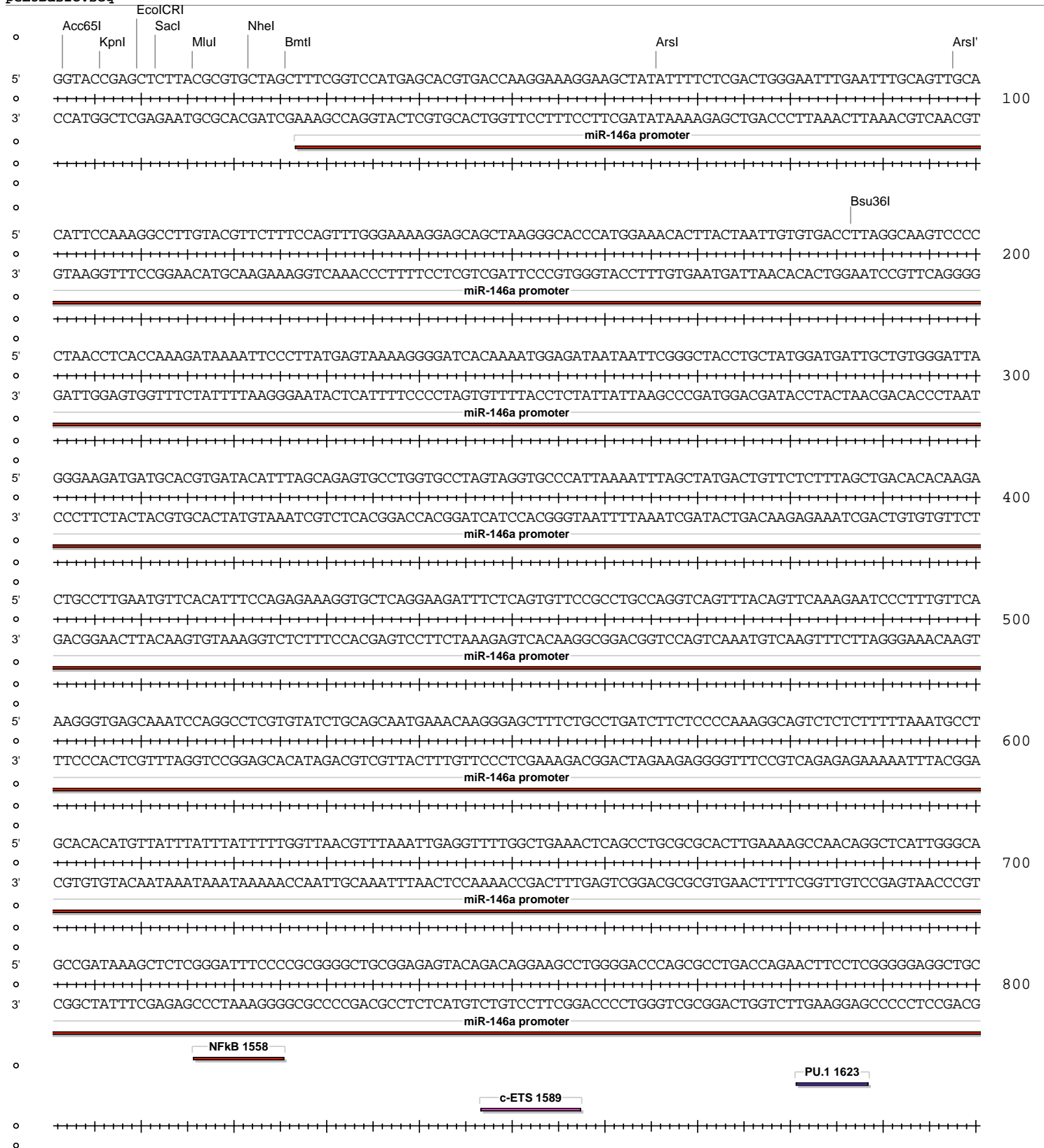
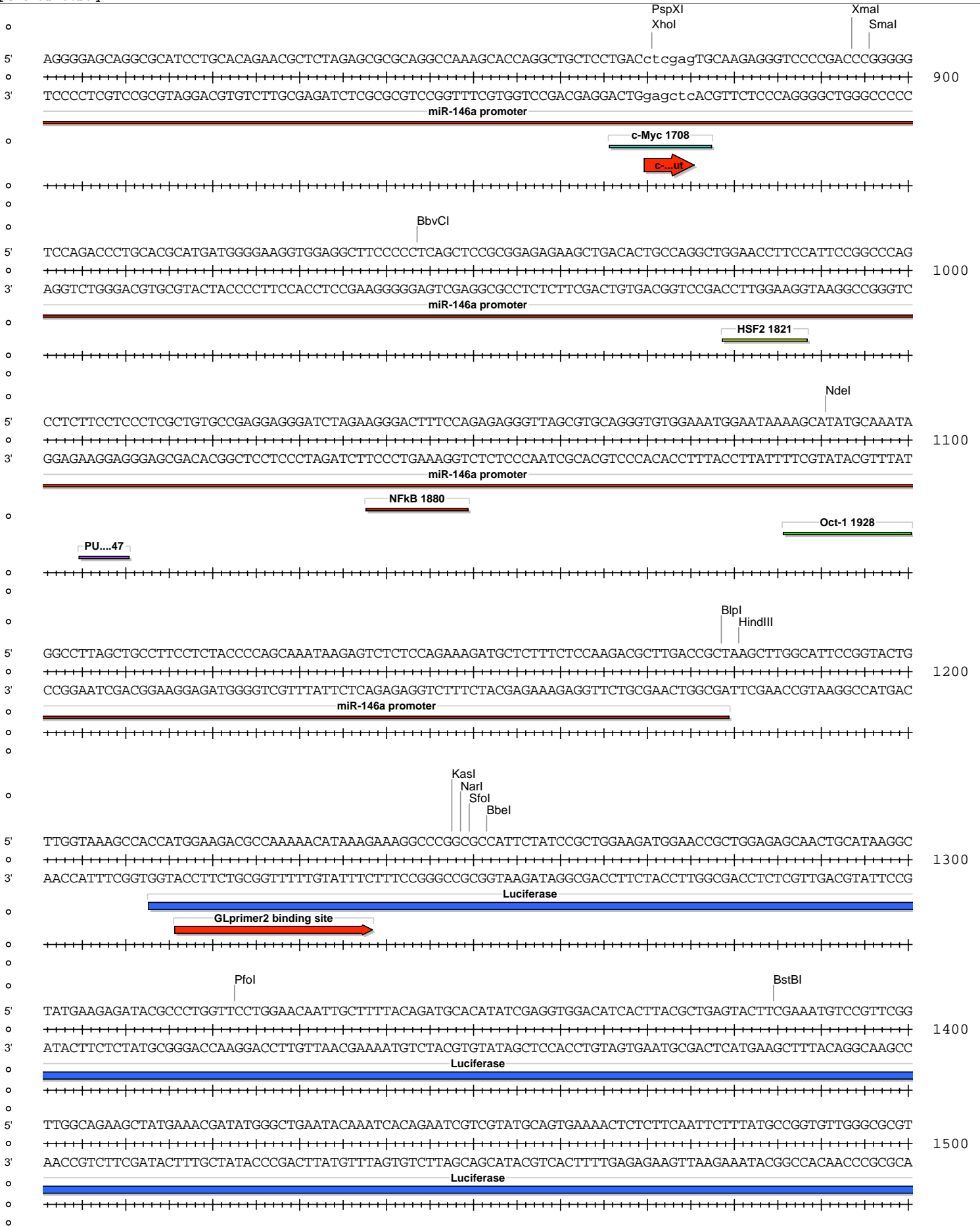


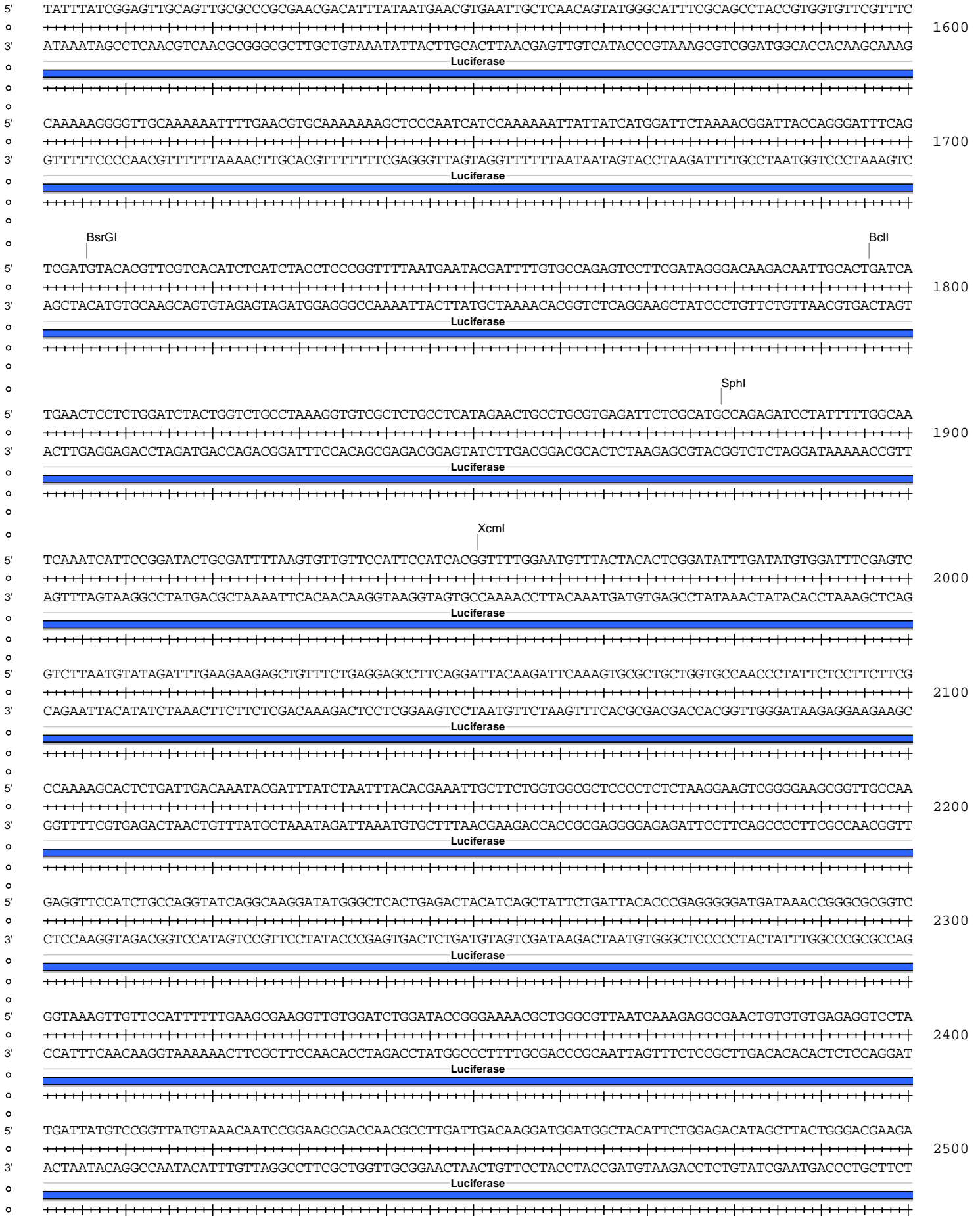
pGL3Basic.seq

Absent Sites	0	AatII, AbsI, AfiIII, AgeI, AjuI, AjuI', AleI, ApaI, AscI, AsiSI, AvrII, BaeI, BaeI', BarI, BarI', BglII, BmgBI, BsiWI, BsmBI, BstAPI, BstEII, BstXI, BstZ17I, CspCI, CspCI', EcoRI, EcoRV, FspAI, MauBI, MreI, MscI, NruI, NsiI, PacI, PaeI, PfiMI, PmeI, PspOMI, PspI, PspI', PvuII, RsrII, SbfI, SexAI, SfiI, SgrDI, SnaBI, SpeI, SrfI, SwaI, Tth111I, ZraI
Acc65I	1	2
AccI	1	3139
AfeI	1	3264
AhdI	1	4281
Alol	1	5501
Alol'	1	5469
Arsl	1	66
Arsl'	1	98
AseI	1	4453
BamHI	1	3132
BbeI	1	1252
BbvCI	1	944
BclI	1	1796
BglI	1	1179
BmtI	1	26
BsaBI	1	3131
BsaI	1	4342
BsrGI	1	1706
BstBI	1	1385
Bsu36I	1	187
BtgZI	1	5425
DraIII	1	5433
EcoICRI	1	10
FseI	1	2889
HindIII	1	1181
KasI	1	1248
KpnI	1	6
MluI	1	16
NarI	1	1249
NdeI	1	1091
NheI	1	22
NotI	1	5779
PfoI	1	1323
PshAI	1	3203
PspXI	1	871
SacI	1	12
SalI	1	3138
SfoI	1	1250
SgrAI	1	2644
Smal	1	896
SphI	1	1879
TstI	1	2779
TstI'	1	2747
XcmI	1	1951
XhoI	1	871
XmaI	1	894
XmnI	1	4880

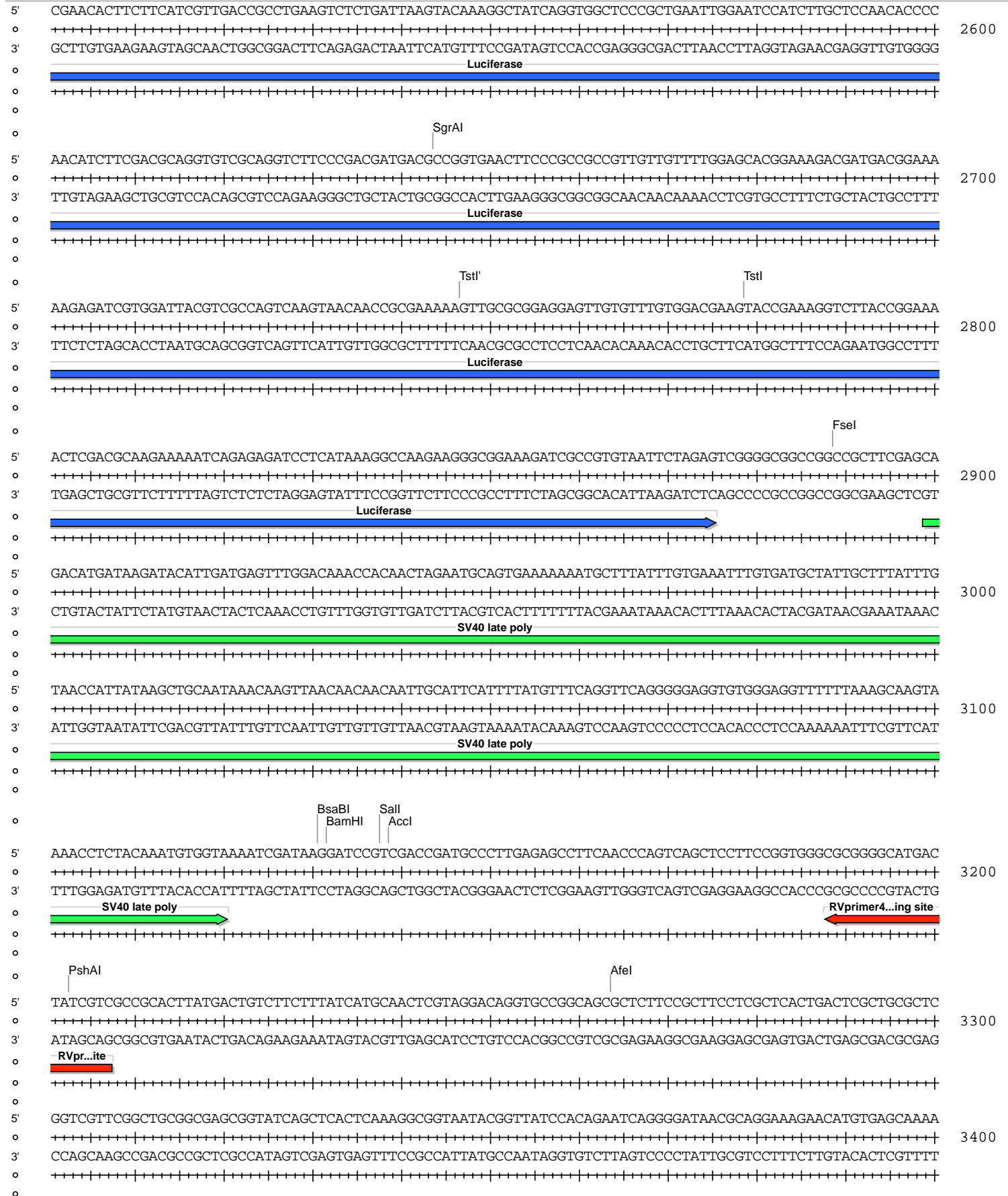




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pGL3Basic.seq



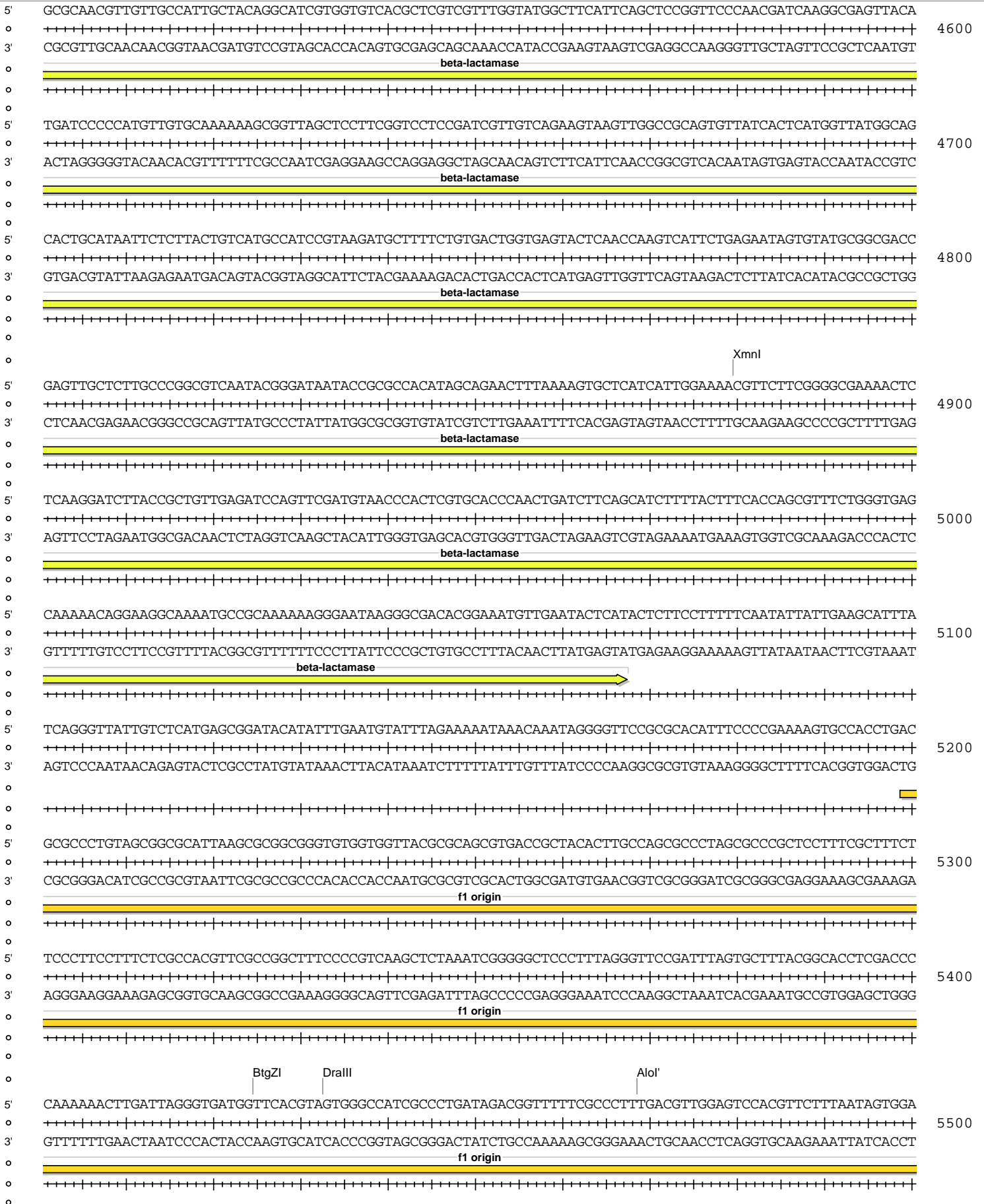
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o
3' CCGGTTCGTTTTCGGTCTCTGGCATTTTCCGGCGCAACGACCGCAAAAAGGTATCCGAGGCCGGGGGACTGCTCGTAGTGTTTTAGCTGCGAGTTCAG
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
o
o
5' AGAGGTGGCGAAAACCCGACAGGACTATAAAGATAACCAGGCGTTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCCCTGCCGTTACCGGATA
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
o
3' TCTCCACCGCTTTGGGCTGTCTGATATTCTATGGTCCGCAAAGGGGACCTTCGAGGGAGCACGCGAGAGGACAAGGCTGGGACGGCGAATGGCCTAT
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
o
o
5' CCTGTCCGCCTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGT
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
o
3' GGACAGGCGGAAAAGGGAAAGCCCTTCGACCCGCAAAGAGTATCGAGTTCGACATCCATAGAGTCAAGCCACATCCAGCAAGCGAGGTTCCGACCCGACA
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
o
o
5' GTGCACGAACCCCCCTTCAGCCGACCGCTGCGCCTTATCCGGTA ACTATCGTCTTGAGTCCAACCCGGAAGACACGACTTATCGCCACTGGCAGCAG
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
o
3' CACGTGCTTGGGGGCAAGTCGGGCTGGCGACCGGAATAGGCCATTGATAGCAGA ACTCAGGTTGGGCGCATCTGTGCTGAATAGCGGTGACCGTCGTC
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
o
o
5' CCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGG
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
o
3' GGTGACCAATTGCTTAATCGTCTCGCTCCATACATCCGCCACGATGTCTCAAGA ACTTCACCACCGGATTGATGCCGATGTGATCTCTTTCATATAAACC
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
o
o
5' TATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGA AAAAGAGTTGGTAGCTTTGATCCGCGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTGTGTTGC
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
o
3' ATAGACGCGAGACGACTTCGGTCAATGGAAGCCTTTTTCTCAACCATCGAGA ACTAGGCCGTTGTTGGTGGCGACCATCGCCACCAAAAAAACAAACG
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
o
o
5' AAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGA
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
o
3' TTCGTGCTCTAATGCGCGTCTTTTTTTCC TAGAGTCTTCTAGGAACTAGAAAAGATGCCCCAGACTGCGAGTCACCTTGCTTTTGAGTGAATTCCCT
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
o
o
5' TTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTA AAAATGAAGTTTAAATCAATCTAAAGTATATATGAGTAACTTGGTC
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
o
3' AAAACCAGTACTCTAATAGTTTTTTCCTAG AAGTGGATCTAGGAAAATTAATTTTTACTTCAAATTTAGTTAGATTTCATATATACTCATTTGAAACCAG
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
o
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5' TGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTC GTTCCATCAGTTGCCTGACTCCCGTCGTGTAGATAACTACG
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
o
3' ACTGTCAATGGTTACGAATTAGTCACTCCG TGGATAGAGTCGCTAGACAGATAAAGCAAGTAGGTATCAACGGACTGAGGGGCAGCACATCTATTGATGC
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
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                                AhdI
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                                beta-lactamase
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o
o
                                BsaI
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                                v
                                +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
o
5' ATACGGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGCGAGACCCACGCTC ACCGGCTCCAGATTTATCAGCAATAAACAGCCAGCCGGAA
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
o
3' TATGCCCTCCCGAATGGTAGACC GGGGTCACGACGTTACTATGGCGCTCTGGGTGCGAGTGGCCGAGGTCATAAATAGTCGTTATTTGGTTCGGTTCGCGCCTT
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
o
o
o
                                beta-lactamase
                                +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
o
o
o
                                AseI
                                |
                                v
                                +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
o
5' GGGCCGAGCGCAGAAGTGGTCTGCACTTTATCCGCCTCCATCCAGTCTATTAATTG TGTGCCGGGAAGCTAGAGTAAGTAGTTCCGCCAGTTAATAGTTT
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
o
3' CCCGGCTCGCGTCTTACCAGGACGTTGAAATAGGCGGAGGTAGGTGAGATAAATTAA CAACGCCCTTCGATCTCATTCATCAAGCGGTCAATTATCAAAA
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
o
o
o
                                beta-lactamase
                                +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
o
o
o

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Cameron et al., Epstein-Barr Virus Latent Membrane Protein 1 Induces Cellular MicroRNA miR-146a, a Modulator of Lymphocyte Signaling Pathways, J. Virol., Feb. 2008, 1946-1958

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pGL3Basic.seq

