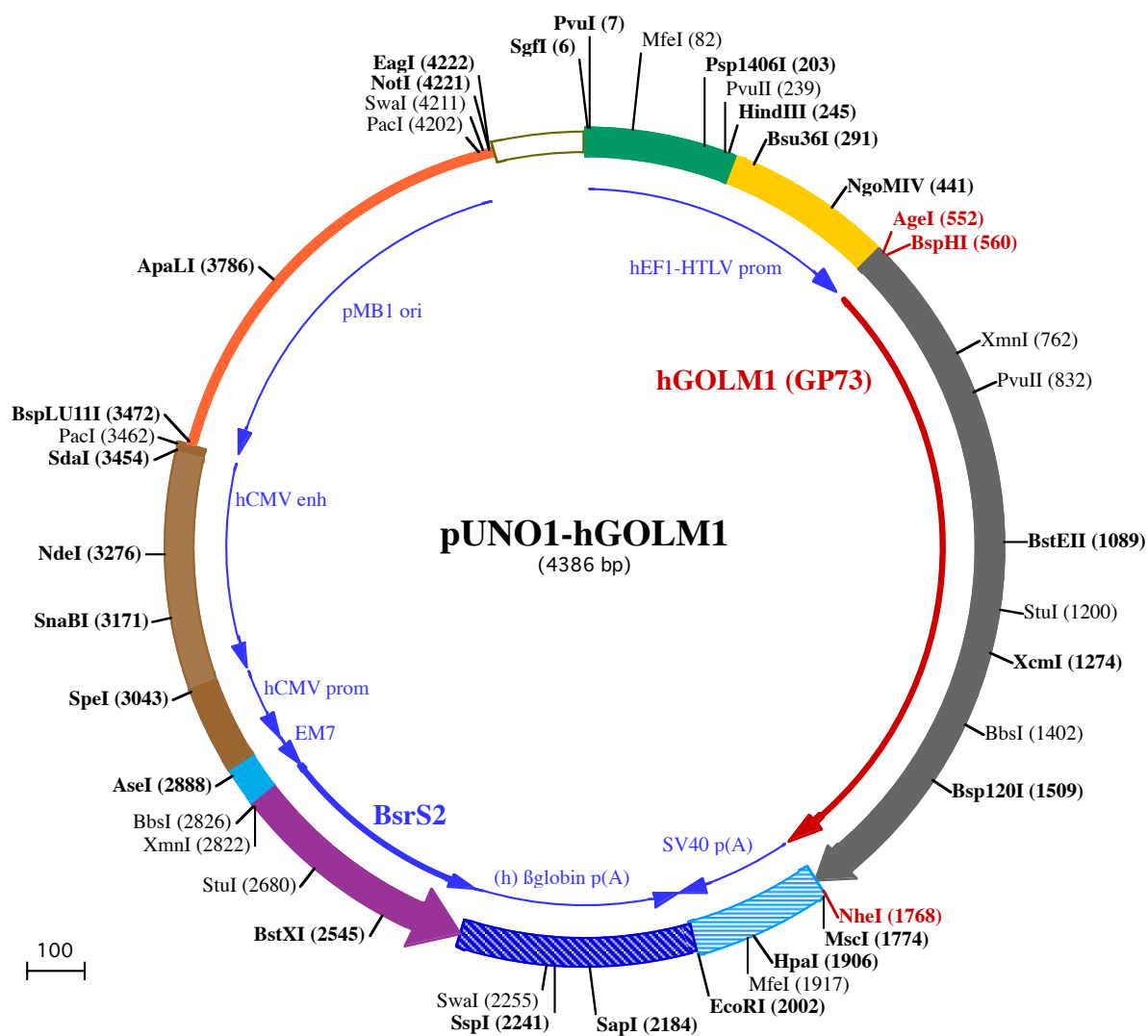




PvuI (7)
SgfI (6)
MfeI (82)

1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
 101 GAGAAAGTGGCGCGGGGTAAACTGGGAAAGTATGTCGTGTACTGGCTCCGCCTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

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

201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCGCCCTACCTGAGGCC
 301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCCTCCCGCCTGTGGTGCTCTCTGAAGTGCCTCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGCCTGACCCTGCTTGCTCAACTCTACGCTTTGTTTCGTTT

AgeI (552) **BspHI (560)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCTACCTGAGATCACCGGTCATCATGATGGGCTTGGGAAACGGGCGTCGCAGCATGAAGTC
 601 GCCGCCCCTCGTCTGGCCGCCCTGGTGGCCTGCATCATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGAGCGTGGACCTCCAGACACGGATC
 13▶ P P L V L A A L V A C I I V L G F N Y W I A S S R S V D L Q T R I

XmnI (762)

701 ATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGCGCGTGGAGCTGAAGAAGAACGAGTTCAGGGAGAGCTGGAGAAGCAGCGGGAGC
 47▶ M E L E G R V R R A A A E R G A V E L K K N E F Q G E L E K Q R E

PvuII (832)

801 AGCTTGACAAATCCAGTCCAGCCACAACCTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGCGGTTTTGGTGAATAACATCACCACAGG
 80▶ Q L D K I Q S S H N F Q L E S V N K L Y Q D E K A V L V N N I T T G
 901 TGAGAGGCTCATCCGAGTGTGCAAGACCAGTTAAAGACCCTGCAGAGGAATTACGGCAGGCTGCAGCAGGATGTCCTCCAGTTTCAAGAACCAGACC
 113▶ E R L I R V L Q D Q L K T L Q R N Y G R L Q Q D V L Q F Q K N Q T

BstEII (1089)

1001 AACCTGGAGAGGAAGTTCTCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTGTGAGGAGCGAATAGAAGAGGTACCAAAA
 147▶ N L E R K F S Y D L S Q C I N Q M K E V K E Q C E E R I E E V T K
 1101 AGGGGAATGAAGCTGTAGCTTCCAGAGACCTGAGTGAAAACAACGACCAGAGACAGCAGTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAGGCAGC
 180▶ K G N E A V A S R D L S E N N D Q R Q Q L Q A L S E P Q P R L Q A A

StuI (1200)
XcmI (1274)

1201 AGGCCTGCCACACAGAGGTGCCACAAGGGAAGGGAACGTGCTTGGTAACAGCAAGTCCCAGACACCAGCCCCAGTTCGGAAGTGGTTTTGGATTCA
 213▶ G L P H T E V P Q G K G N V L G N S K S Q T P A P S S E V V L D S
 1301 AAGAGACAAGTTGAGAAAGAGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGACAGGCTGCCGAGGAGCCAGGCCGGGAGCAGGTGG
 247▶ K R Q V E K E E T N E I Q V V N E E P Q R D R L P Q E P G R E Q V

BbsI (1402)

1401 TGAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGGAGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTCACTGAGCCAGGAAAATCC
 280▶ V E D R P V G G R G F G G A G E L G Q T P Q V Q A A L S V S Q E N P

Bsp120I (1509)

1501 AGAGATGGAGGGCCCTGAGCGAGACCAGCTTGTATCCCCGACGAGGAGGAGGAGCAGGAAGCTGCCGGGGAAGGGAGAAACCAGCAGAAACTGAGA
 313▶ E M E G P E R D Q L V I P D G Q E E E Q E A G E G R N Q Q K L R
 1601 GGAGAAGATGACTACAACATGGATGAAAATGAAGCAGAACTCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATGTTTTAATG
 347▶ G E D D Y N M D E N E A E S E T D K Q A A L A G N D R N I D V F N

MscI (1774)

NheI (1768)

1701 TTGAAGATCAGAAAAGAGACACCATAAATTTACTTGATCAGCGTGAAAAGCGGAATCATACACTCTGAGCTAGCTGGCCAGACATGATAAGATACATTGA
 380▶ V E D Q K R D T I N L L D Q R E K R N H T L •
 1801 TGAGTTTGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAAT

HpaI (1906)
MfeI (1917)

1901 AAACAAGTTAAACAACAACAAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTA

EcoRI (2002)

2001 TGAATCTAAAAATACAGCATAGCAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGCT

SapI (2184)

2101 GTTGCCAAATGTGCATTAGCTGTTTGACGCTCACCTTCTTTTATGAGTAAAGATATAGTGATTTTCCCAAGGTTTGAAGTACGCTTTCATTCTTTA

SspI (2241)
SwaI (2255)

2201 TGTTTTAAATGCACTGACCTCCACATTCCTTTTATGATAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGC
 2301 AGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTATGAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCG
 2401 AGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGTTGCCATTCTCTCAATGAGCAGCAAGCAGTCAG
 141▶ • N R T Y K L P I L E E I T T K V L K G N M E I L V F C D P

BstXI (2545)

2501 GAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAAT
111 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 Y P H R V A V I

StuI (2680)

2601 GGTGTCAAAGTCCTTCTGCCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCA
78 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 Y A E I H V A

2701 GAGATGATCTCCCAAGTCTTGGTCTGATGGCCGCCCGACATGGTGTCTGTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCT
44 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 A V E V L E

BbsI (2826)

XmnI (2822)

2801 CCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAA
11 L D Q Q S I N F T K M

AseI (2888)

2901 AACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTGCGTCAA

SpeI (3043)

3001 TGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGT

SnaBI (3171)

3101 GAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGT

NdeI (3276)

3201 CCCATAAGGTCATGTACTGGGCATAATGCCAGCGGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGC

3301 CAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGG

PacI (3462)

SdaI (3454)

BspLU11I (3472)

3401 CGGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGC

3501 CAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAAC

3601 CCGACAGGACTATAAAGATACCAGGCGTTTCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCGACCTGCCGTTACCGGATACCTGTCCGCTTTT

ApaLI (3786)

3701 TCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCC

3801 CGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGG

3901 ATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGC

4001 TGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGGAAGCAGCAGATTAC

4101 GCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACTCACGTAAAGGGATTTTGGTCATGGCT

EagI (4222)

PacI (4202) **SwaI (4211)** **NotI (4221)**

4201 AGTTAATTAACATTTAAATCAGCGGCCGAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCT

4301 CCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCAAGTGCAAGTGCCAGAGTCCAGAACATTTCTCTATCGAA