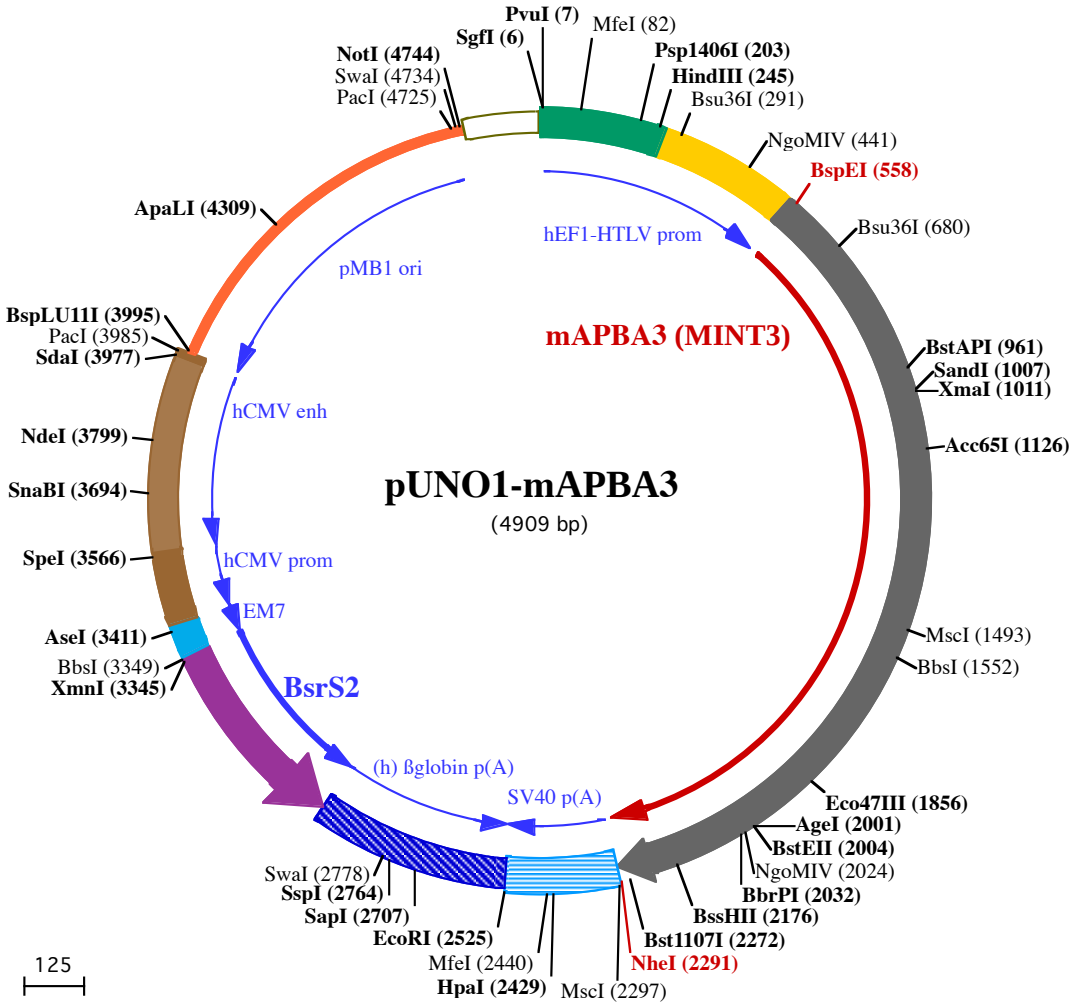
pUNO1-mAPBA3
(4909 bp)
mAPBA3 (MINT3)
hEF1-HTLV prom
pMB1 ori
hCMV enh
hCMV prom
EM7
BsrS2
(h) ßglobin p(A)
SV40 p(A)
PvuI (7)
MfeI (82)
SgfI (6)
NotI (4744)
SwaI (4734)
PacI (4725)
Psp1406I (203)
HindIII (245)
Bsu36I (291)
NgoMIV (441)
BspEI (558)
Bsu36I (680)
BstAPI (961)
SandI (1007)
XmaI (1011)
Acc65I (1126)
MscI (1493)
BbsI (1552)
Eco47III (1856)
AgeI (2001)
BstEII (2004)
NgoMIV (2024)
BbrPI (2032)
BssHII (2176)
Bst1107I (2272)
NheI (2291)
MscI (2297)
HpaI (2429)
MfeI (2440)
EcoRI (2525)
SapI (2707)
SspI (2764)
SwaI (2778)
XmnI (3345)
BbsI (3349)
AseI (3411)
SpeI (3566)
SnaBI (3694)
NdeI (3799)
SdaI (3977)
PacI (3985)
BspLU11I (3995)
ApaLI (4309)
125

PvuI (7)
SgfI (6) MfeI (82)
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

Psp1406I (203) HindIII (245) Bsu36I (291)
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAACTCTACGTCTTTGTTTCGTTT

BspEI (558)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGCTCCGGACACCATGGAGTTCCTGCCAGGACCCCAGCATCCCCC
1 M E F L P G P Q H P P

Bsu36I (680)
601 AGGGCCCCCAACCATGGACTTGGAGGAGCCCAAAGGCCCCGAGGTGCCCTCTGAGAACCACCCCTCTAACACCCAGTCGGCCTTAGGGCCTGGAGGCCCT
11 G P P T M D L E E P K G P E V P S E N H P S N T Q S A L G P G G P
701 GTCACCCTGAGTGAGATGGAGCTGGACACATCCAGTGTGCAGGAGCTGGTTCAGCAGCTAGAAGCTCTACCCAGCGACCTGGGTGGCCCATTCCCAGATG
45 V T L S E M E L D T S S V Q E L V Q Q L E A L P S D L G G P F P D
801 GAGCCCCCTGTCCCCTGCACATTGCTACCGGCCAAGGACTTGCCACCCAGGAGAACCCAGATGCTGGTGGGCTCTTGTCGGCCGAGGCAGGCGGGGACGA
78 G A P C P L H I A T G Q G L A T Q E N P D A G G L L S A E A G G D D

BstAPI (961)
901 CCTTCTGGGTCTGCTGAGGGATGAGGCCTCTTCGCCTGCCCAATCTGTCCCCCAAGATCCTGCACAGACTGCACCCCGCCTTCTGCAGCCGCCAGAGGAC
111 L L G L L R D E A S S P A Q S V P Q D P A Q T A P R L L Q P P E D

XmaI (1011)
SandI (1007)
1001 CCTGATGGGGACCCGGGATGGATGGAAGGGGCATCAGCAGAGCCAGCAGACAGCAGGAGCTCCAGCAGTTCCCCGGAGCCCTGGCTGGAGACAGCACCCC
145 P D G D P G W M E G A S A E P A D S R S S S S S P E P W L E T A P

Acc65I (1126)
1101 TGGTGACACAGCAGGAACCACCTGTGGGTACCCAGAGCCGGGAGACCCTGGCCTCGTGCCCTGCCGTCACCGAGGTCCCAGGTCCCTGTGGGCCGGAGGA
178 L V T Q Q E P P V G T Q S R E T L A S C P A V T E V P G P C G P E E
1201 GCTCATGGATGGTGTCATCTTCGGGGCGAAATACCTGGGCTCCACCCAGCTGCTGTCAGAGCGCAGCCCGGCGCCCAGCACACGCATGGGGCAGGCGCAG
211 L M D G V I F G A K Y L G S T Q L L S E R S P A P S T R M G Q A Q
1301 GAGGCCATGGACCGCGTCAAGGCCCCTGAAGGCGAGACCCAGCCCATGGTGGAAGTGGACATCTTTATCTCCACCAAGCGTGTCAAAGTGTTGGCTGCTG
245 E A M D R V K A P E G E T Q P M V E V D I F I S T K R V K V L A A

MscI (1493)
1401 ACTCCCAGGATGCCCTGATGGACCATGCCCTGCAGACCATCTCCTACATCGCAGACATTGGGCCTGTACTGGTCTTGATGGCCCGGAGGCGGCTGGCCAG
278 D S Q D A L M D H A L Q T I S Y I A D I G P V L V L M A R R R L A R

BbsI (1552)
1501 GAGGACAACTCCCCAGGACCGCCAGCGGCGACTCTACAAGATGCTGTGCCATGTCTTCCACTCAGAGGATGCCCAGCTCATAGCACAAGCCATCGGCCAG
311 R T T P Q D R Q R R L Y K M L C H V F H S E D A Q L I A Q A I G Q
1601 GCCTTCAGCATCGCCTACAGCCAGTTCCTACAGGAGAACAGGATCGACCCCAGCCAGGTGGGCACGCAGCCCTCAACCGCTGCCAGCCACCCGCACAACG
345 A F S I A Y S Q F L Q E N R I D P S Q V G T Q P S T A A S H P H N
1701 GCGACCTGGACCACTTCTGCAACAGCCAGAACTGTAGGGAGGTTTGCATCCAGAAGCGGCCAGGTGAAGGCCTGGGCGTCGCGCTAGTTGAATCAGGCTG
378 G D L D H F C N S Q N C R E V C I Q K R P G E G L G V A L V E S G W

Eco47III (1856)
1801 GGGCTCGCTACTGCCCACTGCGGTCATTGCCAACCTGCTCCATGGGGGCCCTGCCGAGCGCTGCGGGGCCCTGAGCATAGGGGACCGCGTCACTGCCATC
411 G S L L P T A V I A N L L H G G P A E R C G A L S I G D R V T A I
1901 AATGGAACCAGCCTGGTGGGGCTGTCGCTGGCTGCCTGCCAGGCTGCGGTGCGCGAGGTGCGGCGACTTTCATCCGTGACGCTGAGTATTATCCACTGCC
445 N G T S L V G L S L A A C Q A A V R E V R R L S S V T L S I I H C

BstEII (2004) BbrPI (2032)
AgeI (2001) NgoMIV (2024)
2001 CACCGGTCACCACGGCCGTCATCCGCCGGCCCCACGTGCGCGAGCAGCTGGGCTTCTGTGTGGAGGATGGAATCATTTGTAGCCTGCTGCGTGGGGGCGC
478 P P V T T A V I R R P H V R E Q L G F C V E D G I I C S L L R G G A

BssHII (2176)
2101 TGCTGAGCGTGGTGGAGTCCGCGTTGGACACCGCATCATTGAGGTCAACGGGCAGAGCGTGGTGGCTATGCCCCATGCGCGCATCATCCAGCTGCTCACA
511 A E R G G V R V G H R I I E V N G Q S V V A M P H A R I I Q L L T

MscI (2297)
Bst1107I (2272) NheI (2291)
2201 GAGACAAGAGAAATCCACATCAAGACCATGCCAGCTGCCACCTACCGACTGCTCACGGGACAGGAACAACCAGTATACCTATGACTGCCCCGCTAGCTGG
545 E T R E I H I K T M P A A T Y R L L T G Q E Q P V Y L •
2301 CCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTAT

HpaI (2429) MfeI (2440)
2401 TTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCAA

EcoRI (2525)

2501 GTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGA

2601 ATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAGATATAGTGTATTTTCCCAAGGTT

SapI (2707) SspI (2764) SwaI (2778)

2701 TGAACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATG

2801 AAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAAT

2901 AGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCAT

141 • N R T Y K L P I L E E I T T K V L K G N M

3001 CTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAG

119 E I L V F C D P A Y D S I L E R C M G C P S V V R I S R D V E D S

3101 TAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAA

85 Y P H R V A V I T D F D K Q G N S V A S G I A I A E A C V T V R G I

3201 TGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCCTGATGGCCGCCCCGACATGGTGCTTGTTGTCCTCATAGAGCATGGTGATCTT

52 Y 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

BbsI (3349)

XmnI (3345)

3301 CTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATA

19 E T A V E V L E L D Q Q S I N F T K M

AseI (3411)

3401 CTATGCCGATGATTAATTGTCAAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCCACCGTACA

SpeI (3566)

3501 CGCCTACCGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGG

SnaBI (3694)

3601 GGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTA

NdeI (3799)

3701 GATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGC

3801 ATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACAT

PacI (3985)

SdaI (3977) BspLU11I (3995)

3901 ACGTCATTATTGACGTCAATGGGCGGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATG

4001 TGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGAC

4101 GCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCT

4201 TACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAG

ApaLI (4309)

4301 CTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCAC

4401 TGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAAC

4501 AGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTT

4601 TTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCAC

PacI (4725) SwaI (4734) NotI (4744)

4701 GTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGT

4801 GAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTC

4901 TCTATCGAA