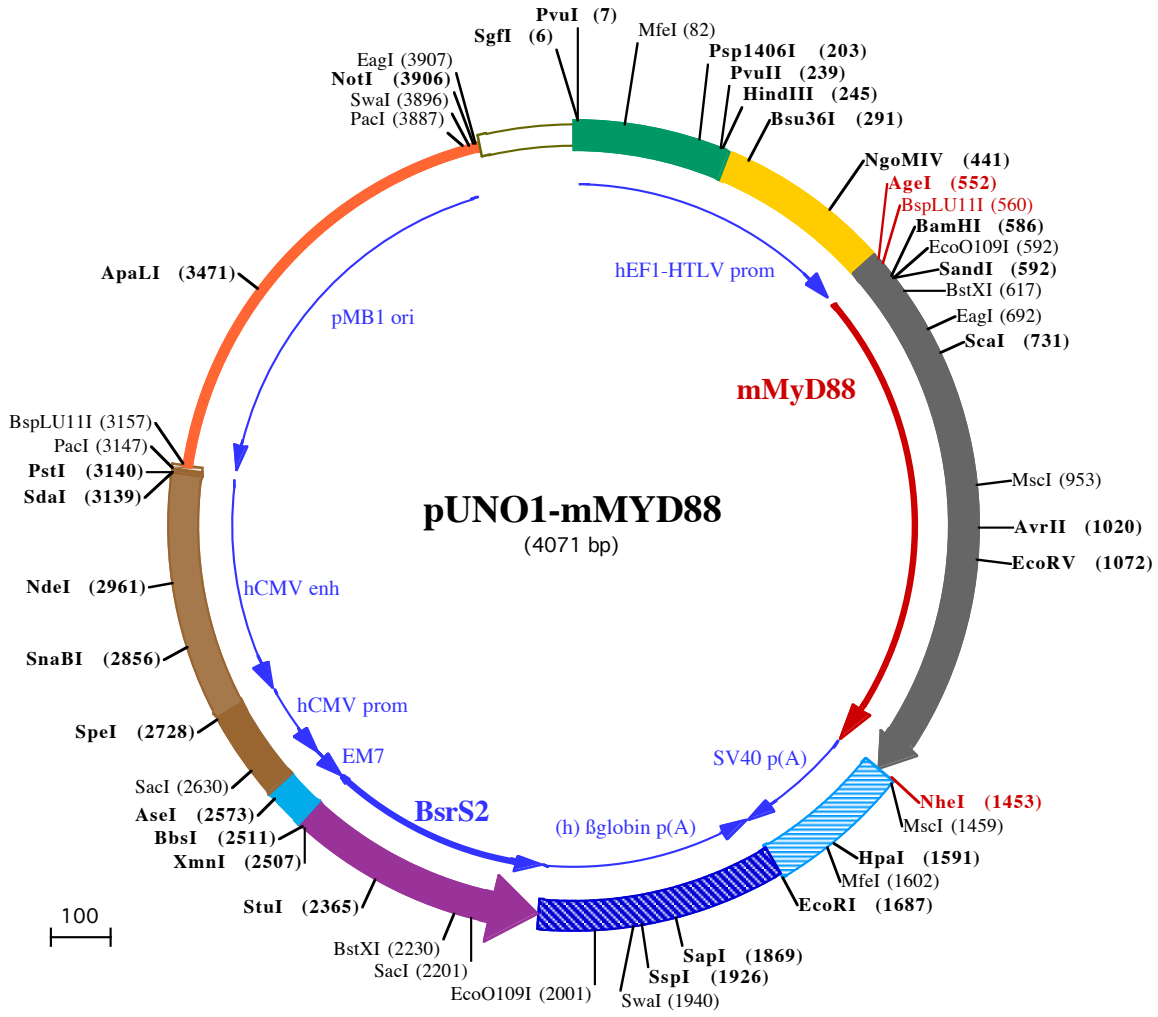
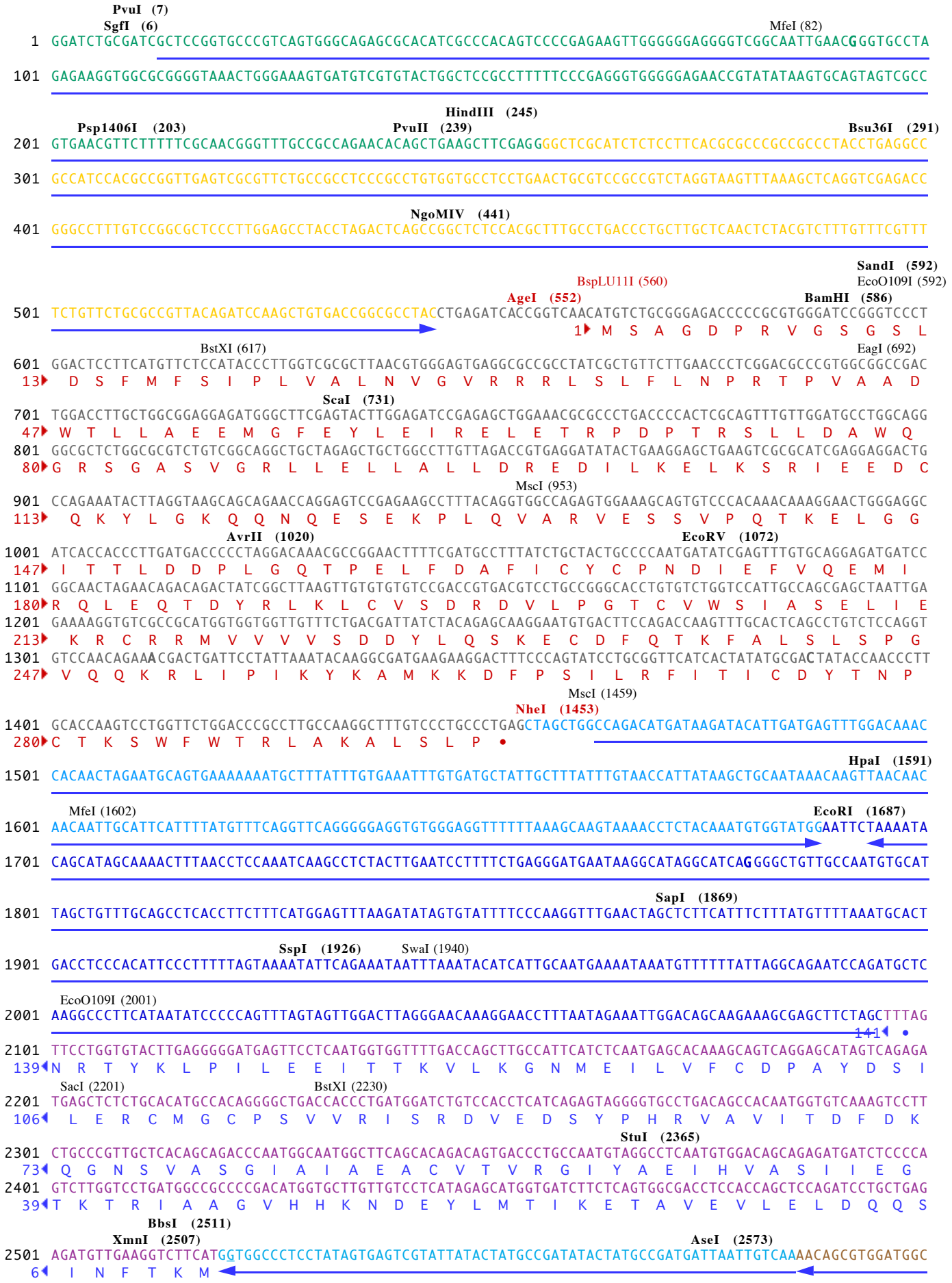
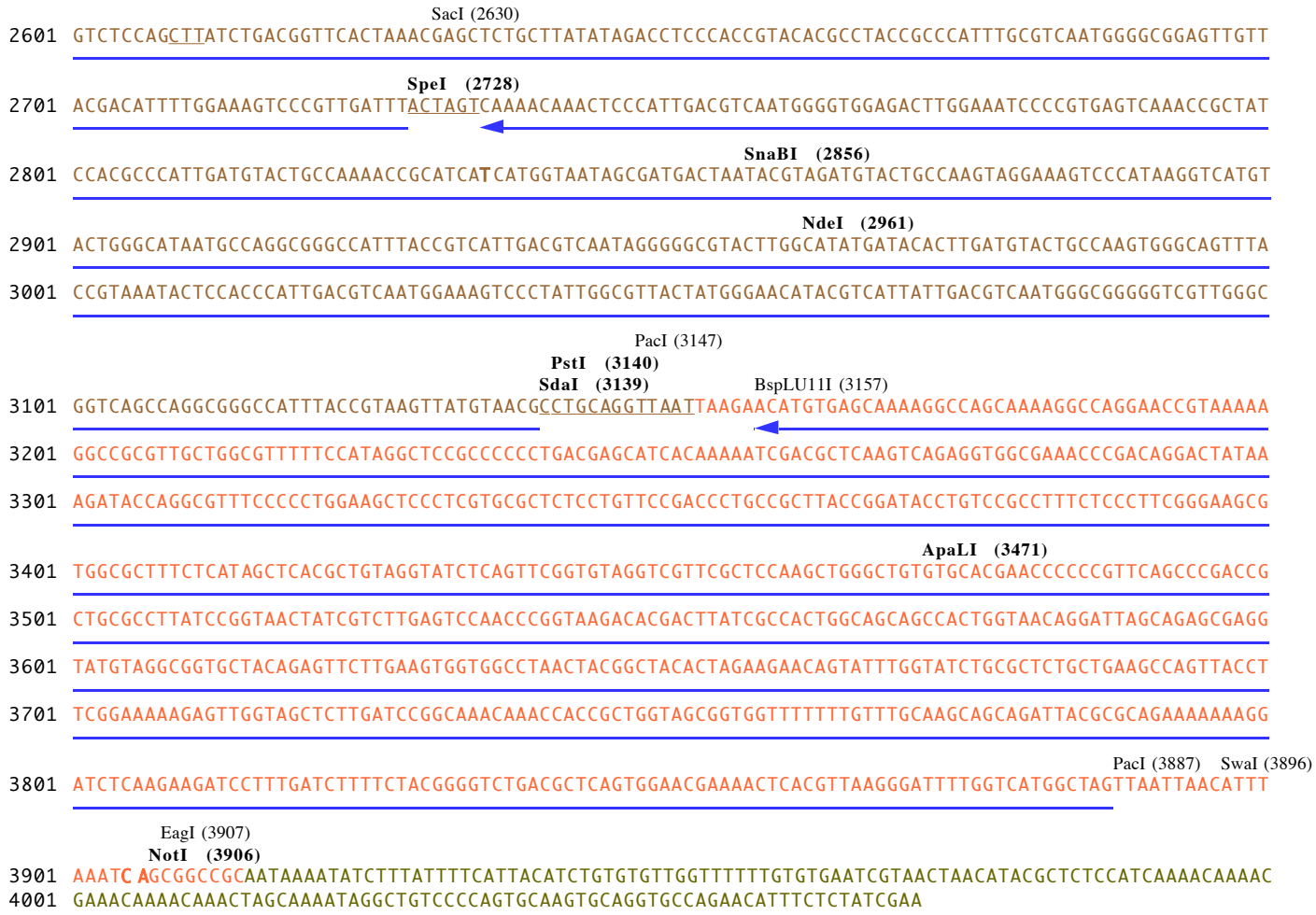

pUNO1-mMYD88
(4071 bp)
mMyD88
BsrS2
hEF1-HTLV prom
pMB1 ori
hCMV enh
hCMV prom
EM7
SV40 p(A)
(h) ßglobin p(A)
PvuI (7)
SgfI (6)
MfeI (82)
Psp1406I (203)
PvuII (239)
HindIII (245)
Bsu36I (291)
NgoMIV (441)
AgeI (552)
BspLU11I (560)
BamHI (586)
EcoO109I (592)
SandI (592)
BstXI (617)
EagI (692)
ScaI (731)
MscI (953)
AvrII (1020)
EcoRV (1072)
NheI (1453)
MscI (1459)
HpaI (1591)
MfeI (1602)
EcoRI (1687)
SapI (1869)
SspI (1926)
SwaI (1940)
EcoO109I (2001)
SacI (2201)
BstXI (2230)
StuI (2365)
XmnI (2507)
BbsI (2511)
AseI (2573)
SacI (2630)
SpeI (2728)
SnaBI (2856)
NdeI (2961)
SdaI (3139)
PstI (3140)
PacI (3147)
BspLU11I (3157)
ApaLI (3471)
PacI (3887)
SwaI (3896)
NotI (3906)
EagI (3907)
100


PvuI (7)
SgfI (6)
MfeI (82)
HindIII (245)
Psp1406I (203)
PvuII (239)
Bsu36I (291)
NgoMIV (441)
SandI (592)
EcoO109I (592)
BspLU11I (560)
AgeI (552)
BamHI (586)
BstXI (617)
EagI (692)
ScaI (731)
MscI (953)
AvrII (1020)
EcoRV (1072)
MscI (1459)
NheI (1453)
HpaI (1591)
MfeI (1602)
EcoRI (1687)
SapI (1869)
SspI (1926)
SwaI (1940)
EcoO109I (2001)
SacI (2201)
BstXI (2230)
StuI (2365)
BbsI (2511)
XmnI (2507)
AseI (2573)


SacI (2630)
2601 GTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCCATTTGCGTCAATGGGGCGGAGTTGTT
SpeI (2728)
2701 ACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTAT
SnaBI (2856)
2801 CCACGCCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCATGT
NdeI (2961)
2901 ACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTA
3001 CCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGGTCGTTGGGC
PacI (3147)
PstI (3140)
SdaI (3139)
BspLU11I (3157)
3101 GGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAA
3201 GGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAA
3301 AGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCG
ApaLI (3471)
3401 TGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCG
3501 CTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGG
3601 TATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCT
3701 TCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGG
PacI (3887)
SwaI (3896)
3801 ATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTT
EagI (3907)
NotI (3906)
3901 AAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAAC
4001 GAAACAAAACAAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA