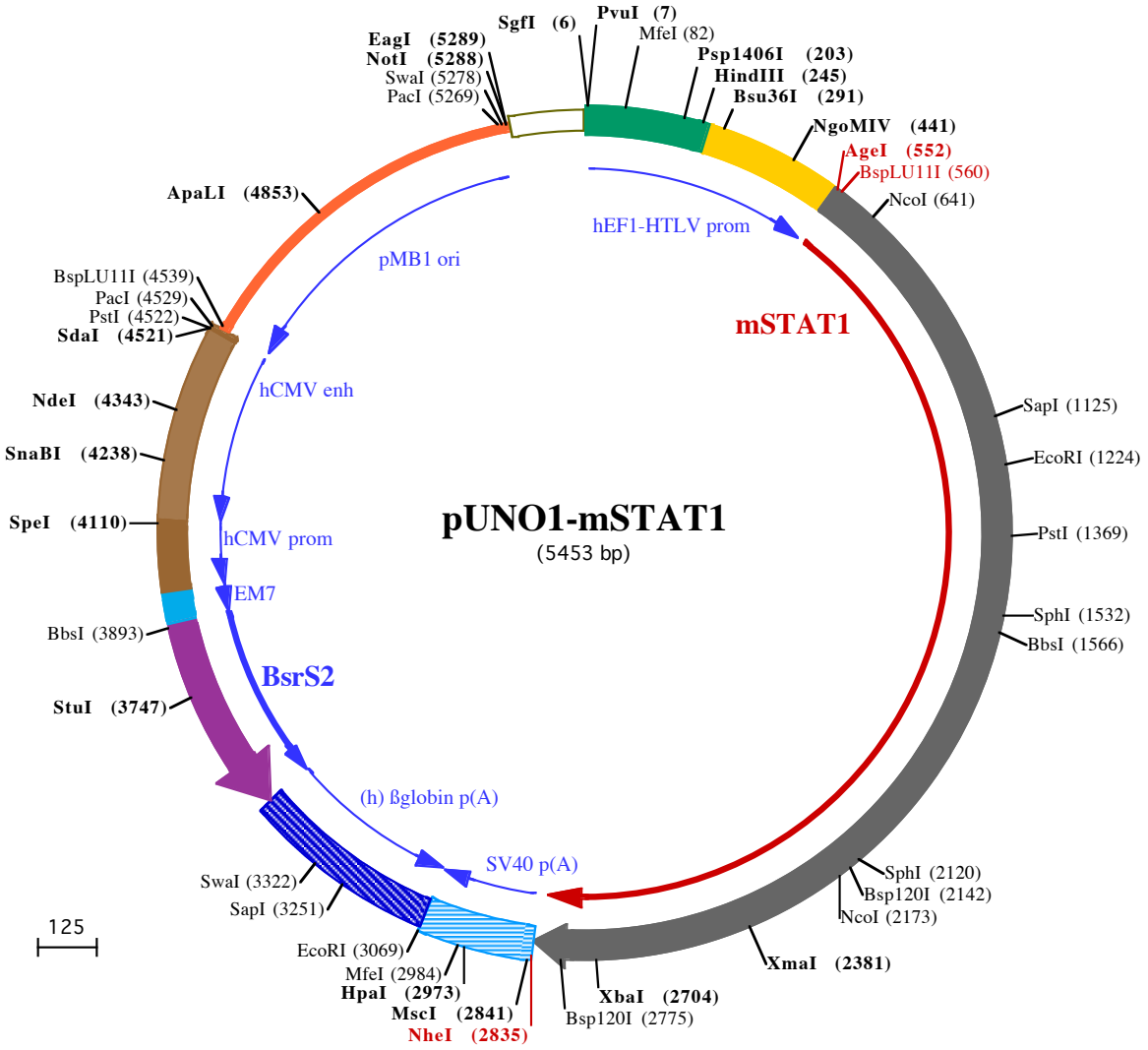
pUNO1-mSTAT1
(5453 bp)
mSTAT1
BsrS2
hEF1-HTLV prom
pMB1 ori
hCMV enh
hCMV prom
EM7
(h) ßglobin p(A)
SV40 p(A)
SgfI (6)
PvuI (7)
MfeI (82)
Psp1406I (203)
HindIII (245)
Bsu36I (291)
NgoMIV (441)
AgeI (552)
BspLU11I (560)
NcoI (641)
SapI (1125)
EcoRI (1224)
PstI (1369)
SphI (1532)
BbsI (1566)
SphI (2120)
Bsp120I (2142)
NcoI (2173)
XmaI (2381)
XbaI (2704)
Bsp120I (2775)
NheI (2835)
MscI (2841)
HpaI (2973)
MfeI (2984)
EcoRI (3069)
SapI (3251)
SwaI (3322)
125
BbsI (3893)
StuI (3747)
SpeI (4110)
SnaBI (4238)
NdeI (4343)
SdaI (4521)
PstI (4522)
PacI (4529)
BspLU11I (4539)
ApaLI (4853)
PacI (5269)
SwaI (5278)
NotI (5288)
EagI (5289)

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

```
   1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA

 101 GAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC
```

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

```
 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCCGCCGCCCTACCTGAGGCC

 301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
```

NgoMIV (441)

```
 401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAACTCTACGTCTTTGTTTCGTTT
```

BspLU11I (560)
AgeI (552)

```
 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTCAACATGTCACAGTGGTTCGAGCTTCAGCAGCTGGACTCCAA
                                                  1▸ M  S  Q  W  F  E  L  Q  Q  L  D  S  K
```

NcoI (641)

```
 601 GTTCCTGGAGCAGGTCCACCAGCTGTACGATGACAGTTTCCCCATGGAAATCAGACAGTACCTGGCCCAGTGGCTGGAAAAGCAAGACTGGGAGCACGCT
  13▸  F  L  E  Q  V  H  Q  L  Y  D  D  S  F  P  M  E  I  R  Q  Y  L  A  Q  W  L  E  K  Q  D  W  E  H  A
 701 GCCTATGATGTCTCGTTTGCGACCATCCGCTTCCATGACCTCCTCTCACAGCTGGACGACCAGTACAGCCGCTTTTCTCTGGAGAATAATTTCTTGTTGC
  47▸ A  Y  D  V  S  F  A  T  I  R  F  H  D  L  L  S  Q  L  D  D  Q  Y  S  R  F  S  L  E  N  N  F  L  L
 801 AGCACAACATACGGAAAAGCAAGCGTAATCTCCAGGATAACTTCCAAGAAGATCCCGTACAGATGTCCATGATCATCTACAACTGTCTGAAGGAAGAAAG
  80▸Q  H  N  I  R  K  S  K  R  N  L  Q  D  N  F  Q  E  D  P  V  Q  M  S  M  I  I  Y  N  C  L  K  E  E  R
 901 GAAGATTTTGGAAAATGCCCAAAGATTTAATCAGGCCCAGGAGGGAAATATTCAGAACACTGTGATGTTAGATAAACAGAAGGAGCTGGACAGTAAAGTC
 113▸  K  I  L  E  N  A  Q  R  F  N  Q  A  Q  E  G  N  I  Q  N  T  V  M  L  D  K  Q  K  E  L  D  S  K  V
1001 AGAAATGTGAAGGATCAAGTCATGTGCATAGAGCAGGAAATCAAGACCCTAGAAGAATTACAAGATGAATATGACTTTAAATGCAAAACCTCTCAGAACA
 147▸ R  N  V  K  D  Q  V  M  C  I  E  Q  E  I  K  T  L  E  E  L  Q  D  E  Y  D  F  K  C  K  T  S  Q  N
```

SapI (1125)

```
1101 GAGAAGGTGAAGCCAATGGTGTGGCGAAGAGCGACCAAAAACAGGAACAGCTGCTGCTCCACAAGATGTTTTTAATGCTTGACAATAAGAGAAAGGAGAT
 180▸R  E  G  E  A  N  G  V  A  K  S  D  Q  K  Q  E  Q  L  L  L  H  K  M  F  L  M  L  D  N  K  R  K  E  I
```

EcoRI (1224)

```
1201 AATTCACAAAATCAGAGAGTTGCTGAATTCCATCGAGCTCACTCAGAACACTCTGATTAATGACGAGCTCGTGGAGTGGAAGCGAAGGCAGCAGAGCGCC
 213▸  I  H  K  I  R  E  L  L  N  S  I  E  L  T  Q  N  T  L  I  N  D  E  L  V  E  W  K  R  R  Q  Q  S  A
```

PstI (1369)

```
1301 TGCATCGGGGGACCGCCCAACGCCTGCCTGGATCAGCTGCAAAGCTGGTTCACCATTGTTGCAGAGACCCTGCAGCAGATCCGTCAGCAGCTTAAAAAGC
 247▸ C  I  G  G  P  P  N  A  C  L  D  Q  L  Q  S  W  F  T  I  V  A  E  T  L  Q  Q  I  R  Q  Q  L  K  K
1401 TGGAGGAGTTGGAACAGAAATTCACCTATGAGCCCGACCCTATTACAAAAAACAAGCAGGTGTTGTCAGATCGAACCTTCCTCCTCTTCCAGCAGCTCAT
 280▸L  E  E  L  E  Q  K  F  T  Y  E  P  D  P  I  T  K  N  K  Q  V  L  S  D  R  T  F  L  L  F  Q  Q  L  I
```

SphI (1532) BbsI (1566)

```
1501 TCAGAGCTCCTTCGTGGTAGAACGACAGCCGTGCATGCCCACTCACCCGCAGAGGCCCCTGGTCTTGAAGACTGGGGTACAGTTCACTGTCAAGCTGAGA
 313▸  Q  S  S  F  V  V  E  R  Q  P  C  M  P  T  H  P  Q  R  P  L  V  L  K  T  G  V  Q  F  T  V  K  L  R
1601 CTGTTGGTGAAATTGCAAGAGCTGAACTATAACTTGAAAGTGAAAGTCTCATTTGACAAAGATGTGAACGAGAAAAACACAGTTAAAGGATTTCGGAAGT
 347▸ L  L  V  K  L  Q  E  L  N  Y  N  L  K  V  K  V  S  F  D  K  D  V  N  E  K  N  T  V  K  G  F  R  K
1701 TCAACATCTTGGGTACGCACACAAAAGTGATGAACATGGAAGAATCCACCAACGGAAGTCTGGCAGCTGAGTTCCGACACCTGCAACTGAAGGAACAGAA
 380▸F  N  I  L  G  T  H  T  K  V  M  N  M  E  E  S  T  N  G  S  L  A  A  E  F  R  H  L  Q  L  K  E  Q  K
1801 AAACGCTGGGAACAGAACTAATGAGGGGCCTCTCATTGTCACCGAAGAACTTCACTCTCTTAGCTTTGAAACCCAGTTGTGCCAGCCAGGCTTGGTGATT
 413▸  N  A  G  N  R  T  N  E  G  P  L  I  V  T  E  E  L  H  S  L  S  F  E  T  Q  L  C  Q  P  G  L  V  I
1901 GACCTGGAGACCACCTCTCTTCCTGTCGTGGTGATCTCCAACGTCAGCCAGCTCCCCAGTGGCTGGGCGTCTATCCTGTGGTACAACATGCTGGTGACAG
 447▸ D  L  E  T  T  S  L  P  V  V  V  I  S  N  V  S  Q  L  P  S  G  W  A  S  I  L  W  Y  N  M  L  V  T
2001 AGCCCAGGAATCTCTCCTTCTTCCTGAACCCCCCGTGCGCGTGGTGGTCCCAGCTCTCAGAGGTGTTGAGTTGGCAGTTTTCATCAGTCACCAAGAGAGG
 480▸E  P  R  N  L  S  F  F  L  N  P  P  C  A  W  W  S  Q  L  S  E  V  L  S  W  Q  F  S  S  V  T  K  R  G
```

SphI (2120) Bsp120I (2142) NcoI (2173)

```
2101 TCTGAACGCAGACCAGCTGAGCATGCTGGGAGAGAAGCTGCTGGGCCCTAATGCTGGCCCTGATGGTCTTATTCCATGGACAAGGTTTTGTAAGGAAAAT
 513▸  L  N  A  D  Q  L  S  M  L  G  E  K  L  L  G  P  N  A  G  P  D  G  L  I  P  W  T  R  F  C  K  E  N
2201 ATTAATGATAAAAATTTCTCCTTCTGGCCTTGGATTGACACCATCCTAGAGCTCATTAAGAAGCACCTGCTGTGCCTCTGGAATGATGGGTGCATTATGG
 547▸ I  N  D  K  N  F  S  F  W  P  W  I  D  T  I  L  E  L  I  K  K  H  L  L  C  L  W  N  D  G  C  I  M
```

XmaI (2381)

```
2301 GCTTCATCAGCAAGGAGCGAGAACGCGCTCTGCTCAAGGACCAGCAGCCAGGGACGTTCCTGCTTAGATTCAGTGAGAGCTCCCGGGAAGGGGCCATCAC
 580▸G  F  I  S  K  E  R  E  R  A  L  L  K  D  Q  Q  P  G  T  F  L  L  R  F  S  E  S  S  R  E  G  A  I  T
2401 ATTCACATGGGTGGAACGGTCCCAGAACGGAGGTGAACCTGACTTCCATGCCGTGGAGCCCTACACGAAAAAAGAACTTTCAGCTGTTACTTTCCCAGAT
 613▸  F  T  W  V  E  R  S  Q  N  G  G  E  P  D  F  H  A  V  E  P  Y  T  K  K  E  L  S  A  V  T  F  P  D
2501 ATTATTCGCAACTACAAAGTCATGGCTGCCGAGAACATACCAGAGAATCCCCTGAAGTATCTGTACCCCAATATTGACAAAGACCACGCCTTTGGGAAGT
 647▸ I  I  R  N  Y  K  V  M  A  A  E  N  I  P  E  N  P  L  K  Y  L  Y  P  N  I  D  K  D  H  A  F  G  K
2601 ATTATTCCAGACCAAAGGAAGCACCAGAACCGATGGAGCTTGACGACCCTAAGCGAACTGGATACATCAAGACTGAGTTGATTTCTGTGTCTGAAGTCCA
 680▸Y  Y  S  R  P  K  E  A  P  E  P  M  E  L  D  D  P  K  R  T  G  Y  I  K  T  E  L  I  S  V  S  E  V  H
```

XbaI (2704) Bsp120I (2775)

```
2701 CCCTTCTAGACTTCAGACCACAGACAACCTGCTTCCCATGTCTCCAGAGGAGTTTGATGAGATGTCCCGGATAGTGGGCCCCGAATTTGACAGTATGATG
 713▸  P  S  R  L  Q  T  T  D  N  L  L  P  M  S  P  E  E  F  D  E  M  S  R  I  V  G  P  E  F  D  S  M  M
```

MscI (2841)
NheI (2835)

```
2801 AGCACAGTATAAACACGAATTTCTCTCTGGCGACAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTG
 747▸ S  T  V  •
```

HpaI (2973) MfeI (2984)

2901 AAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCATTTT

EcoRI (3069)

3001 ATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAAACTTTA

3101 ACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCA

SapI (3251)

3201 CCTTCTTTCATGGAGTTTAAGATATAGTGTATTTTCCCAAGGTTTGAACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCCTT

SwaI (3322)

3301 TTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATC

3401 CCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGG

141 • N R T Y K L

3501 GGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGC

133 P I L E E I T T K V L K G N M E I L V F C D P A Y D S I L E R C M G

3601 CACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCCGTTGCTCACAGC

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

StuI (3747)

3701 AGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCCTGATGGCC

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

BbsI (3893)

3801 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

3901 TGGTGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAAACAGCGTGGATGGCGTCTCCAGCTTATCTGAC

0

4001 GGTTCACTAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTC

SpeI (4110)

4101 CCGTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCCATTGATGTAC

SnaBI (4238)

4201 TGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTACTGGGCATAATGCCAGG

NdeI (4343)

4301 CGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCA

4401 TTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCA

PacI (4529)

PstI (4522)

SdaI (4521) BspLU11I (4539)

4501 TTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTT

4601 TTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCC

4701 CCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCT

ApaLI (4853)

4801 CACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAA

4901 CTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACA

5001 GAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTA

5101 GCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTT

EagI (5289)

PacI (5269) SwaI (5278) **NotI (5288)**

5201 GATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATA

5301 AAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAAACTAGC

5401 AAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA