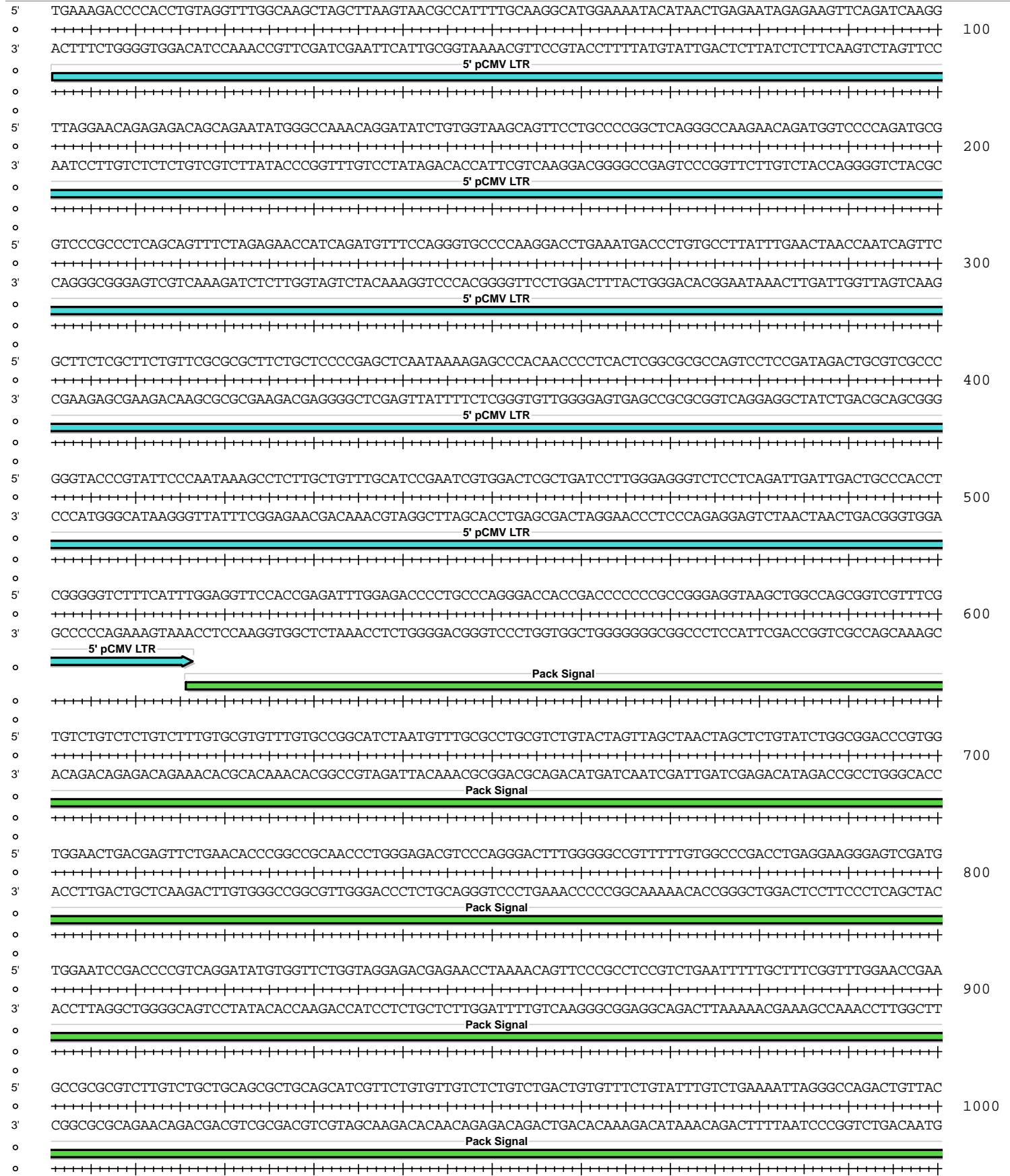
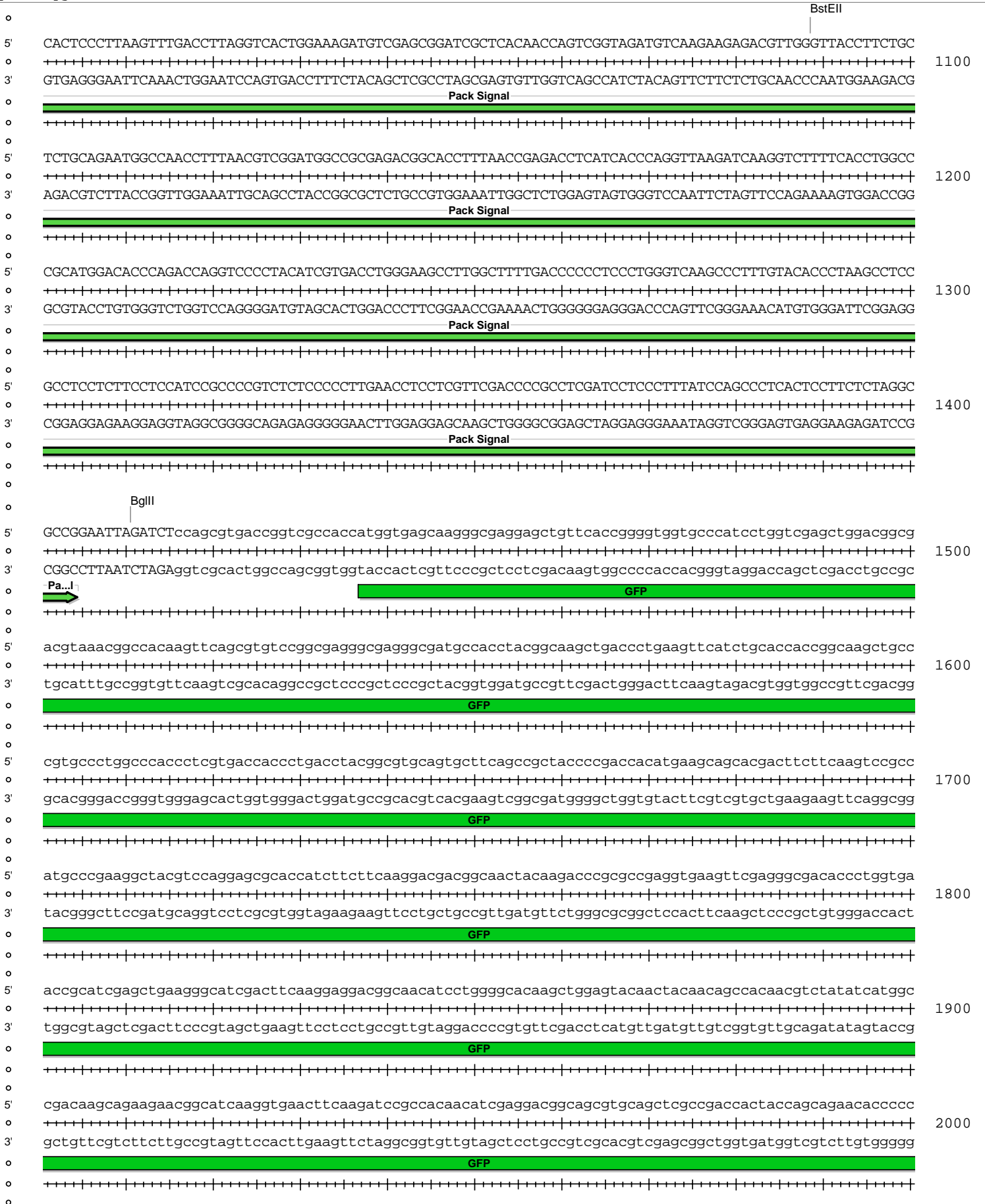
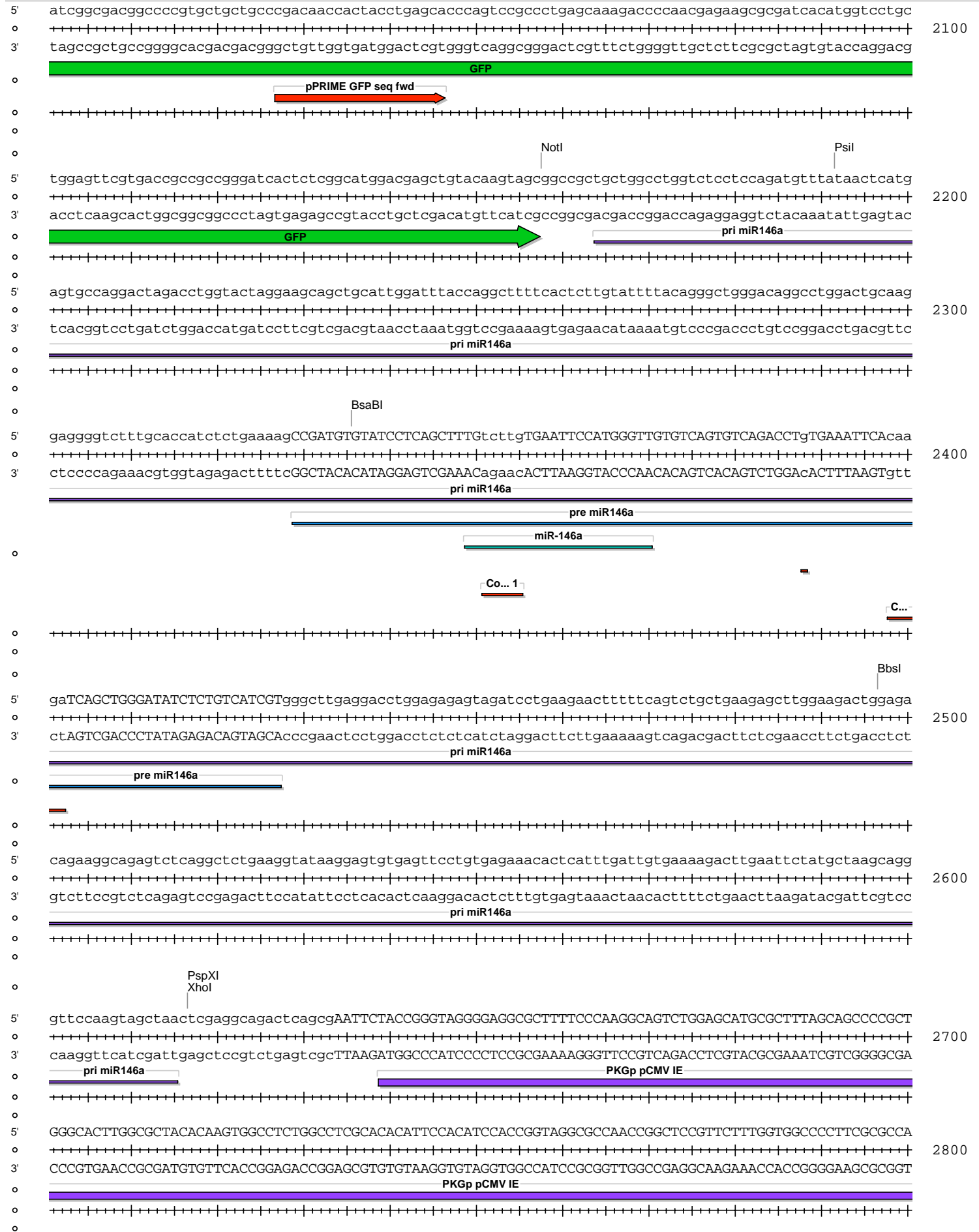
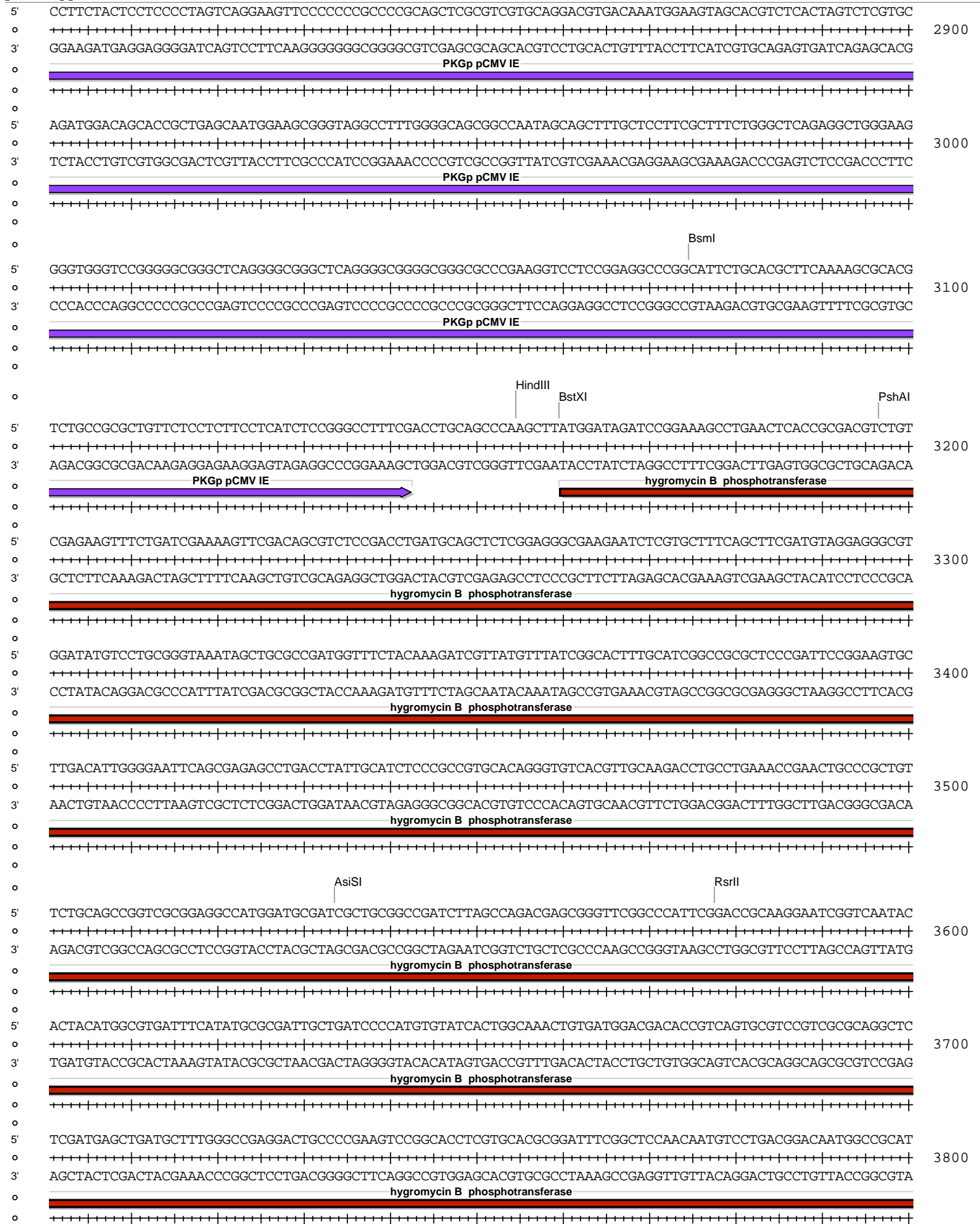


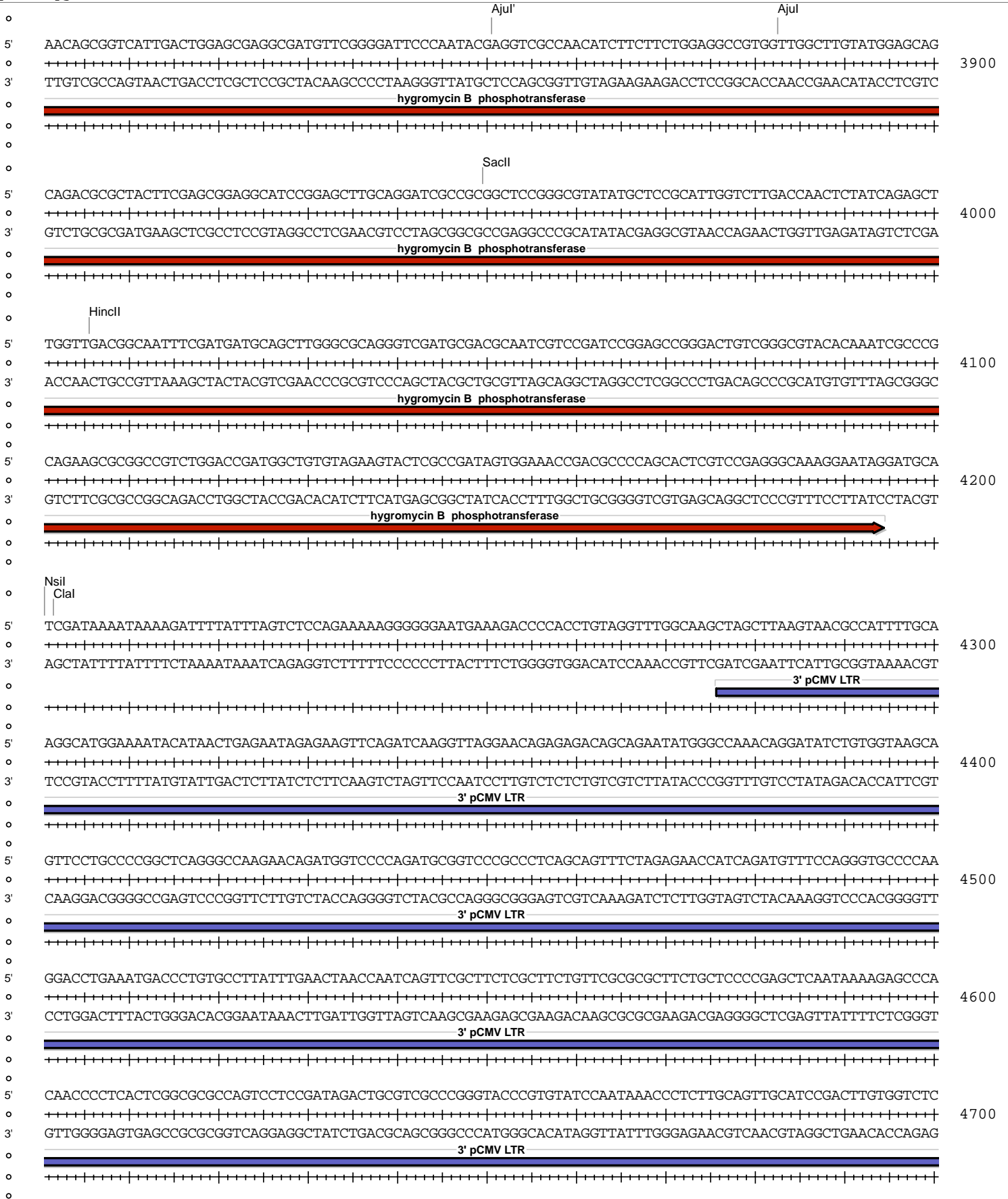
Absent Sites	0	AarI, AbsI, Accl, AflI, AflI', Apal, AvrII, BamHI, BarI, BarI', BclI, BsaAI, BsiWI, BstBI, BstZ17I, CspCI, CspCI', FseI, FspAI, HpaI, MauBI, MfeI, MluI, MreI, NruI, PacI, PflMI, PmeI, PmlI, PspOMI, PstI, PstI', Sall, SanDI, SbfI, SfiI, SgrDI, SnaBI, SrfI, SwaI, XcmI
AfIII	1	5271
AjuI	1	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' TATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTCTCGCGCTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCG
o ++++++
3' ATAGTACTGTAATTGGATATTTTATCCGCATAGTGCTCCGGGAAAGCAGAGCGCGCAAAGCCACTACTGCCACTTTTGGAGACTGTGTACGTGAGGGC
o ++++++
o
5' GAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTGGCGGGTGTGGGGCTGGCTTAACTATG
o ++++++
3' CTCTGCCAGTGTGCAACAGACATTGCGCTACGGCCCTCGTCTGTTTCGGGCAGTCCCGCGCAGTCGCCACAACCGCCACAGCCCCGACCGAATTGATAC
o ++++++
o
5' CGGCATCAGAGCAGATTGTAAGTGTGAGAGTGCACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCCATTTCGCCATT
o ++++++
3' GCCGTAGTCTCGTCTAACATGACTCTCACGTGGTATACGCCACACTTTATGGCGTGTCTACGCATTCTCTTTTATGGCGTAGTCCGCGGTAAGCGGTAA
o ++++++
o
5' CAGGCTGCGCAACTGTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTA
o ++++++
3' GTCCGACGCGTTGACAACCTTCCCGCTAGCCACGCCCGGAGAAGCGATAATGCGGTGACCGCTTTCCCTTACACGACGTTCCGCTAATTCAACCCAT
o ++++++
o
5' ACGCCAGGGTTTTCCAGTACGACGTTGTAAAACGACGGCGCAAGGAATGGTGCATGCAAGGAGATGGCGCCCAACAGTCCCCGGCCACGGGGCCTGC
o ++++++
3' TGCGGTCCCAAAGGGTCAGTGTGCAACATTTGCTGCGCGTTCCTTACCACGTACGTTCTCTACCGCGGTTGTGTCAGGGGCGCGGTGCCCGGACG
o ++++++
o
5' CACCATAACCCACGCCGAAACAAGCGCTCATGAGCCGAAGTGGCGAGCCCGATCTTCCCATCGGTGATGTGCGCGATATAGGCGCCAGCAACCGCACCT
o ++++++
3' GTGGTATGGGTGCGGCTTTGTTTCGCGAGTACTCGGGCTTACCAGTCTAGAGGGGTAGCCACTACAGCCGCTATATCCGCGGTGTTGGCGTGGA
o ++++++
o
o
o
SgrAI
o
5' GTGGCGCGGTGATGCCGGCCACGATGCGTCCGGCGTAGAGGCGATTAGTCCAATTTGTTAAAGACAGGATATCAGTGGTCCAGGCTCTAGTTTTGACTC
o ++++++
3' CACCGCGGCCACTACGGCCGGTGCTACGCAGGCCGATCTCCGCTAATCAGTTAAACAATTTCTGTCTATAGTCACCAGGTCCGAGATCAAACCTGAG
o ++++++
o
5' AACAAATATCACCAGCTGAAGCCTATAGAGTACGAGCCATAGATAAAAATAAAGATTTTATTTAGTCTCCAGAAAAGGGGGGAA
o ++++++
3' TTGTTATAGTGGTCGACTTCGGATATCTCATGCTCGGTATCTATTTTATTTCTAAAATAAATCAGAGGTCTTTTCCCGCCTT
o ++++++
o
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