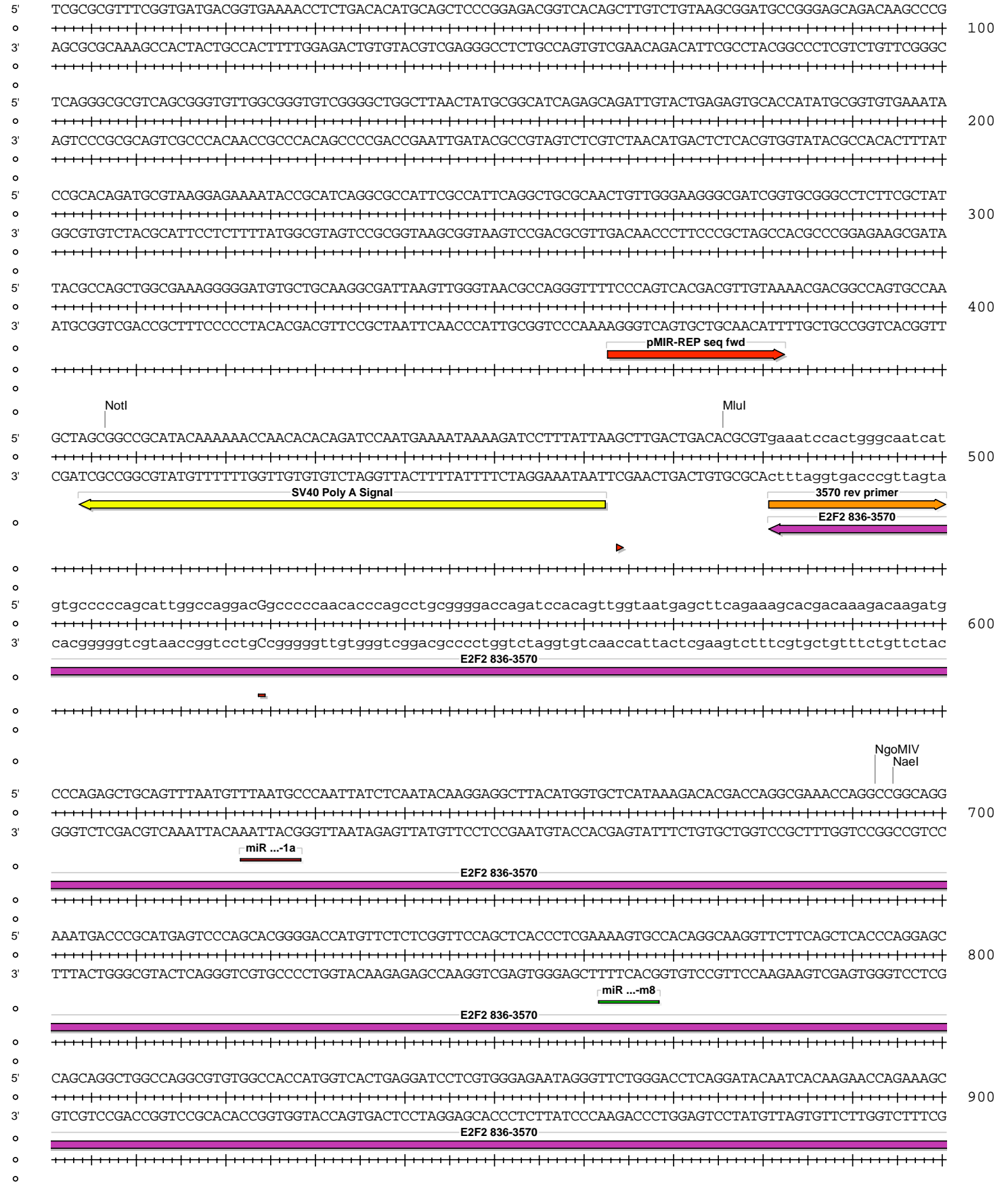


Absent Sites	0	AarI,Abst,AfeI,AfIII,AleI,AscI,AsiSI,BaeI,BaeI',BarI,BarI',BmgBI,FseI,FspAI,MauBI,MreI,NruI,PmeI,PmlI,SgrDI,SpeI,SrfI,Swal
Acc65I	1	5152 (8822)
AgeI	1	8455 (8822)
AhdI	1	6509 (8822)
AjuI	1	3998 (8822)
AjuI'	1	4030 (8822)
Alol	1	4911 (8822)
Alol'	1	4879 (8822)
Arsl	1	3699 (8822)
Arsl'	1	3731 (8822)
AvrII	1	8506 (8822)
BbvCI	1	1587 (8822)
BclI	1	2705 (8822)
BglII	1	3217 (8822)
BsaBI	1	7671 (8822)
BsmI	1	7584 (8822)
BsrGI	1	4388 (8822)
BssHII	1	7939 (8822)
BstZ17I	1	2846 (8822)
BtgZI	1	5137 (8822)
ClaI	1	3515 (8822)
CspCI	1	5101 (8822)
CspCI'	1	5066 (8822)
EcoICRI	1	2914 (8822)
EcoRV	1	3544 (8822)
HpaI	1	7570 (8822)
KpnI	1	5156 (8822)
MluI	1	476 (8822)
NaeI	1	695 (8822)
NgoMIV	1	693 (8822)
NotI	1	407 (8822)
PacI	1	3560 (8822)
PciI	1	5616 (8822)
PfIMI	1	2076 (8822)
PspXI	1	3228 (8822)
RsrII	1	8279 (8822)
SacI	1	2916 (8822)
SacII	1	8186 (8822)
Sall	1	8286 (8822)
SanDI	1	2180 (8822)
Scal	1	6989 (8822)
SgrAI	1	3450 (8822)
SnaBI	1	5135 (8822)
SspI	1	7313 (8822)
Tth111I	1	8355 (8822)
XhoI	1	3228 (8822)

pMIR-REP-dCMV E2F2 836-3570 (mod Hind-Mlu)



pMIR-REP-dCMV E2F2 836-3570 (mod Hind-Mlu)

5' TGCTTCCAAACAACCCAGAGGTTTTCACTTCACATGCGCTAAGCCACACAACACCTGGATGCTGGGGCACCCAAACCTTTCCCTAAAACCTCTGAACA
 1000
 3' ACGAAGGTTTGTGGGGTCTTCCAAAAGTGAAGTGTACGCGATTCCGGTGTGTGTGGACCTACGACCCCGTGGGTTTGGGAAAGGGATTTTGTAGACTTGT
 E2F2 836-3570

5' CTGCAGAATGGAGGTTGAGAACAACCTGGGGAGGGAGAACAAGTCAAGCCATCCTAAAGCCAGTTTTTCAAGCTTGACCACCTCCCTCTCTCTCCCTGA
 1100
 3' GACGCTTACCTCCAACCTCTTGTGAACCCCTCCCTCTTGTTCAGTCTTGGTAGGATTTCCGGTCAAAAAGTTTCAAGCTGGTGGAGGGAGAAGGAGGGACT
 E2F2 836-3570

5' AGGCACACCAGCCGATCCCATTAAGTGTGGAAAAGGGACACCCCTCTGGTCTATTCTAACACCTTTAATGGGAAAGGAGTTAGGAGCATGTCCCTGGCTTCA
 1200
 3' TCCGTGTGGTCCGCTAGGGTAATGACACCTTTTCCCTGTGGGAGACCAGATAAGATTGTGGAAATTACCCTTTCCCTCAATCCTCGTACAGGGACCGAAGT
 E2F2 836-3570

5' AGAAATCTCTGAATCTCCAACCTACTGGATGATTTCCCTGGAGCCCAAGCTTTAGAAAGTCCCTGGGGACACGAGTGATTTTTTGGGGGGCTGTGGT
 1300
 3' TCTTTAGAGACTTAGAGGTTGAGATGACCTACTAAAGGACCTCGGGGTTGAAATCTTCAGGGACCCCTGTGCTCACTAAAAAATCCCCCGACGACCA
 E2F2 836-3570

5' GGGGCTGGGAAGTTTCTGGCAGAAATATTTACCTCAGAAAGACACTGGCTTTTCTTACCCTCGTTTTAAAGTCTACCTGGTCCCTAAAGAAAATAC
 1400
 3' CCCCAGCCCTTCAAAGGACCGTCTTTAATAAATGGAGTCTTCTGTGACCGAAAAGAGAATGGGAGCAAATTTAGATGGACCAGGGATTCTTTTATG
 E2F2 836-3570

5' CACTCAGGCTGGGCTGGTGGCTCGTGCCTGTCTCAACACTTTGGGAGGCCGAGGTGGTGGATCACTTGAGGTGAGGTTCAAGACCAGCCTGACT
 1500
 3' GTGAGTCCGACCCGGACCCGAGCAGCAGTAGAGTTGTGAAACCCCTCCGGCTCCACCACCTAGTGAACCTCAGTCTCAAGTTCTGGTCCGACTGA
 E2F2 836-3570

5' AACATGGCAAACCCCGTCTCGACCAAAAATACAAAATTAGCCGGGCGTGGTGGTGCATGTCTATAGTCCCAGCTACTCTGGAGGCTGAGGAGAGAGAAT
 1600
 3' TTGTACCGTTTGGGGCAGAGCTGGTTTTATGTTTAAATCGGCCCGCACCACCACGTACAGATATCAGGGTGCATGAGACCTCCGACTCCGTCTCTTA
 E2F2 836-3570

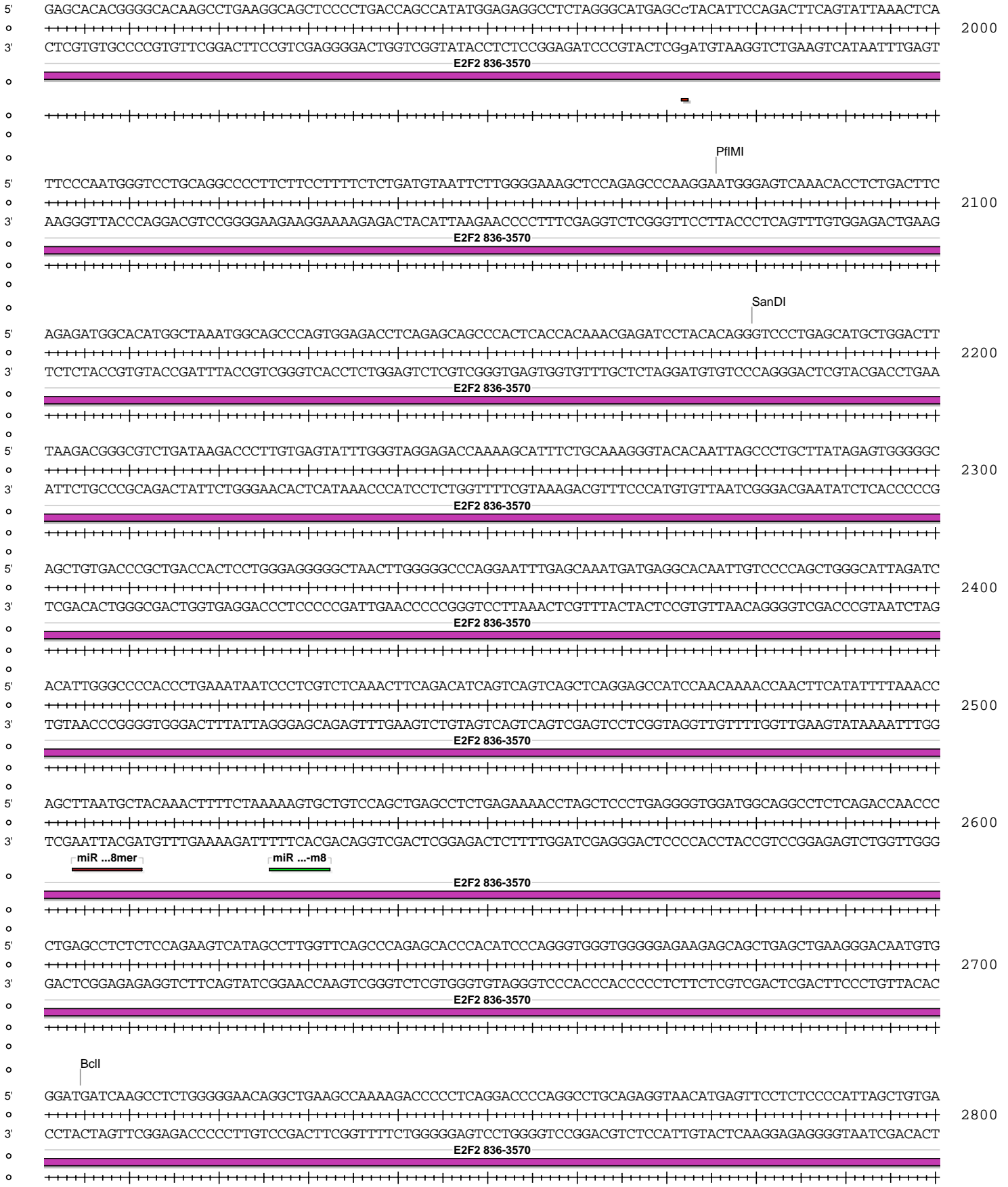
5' CGCTTGAACCTGGGAGGCAGAGTTGCAGTGAGCCGAGATCAGGCCACTGCACTCCAGCCTGGGCAACAGAGtGAGACTCCATCTCAAAAAAAAAAAAAA
 1700
 3' GCGAACTTGGACCCTCCGTCTCAACGTCACTCGGCTCTAGTCCGGTGACGTGAGGTCCGACCCGTTGTCTCaCTCTGAGGTAGAGTTTTTTTTTTTTT
 E2F2 836-3570

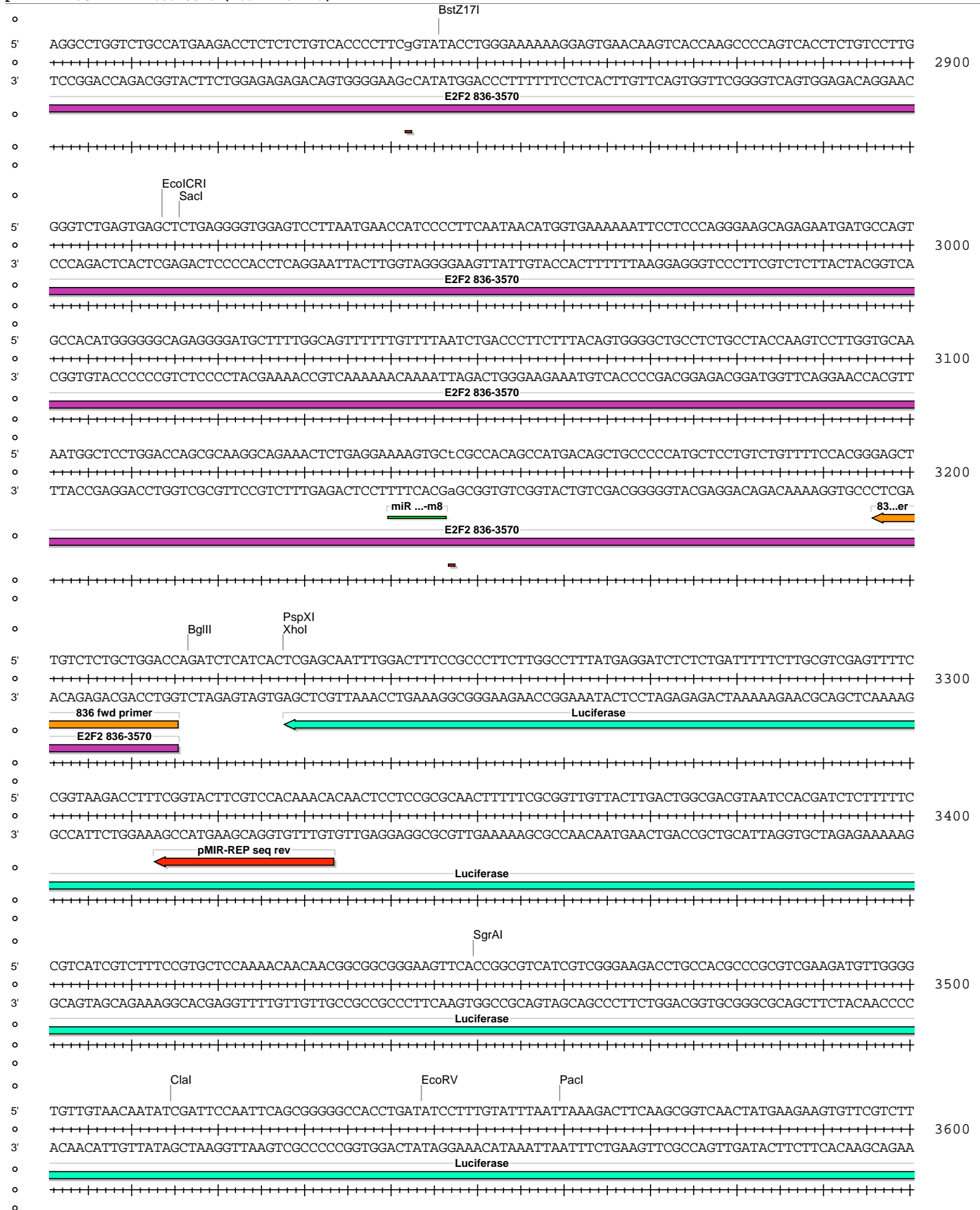
5' AGAAGAAAAAAGAAAAGAAAATACCACTCAAAATGTGTCTGAAGCACTCTGTGGAAGTCGGGAGGCTTCAAGTGTCACTGGCAAGACGGGGCATGAG
 1800
 3' TCTTCTTTTTTCTTTCTTTTATGGTGGTGTGTTTACACAGGACTTCGTGAGACACCTTCAGCCCTCCGAAGTTCACAGTGACCGTTCTGCCCCGTACTC
 E2F2 836-3570

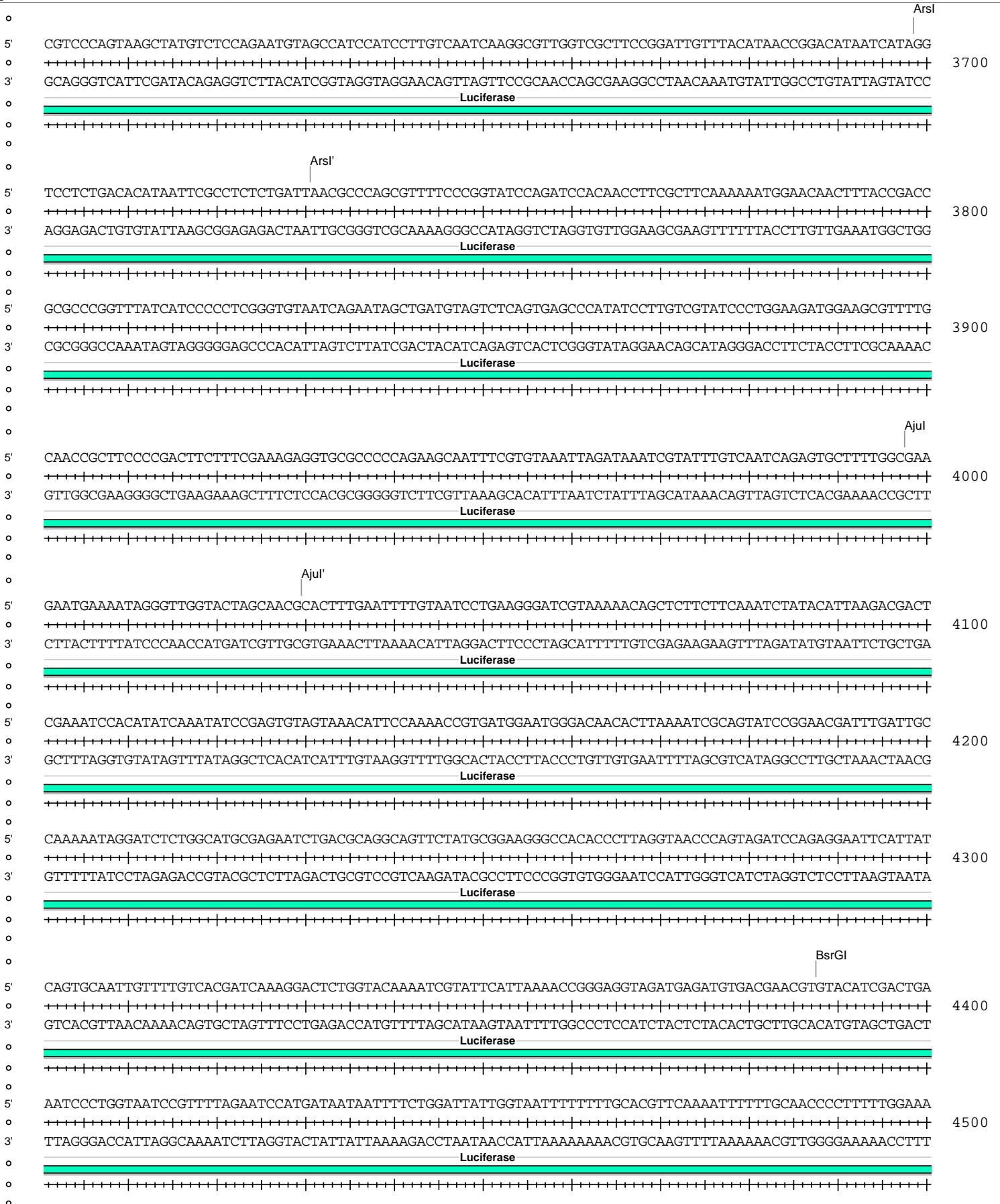
5' CTTGTGTCTGCACTGAATCTGAGGCTTAGCCTGGGAGGTTAGCCCTTTGGCCAGGCAAGGTGTGAAAGGGACAGTAGAGGGGACAGAGGCAGCTGCT
 1900
 3' GAACACAGGACGTGACTTAGACTCCGAATCGGACCCCTCCAGATCGGGGAACCGGTTCCACACTTCCCTGTCTCCCCCTGTCTCCGTCCGACGA
 E2F2 836-3570

BbvCI

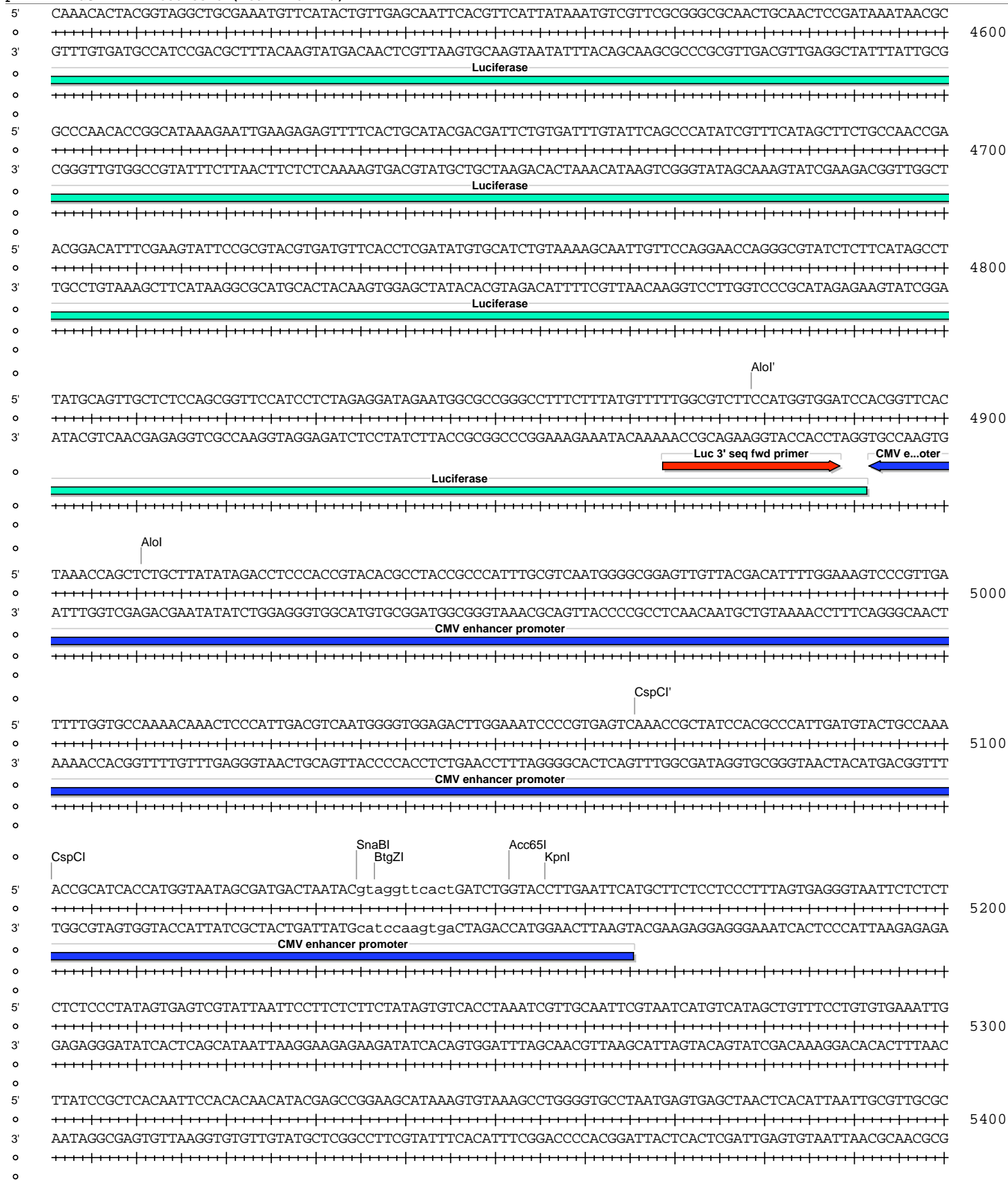
pMIR-REP-dCMV E2F2 836-3570 (mod Hind-Mlu)



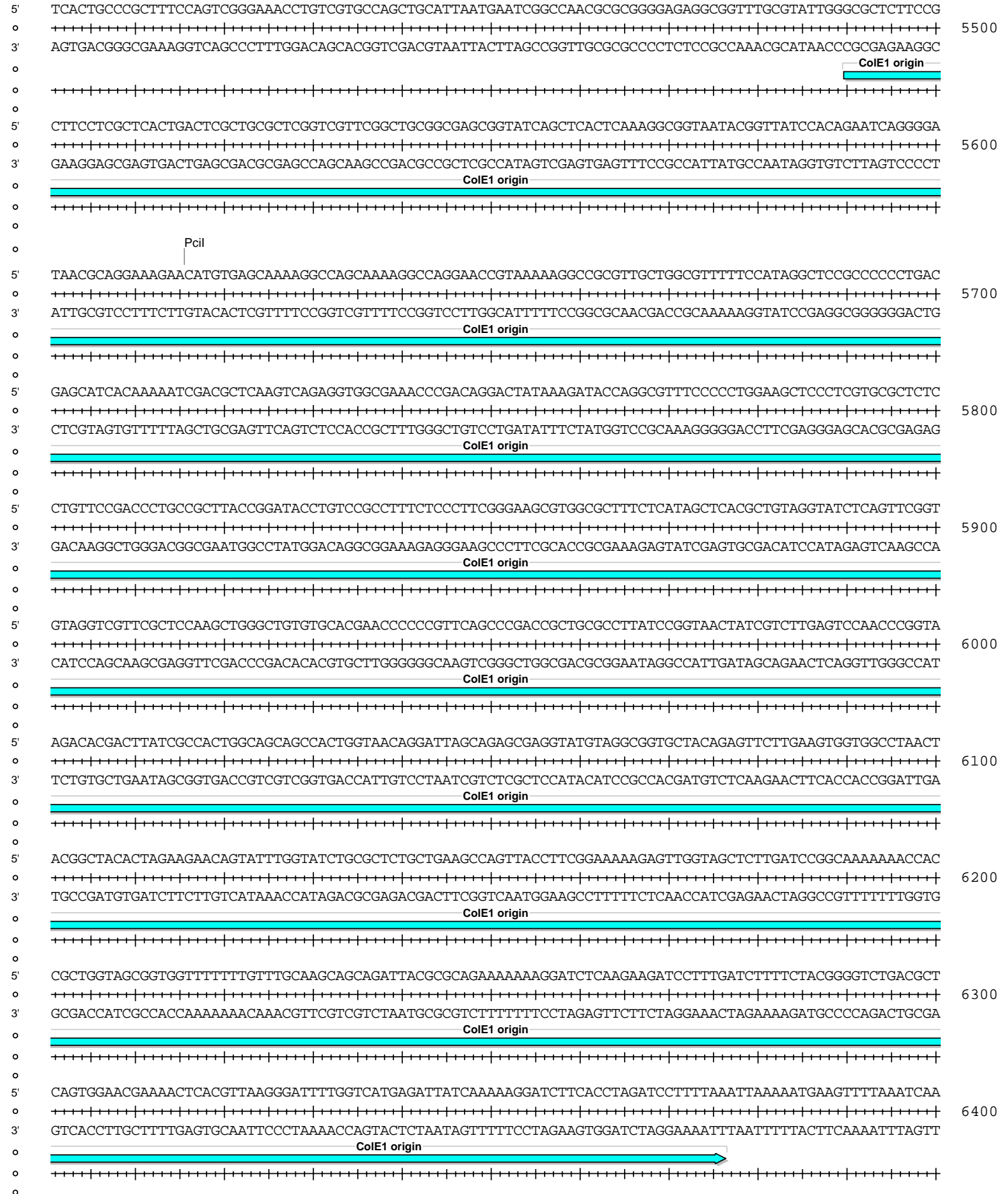




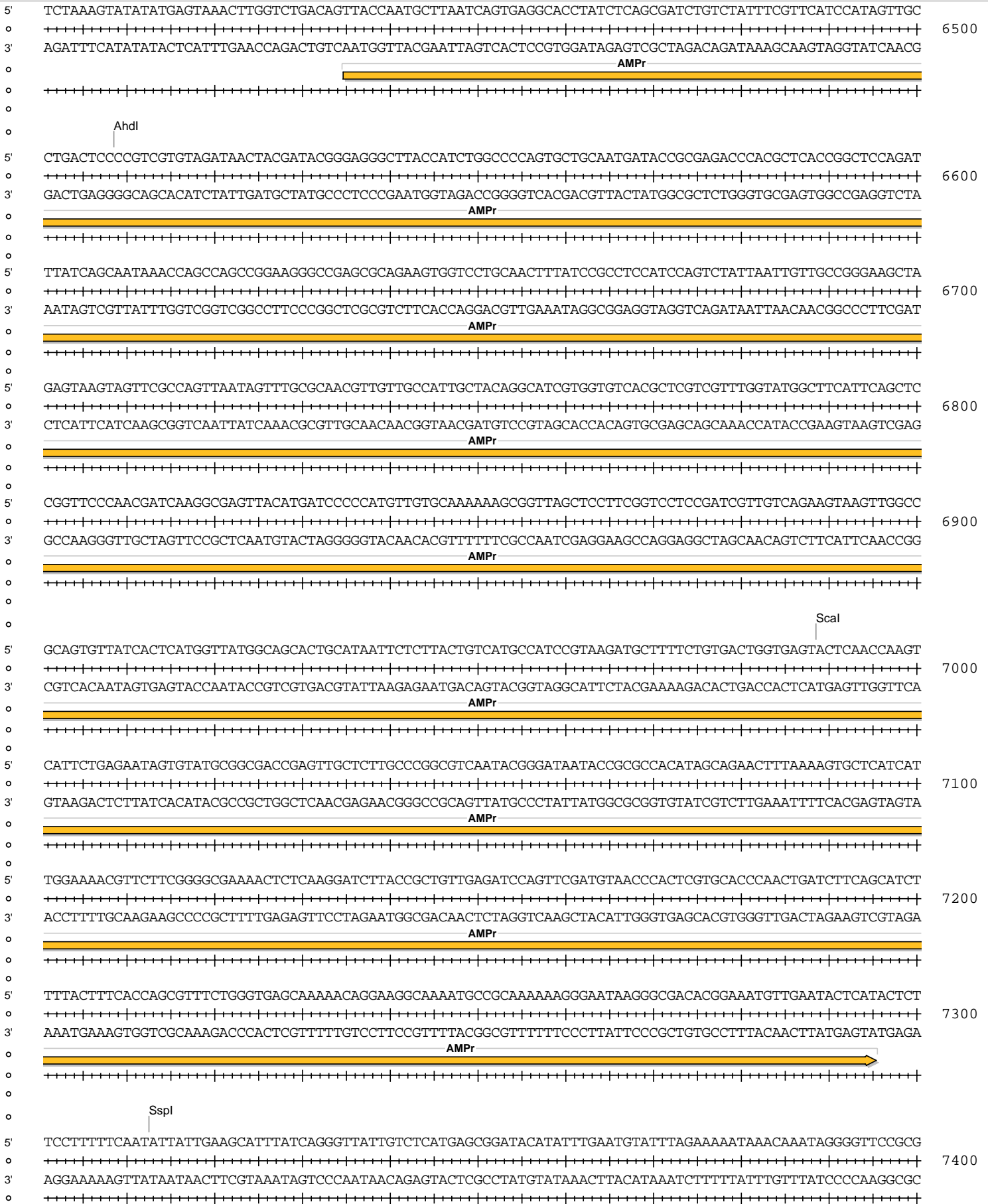
pMIR-REP-dCMV E2F2 836-3570 (mod Hind-Mlu)



pMIR-REP-dCMV E2F2 836-3570 (mod Hind-Mlu)



pMIR-REP-dCMV E2F2 836-3570 (mod Hind-Mlu)



pMIR-REP-dCMV E2F2 836-3570 (mod Hind-Mlu)

