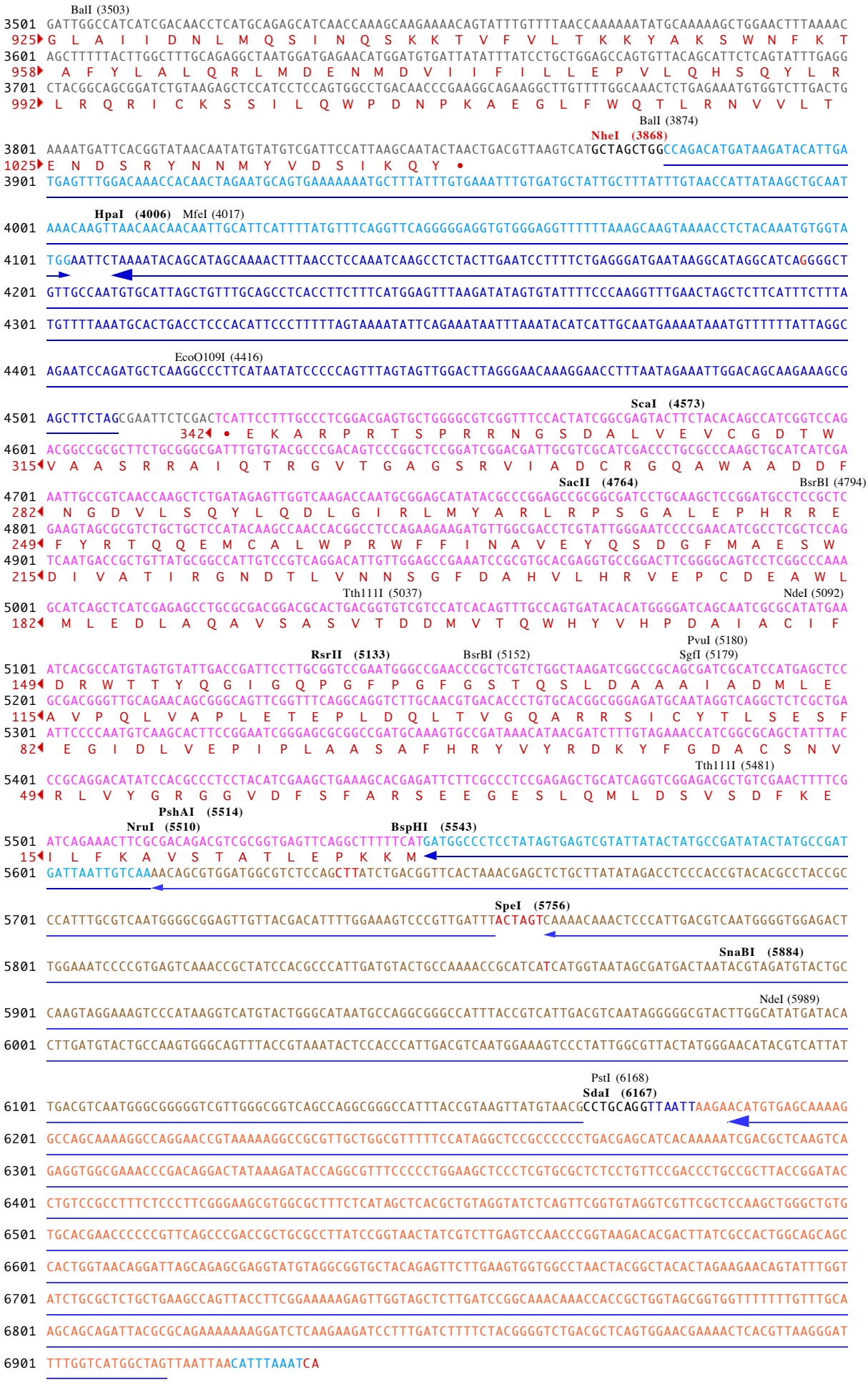
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925 G L A I I D N L M Q S I N Q S K K T V F V L T K K Y A K S W N F K T
3601 AGCTTTTTACTTGGCTTTGCAGAGGCTAATGGATGAGAACATGGATGTGATTATATTTATCCTGCTGGAGCCAGTGTTACAGCATTCTCAGTATTTGAGG
958 A F Y L A L Q R L M D E N M D V I I F I L L E P V L Q H S Q Y L R
3701 CTACGGCAGCGGATCTGTAAGAGCTCCATCCTCCAGTGGCCTGACAACCCGAAGGCAGAAGGCTTGTTTTGGCAAACTCTGAGAAATGTGGTCTTGACTG
992 L R Q R I C K S S I L Q W P D N P K A E G L F W Q T L R N V V L T
BalI (3874)
NheI (3868)
3801 AAAATGATTCACGGTATAACAATATGTATGTCGATTCCATTAAGCAATACTAACTGACGTTAAGTCATGCTAGCTGGCCAGACATGATAAGATACATTGA
1025 E N D S R Y N N M Y V D S I K Q Y •
3901 TGAGTTTGGACAAACCACAACTAGAATGCAGTGAAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAAT
HpaI (4006) MfeI (4017)
4001 AAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTA
4101 TGGAATTCTAAAATACAGCATAGCAAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCT
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EcoO109I (4416)
4401 AGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCG
ScaI (4573)
4501 AGCTTCTAGCGAATTCTCGACTCATTCCTTTGCCCTCGGACGAGTGCTGGGGCGTCGGTTTCCACTATCGGCGAGTACTTCTACACAGCCATCGGTCCAG
342 • E K A R P R T S P R R N G S D A L V E V C G D T W
4601 ACGGCCGCGCTTCTGCGGGCGATTTGTGTACGCCCGACAGTCCCGGCTCCGGATCGGACGATTGCGTCGCATCGACCCTGCGCCCAAGCTGCATCATCGA
315 V A A S R R A I Q T R G V T G A G S R V I A D C R G Q A W A A D D F
SacII (4764)
BsrBI (4794)
4701 AATTGCCGTCAACCAAGCTCTGATAGAGTTGGTCAAGACCAATGCGGAGCATATACGCCCGGAGCCGCGGCGATCCTGCAAGCTCCGGATGCCTCCGCTC
282 N G D V L S Q Y L Q D L G I R L M Y A R L R P S G A L E P H R R E
4801 GAAGTAGCGCGTCTGCTGCTCCATACAAGCCAACCACGGCCTCCAGAAGAAGATGTTGGCGACCTCGTATTGGGAATCCCCGAACATCGCCTCGCTCCAG
249 F Y R T Q Q E M C A L W P R W F F I N A V E Y Q S D G F M A E S W
4901 TCAATGACCGCTGTTATGCGGCCATTGTCCGTCAGGACATTGTTGGAGCCGAAATCCGCGTGCACGAGGTGCCGGACTTCGGGGCAGTCCTCGGCCCAAA
215 D I V A T I R G N D T L V N N S G F D A H V L H R V E P C D E A W L
Tth111I (5037)
NdeI (5092)
5001 GCATCAGCTCATCGAGAGCCTGCGCGACGGACGCACTGACGGTGTCGTCCATCACAGTTTGCCAGTGATACACATGGGGATCAGCAATCGCGCATATGAA
182 M L E D L A Q A V S A S V T D D M V T Q W H Y V H P D A I A C I F
PvuI (5180)
RsrII (5133)
BsrBI (5152)
SgfI (5179)
5101 ATCACGCCATGTAGTGTATTGACCGATTCCTTGCGGTCCGAATGGGCCGAACCCGCTCGTCTGGCTAAGATCGGCCGCAGCGATCGCATCCATGAGCTCC
149 D R W T T Y Q G I G Q P G F P G F G S T Q S L D A A A I A D M L E
5201 GCGACGGGTTGCAGAACAGCGGGCAGTTCGGTTTCAGGCAGGTCTTGCAACGTGACACCCTGTGCACGGCGGGAGATGCAATAGGTCAGGCTCTCGCTGA
115 A V P Q L V A P L E T E P L D Q L T V G Q A R R S I C Y T L S E S F
5301 ATTCCCCAATGTCAAGCACTTCCGGAATCGGGAGCGCGGCCGATGCAAAGTGCCGATAAACATAACGATCTTTGTAGAAACCATCGGCGCAGCTATTTAC
82 E G I D L V E P I P L A A S A F H R Y V Y R D K Y F G D A C S N V
Tth111I (5481)
5401 CCGCAGGACATATCCACGCCCTCCTACATCGAAGCTGAAAGCACGAGATTCTTCGCCCTCCGAGAGCTGCATCAGGTCGGAGACGCTGTCGAACTTTTCG
49 R L V Y G R G G V D F S F A R S E E G E S L Q M L D S V S D F K E
PshAI (5514)
NruI (5510)
BspHI (5543)
5501 ATCAGAAACTTCGCGACAGACGTCGCGGTGAGTTCAGGCTTTTTCATGATGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGAT
15 I L F K A V S T A T L E P K K M
5601 GATTAATTGTCAAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGC
SpeI (5756)
5701 CCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACT
SnaBI (5884)
5801 TGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGC
NdeI (5989)
5901 CAAGTAGGAAAGTCCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACA
6001 CTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTAT
PstI (6168)
SdaI (6167)
6101 TGACGTCAATGGGCGGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAG
6201 GCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCA
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