

pMSCV-Hyg-GFP miR-146a

Absent Sites	0	AarI, AbsI, Accl, AflI, AflI', Apal, AvrII, BamHI, BarI, BarI', BclI, BsaAI, BsiWI, BstBI, BstZ17I, CspCI, CspCI', FseI, FspAI, HpaI, MauBI, MfeI, MluI, MreI, NruI, PacI, PflMI, PmeI, PmlI, PspOMI, PstI, PstI', Sall, SanDI, SbfI, SfiI, SgrDI, SnaBI, SrfI, SwaI, XcmI
AfIII	1	5271
AjuI	1	3883
AjuI'	1	3851
AsiSI	1	3534
BbsI	1	2497
BglII	1	1411
BsaBI	1	2336
BsmI	1	3075
BstEII	1	1089
BstXI	1	3160
Clal	1	4202
HincII	1	4006
HindIII	1	3155
NotI	1	2158
NsiI	1	4201
PciI	1	5271
PshAI	1	3197
PsiI	1	2192
PspXI	1	2617
RsrII	1	3578
SacII	1	3950
SgrAI	1	7707
XhoI	1	2617

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5' TGAAAGACCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGAAGGCATGGAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGG
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 3' ACTTCTGTTGGGTGGACATCCAAACCGTTCGATCGAATTCATTGCGGTAACCGTTCCTGACCTTTTATGTATTGACTCTTATCTCTTCAAGTCTAGTTCC
 5' pCMV LTR

5' TTAGGAACAGAGAGACAGCAGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCG
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 3' AATCCTTGTCTCTCTGTGCTTATACCCGGTTTGTCTTATAGACACCATTTCGTCAAGGACGGGGCCGAGTCCCGGTTCTTGTCTACCAGGGGTCTACGC
 5' pCMV LTR

5' GTCCCGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTC
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 3' CAGGGCCGGGAGTCGTCAAAGATCTCTTGGTAGTCTACAAAGTCCACGGGGTTCCTGGACTTTACTGGGACACGGAATAAACTTGATTGGTTAGTCAAG
 5' pCMV LTR

5' GCTTCTCGTCTCTGTTCGCGCTTCTGCTCCCCGAGCTCAATAAAAAGAGCCACAAACCCCTCACTCGGCGCGCAGTCTCCGATAGACTGCGTCCCC
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5' GGGTACCCGTATTCCCAATAAAGCCTCTTGCTGTTTGCATCCGAATCGTGGACTCGCTGATCCTTGGGAGGGTCTCCTCAGATTGATTGACTGCCACCT
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 5' pCMV LTR

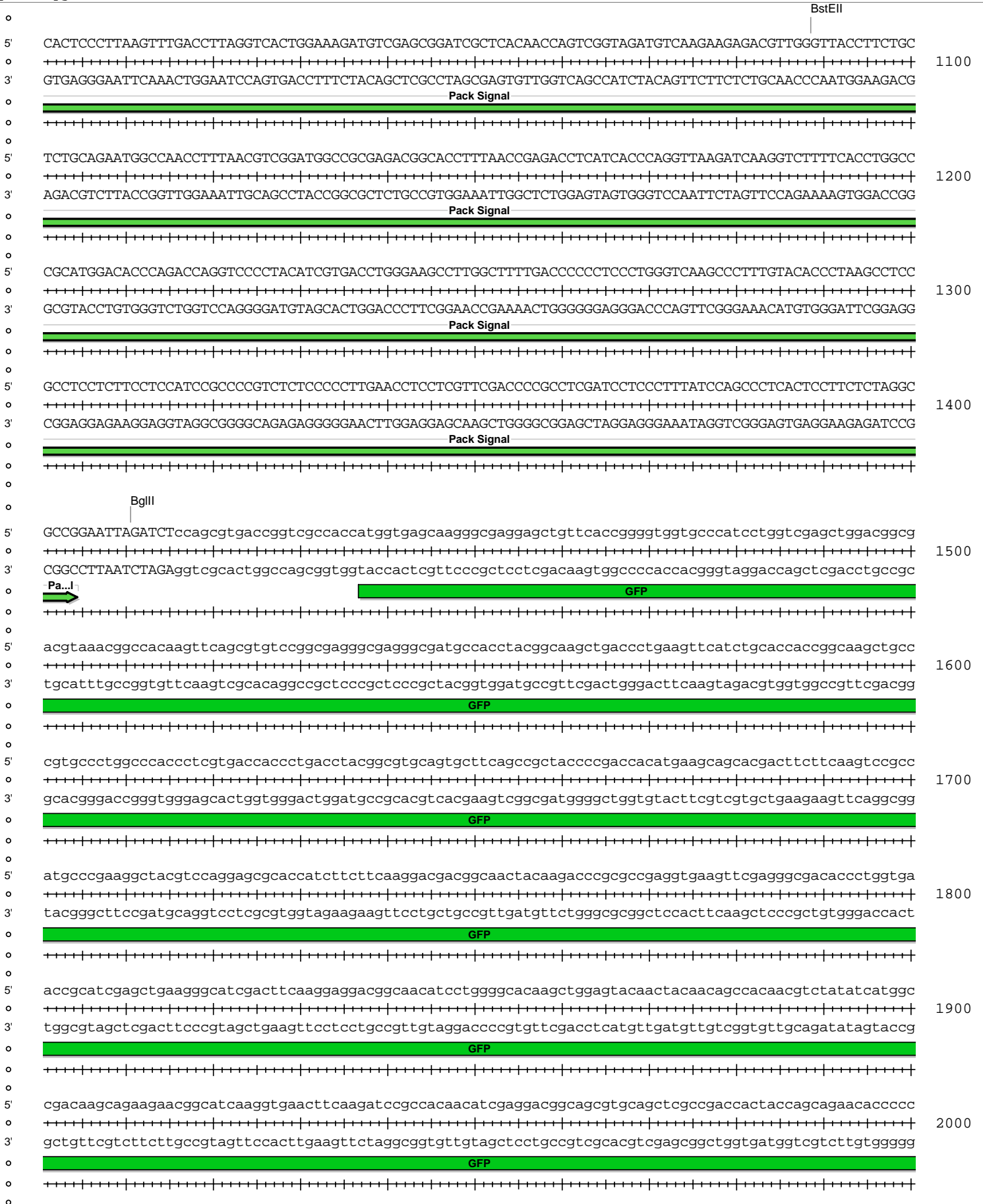
Pack Signal

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 3' ACAGACAGAGACAGAAACACGCACAAACACGGCCGTAGATTACAAACCGCGACGCAGACATGATCAATCGATTGATCGAGACATAGACCGCTGGGCACC
 Pack Signal

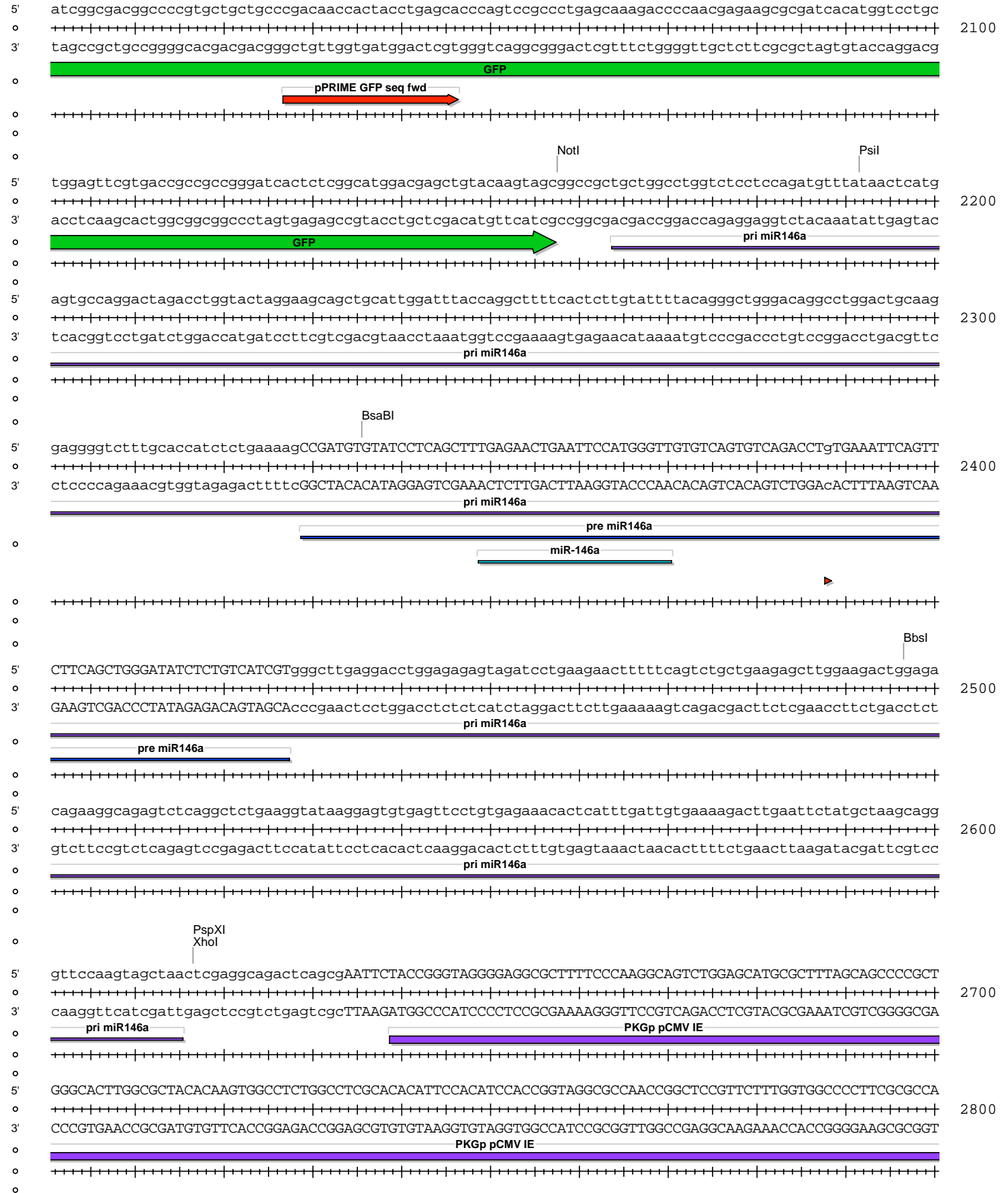
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 Pack Signal

5' TGGAATCCGACCCCGTCAGGATATGTGGTTCTGGTAGGAGACGAGAACC'TAAACAGTTCCCGCCTCCGTCTGAATTTTGTCTTTCGGTTTGAACCGAA
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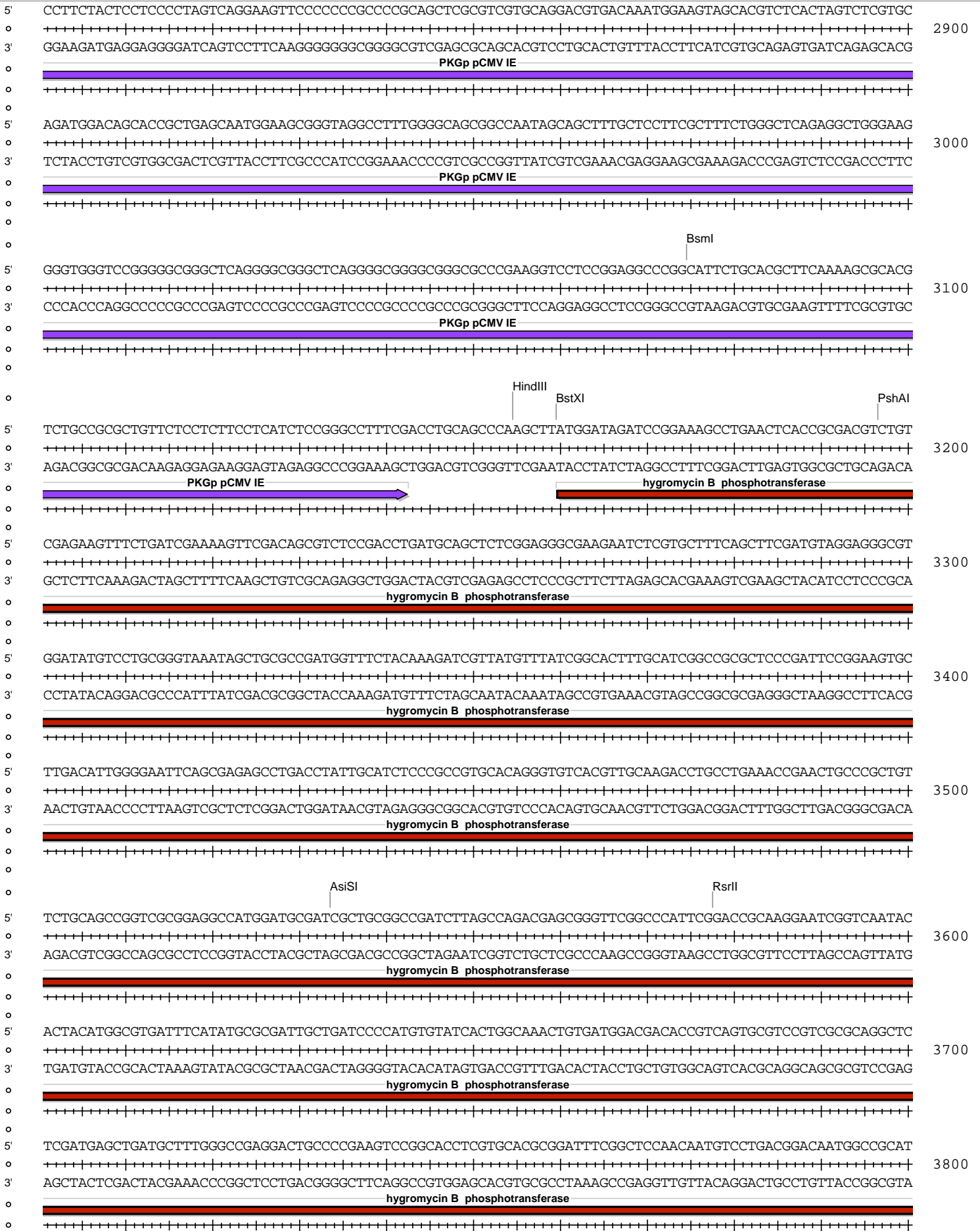
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 Pack Signal

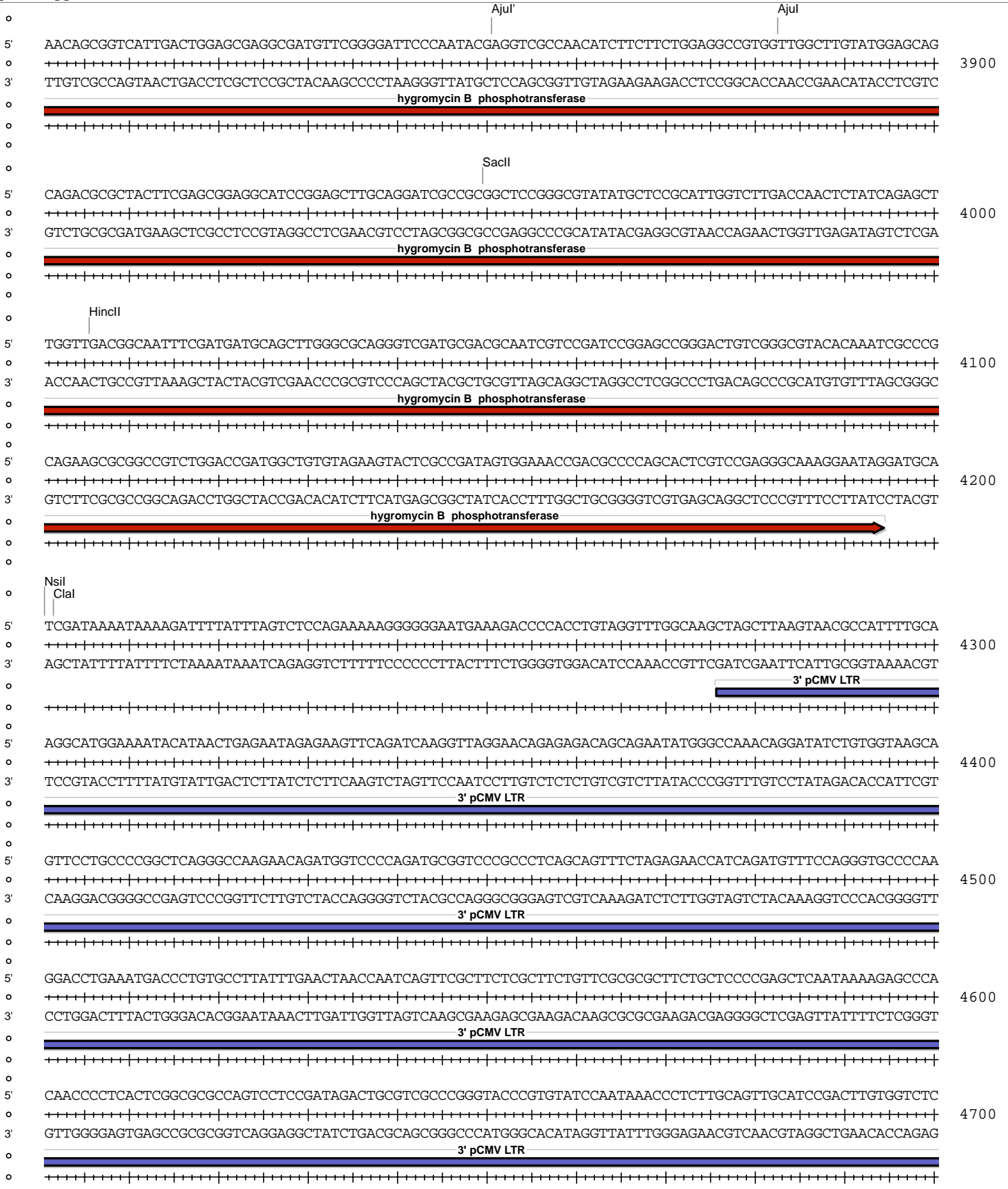


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 3' CGACAAGGAACCCCTCCAGAGGAGACTCACTAACTGATGGGCAGTCGCCCCAGAAAAGTACCCATTGTCAAAGAACTTCAACCTCTTGTGTAAGACTCC
 3' pCMV LTR
 5' GTAGGAGTCGAATATTAAGTAATCCTGACTCAATTAGCCACTGTTTGAATCCACATACTCCAATACTCCTGAAATAGTTTCATTATGGACAGCGCAGAAG
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 AfilIII
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 5300
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 3' GTCTTTTTCTCTAGAGTTCTCTAGGAACTAGAAAAGATGCCCCAGACTGCGAGTCACCTTGTCTTTGAGTGAATTCCTAAACAGTACTCTAAT

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5' TCAAAAAGGATCTTCACCTAGATCCTTTTAAATTA AAAATGAAGTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCT
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 7100
 3' ACTCGCCTATGTATAAACTTACATAAATCTTTTATTTGTTTATCCCAAGCGCGTGTAAAGGGGCTTTTACGGTGGACTGCAGATTCTTTGGTAAATA
 Amp Res

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o ++++++
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o ++++++
o
5' GAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTGGCGGGTGTGGGGCTGGCTTAACTATG
o ++++++
3' CTCTGCCAGTGTGCAACAGACATTGCGCTACGGCCCTCGTCTGTTTCGGGCAGTCCCGCGCAGTCGCCACAACCGCCACAGCCCCGACCGAATTGATAC
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o
5' CGGCATCAGAGCAGATTGTAAGTACTGAGAGTGCACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCCATTGCCATT
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o ++++++
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5' CACCATAACCCACGCCGAAACAAGCGCTCATGAGCCGAAGTGCGGAGCCCGATCTTCCCATCGGTGATGTGCGCGATATAGGCGCCAGCAACCGCACCT
o ++++++
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o ++++++
o
o
SgrAI
o |
5' GTGGCGCCGGTGATGCCGGCCACGATGCGTCCGGCGTAGAGGCGATTAGTCCAATTTGTTAAAGACAGGATATCAGTGGTCCAGGCTCTAGTTTTGACTC
o ++++++
3' CACCGCGGCCACTACGGCCGGTGCTACGCAGGCCGATCTCCGCTAATCAGTTAAACAATTTCTGTCTATAGTCACCAGGTCCGAGATCAAACCTGAG
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5' AACAAATATCACCAGCTGAAGCCTATAGAGTACGAGCCATAGATAAAAATAAAGATTTTATTTAGTCTCCAGAAAAGGGGGGAA
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3' TTGTTATAGTGGTGCAGTTCGGATATCTCATGCTCGGTATCTATTTTATTTCTAAAATAAATCAGAGGTCTTTTCCCGCCTT
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