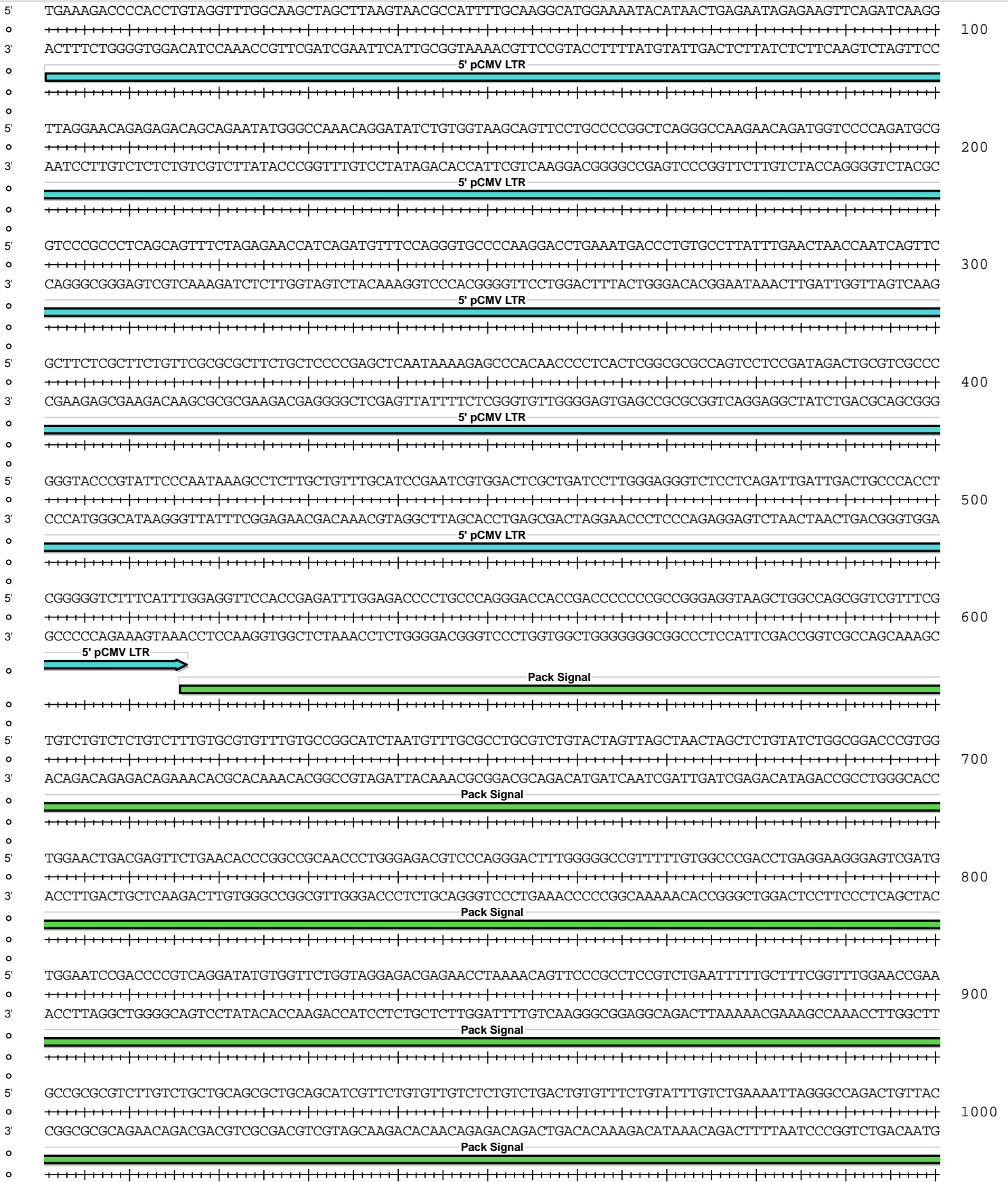


## pMSCV-Puro-GFP miR-146a

Absent Sites	0	AarI, AbsI, Accl, AjuI, AjuI', AlfI, AlfI', ApaI, AsiSI, AvrII, BamHI, BarI, BarI', BclI, BsaAI, BstBI, BstXI, BstZ17I, CspCI, CspCI', FseI, FspAI, HincII, HpaI, MauBI, MfeI, MluI, MreI, NruI, PacI, PfiMI, PmeI, PmlI, PshAI, PspOMI, PstI, PstI', Sall, SanDI, SbfI, SfiI, SgrDI, SnaBI, SrfI, SwaI, XcmI
AfIII	1	4887
ArsI	1	1732
ArsI'	1	1700
BbsI	1	2497
BglIII	1	1411
BsaBI	1	2336
BsiWI	1	3220
BsmI	1	3075
BspMI	1	3153
BtgZI	1	1559
Clal	1	3818
DrallI	1	3735
HindIII	1	3155
NdeI	1	6951
NotI	1	2158
NsiI	1	3817
PciI	1	4887
PsiI	1	2192
PspXI	1	2617
RsrII	1	3280
SacII	1	3378
Scal	1	6260
SgrAI	1	7323
XhoI	1	2617

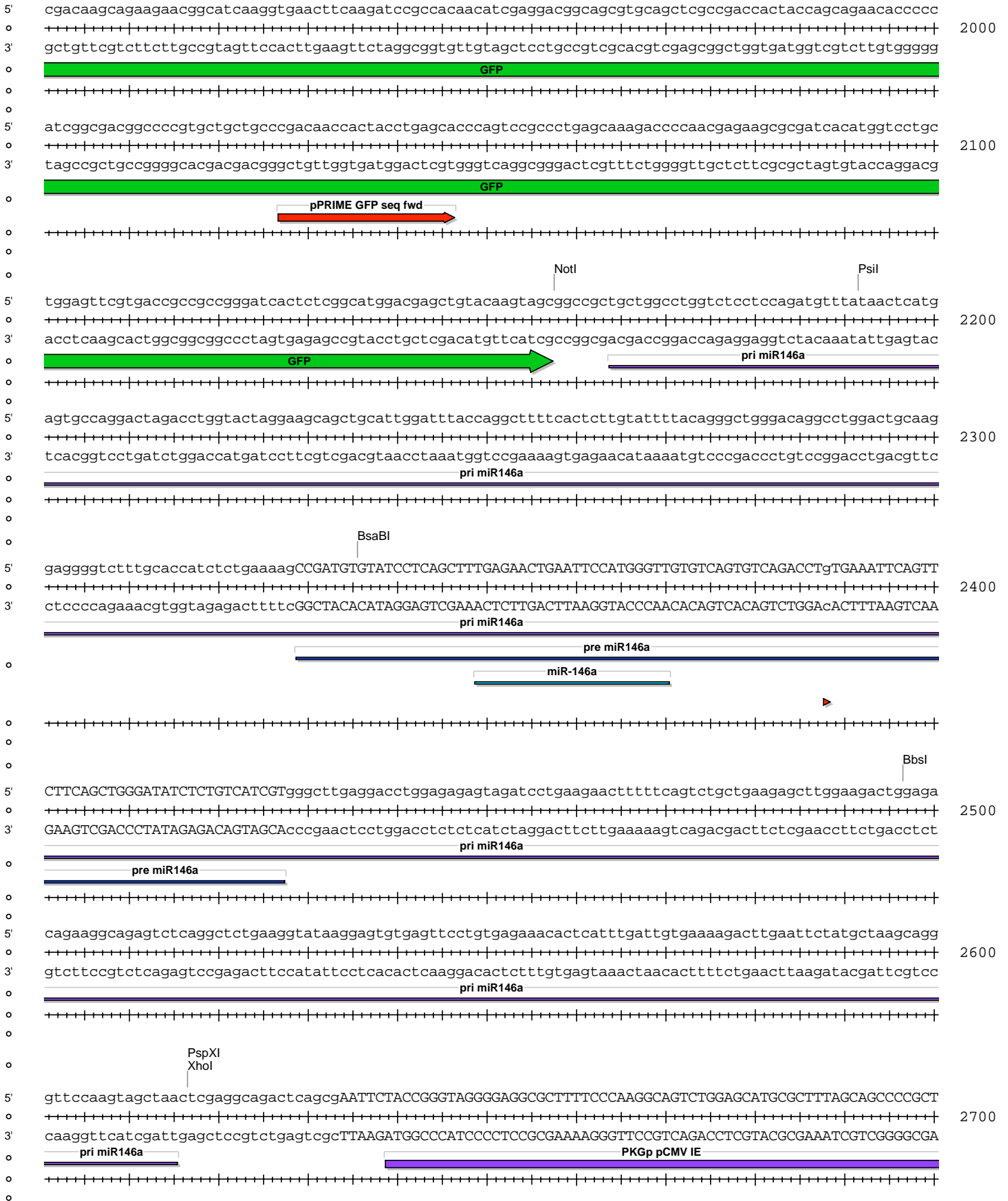
pMSCV-Puro-GFP miR-146a



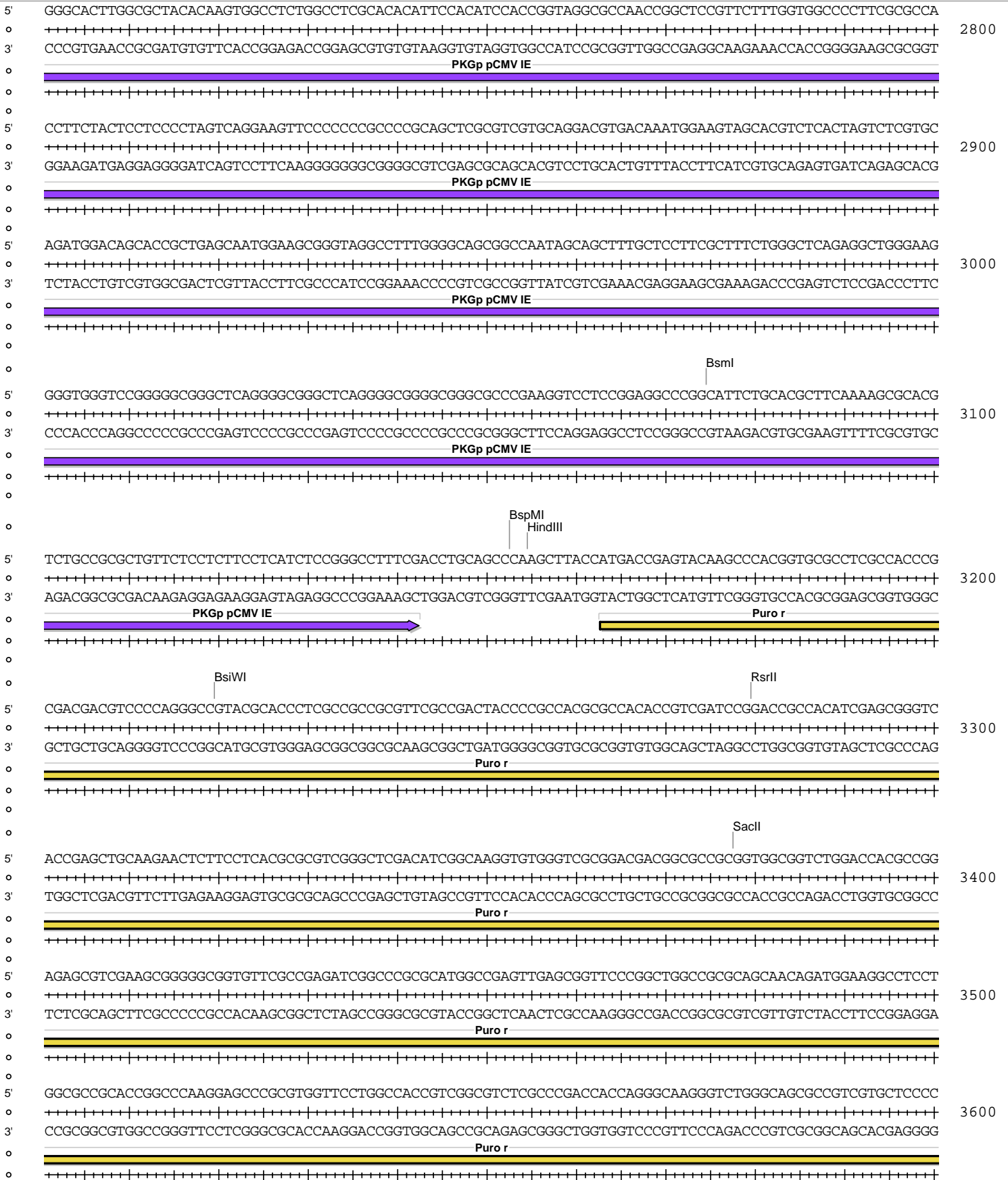
pMSCV-Puro-GFP miR-146a



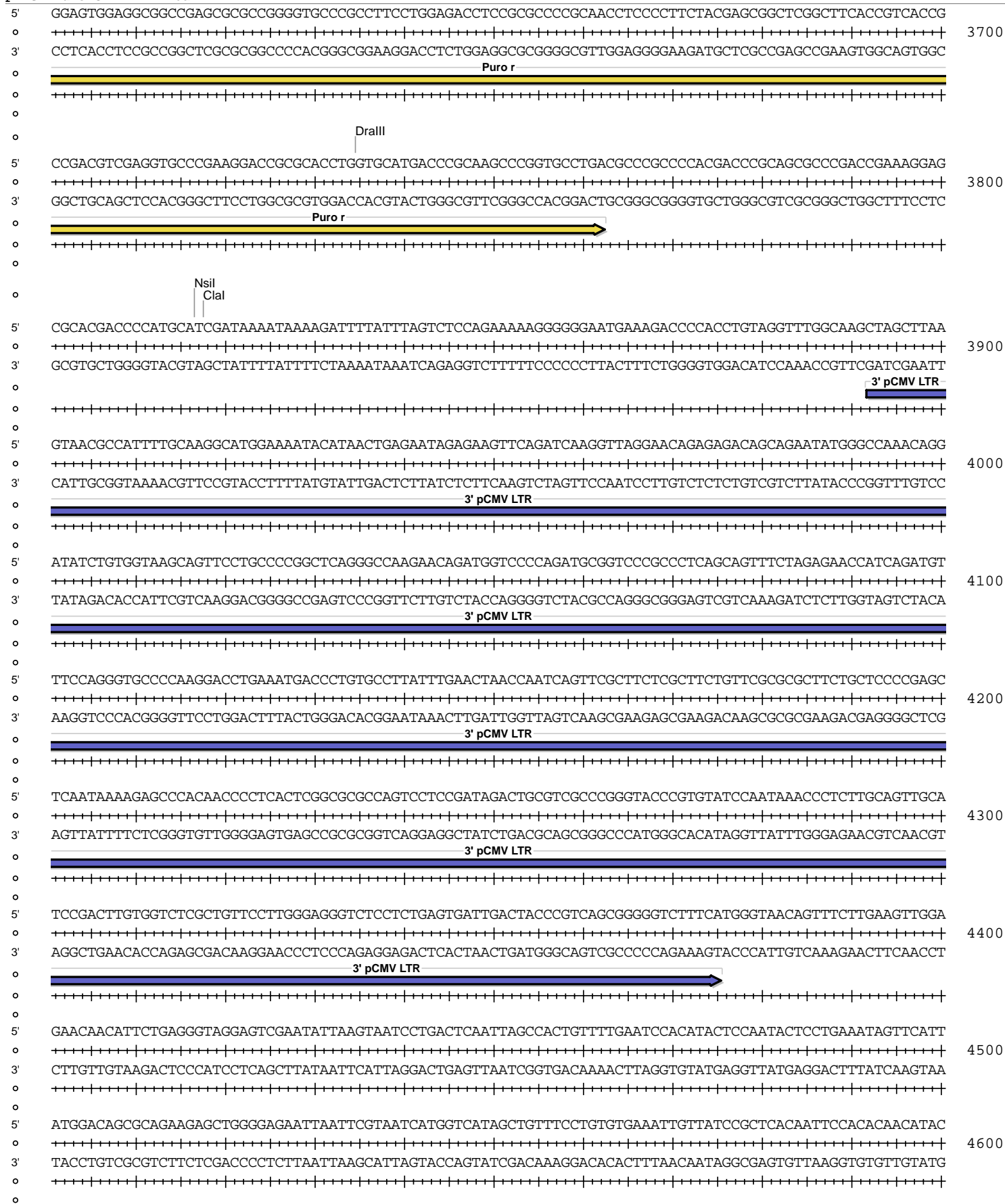
pMSCV-Puro-GFP miR-146a



pMSCV-Puro-GFP miR-146a



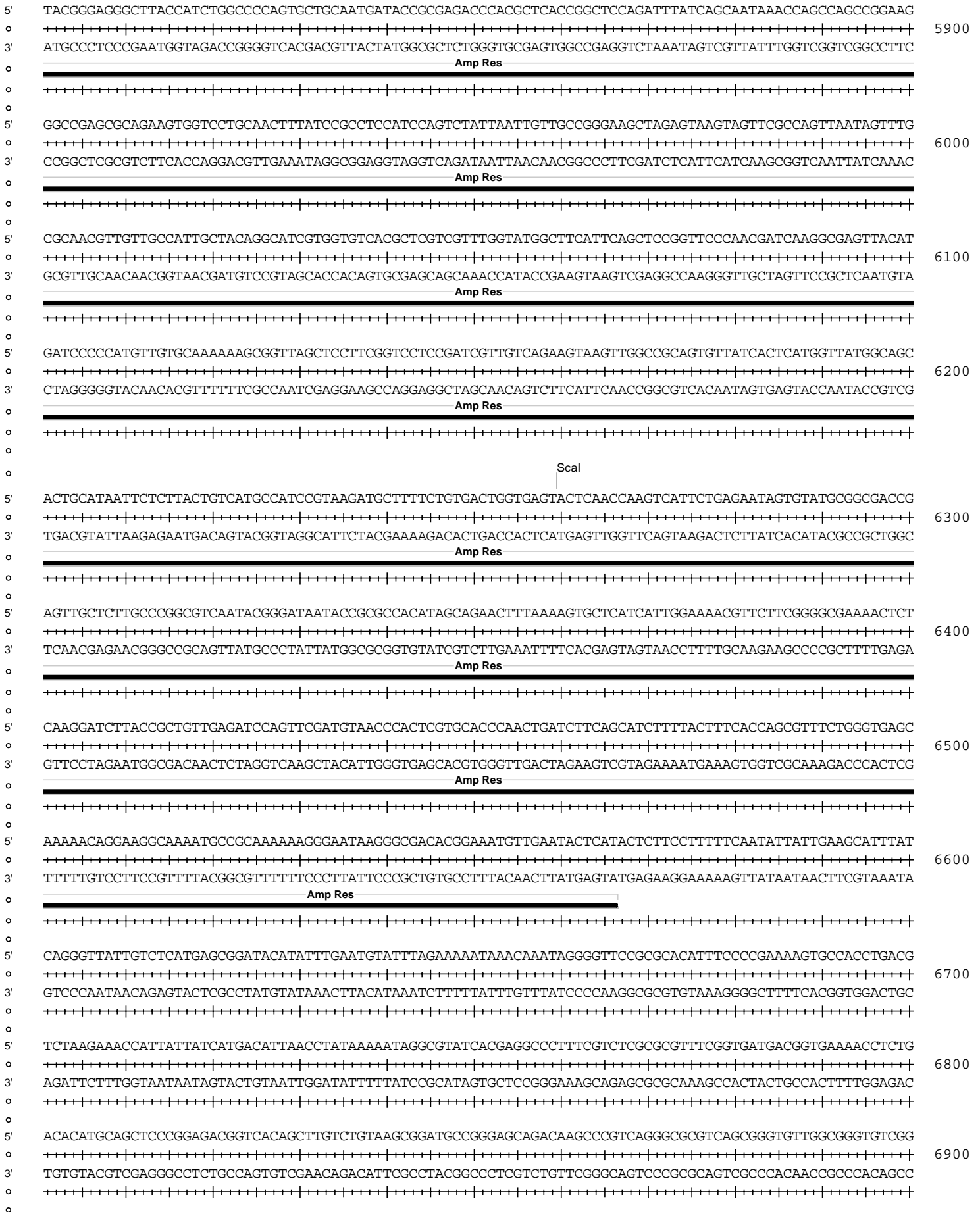
pMSCV-Puro-GFP miR-146a







pMSCV-Puro-GFP miR-146a



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NdeI

5' GGCTGGCTTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCA  
o ++++++  
3' CCGACCGAATTGATACGCCGTAGTCTCGTCTAACATGACTCTCACGTGGTATACGCCACACTTTATGGCGTGTCTACGCATTCTCTTTTATGGCGTAGT  
o ++++++ 7000

o

5' GGCGCCATTTCGCCATTTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAG  
o ++++++ 7100

3' CCGCGGTAAGCGGTAAGTCCGACGCGTTGACAACCCCTTCCCGCTAGCCACGCCGAGAAGCGATAATGCGGTGACCGCTTCCCCCTACACGACGTTT  
o ++++++

o

5' GCGATTAAGTTGGGTAACGCCAGGGTTTTCCAGTCACGAGTTGTAAAACGACGGCGCAAGGAATGGTGCATGCAAGGAGATGGCGCCCAACAGTCCCC  
o ++++++ 7200

3' CGCTAATTCAACCCATTGCGGTCCCAAAGGGTCAGTGTGCAACATTTTGTCTGCCGCTTCTTACCACGTACGTTCTCTACCGGGTTGTGTCAGGGG  
o ++++++

o

5' CGGCCACGGGGCTGCCACCATACCCACGCCGAAACAAGCGCTCATGAGCCCGAAGTGGCGAGCCCGATCTTCCCATCGGTGATGTGCGCGATATAGGC  
o ++++++ 7300

3' GCCGGTGCCCGGACGGTGGTATGGGTGCGGCTTTGTTTCGCGAGTACTCGGGCTTACCCTCGGGCTAGAAGGGGTAGCCACTACAGCCGCTATATCCG  
o ++++++

o

SgrAI

5' GCCAGCAACCGCACCTGTGGCGCCGGTGTGTCGGGCCACGATGCGTCCGGCTAGAGGCGATTAGTCCAATTTGTTAAAGACAGGATATCAGTGGTCCAG  
o ++++++ 7400

3' CCGTCGTTGGCGTGGACACCGCGCCACTACGGCCGGTGTCTACGAGCCGCATCTCCGCTAATCAGGTTAAACAATTTCTGTCTATAGTCACCAGGTC  
o ++++++

o

5' GCTCTAGTTTTGACTCAACAATATCACCAGCTGAAGCCTATAGAGTACGAGCCATAGATAAAAATAAAAGATTTATTTAGTCTCCAGAAAAGGGGGAA  
o ++++++ 7500

3' CGAGATCAAACTGAGTTGTTATAGTGGTGCACCTTCGGATATCTCATGCTCGGTATCTATTTTATTTTCTAAAATAAATCAGAGGTCTTTTCCCCCTT  
o ++++++

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