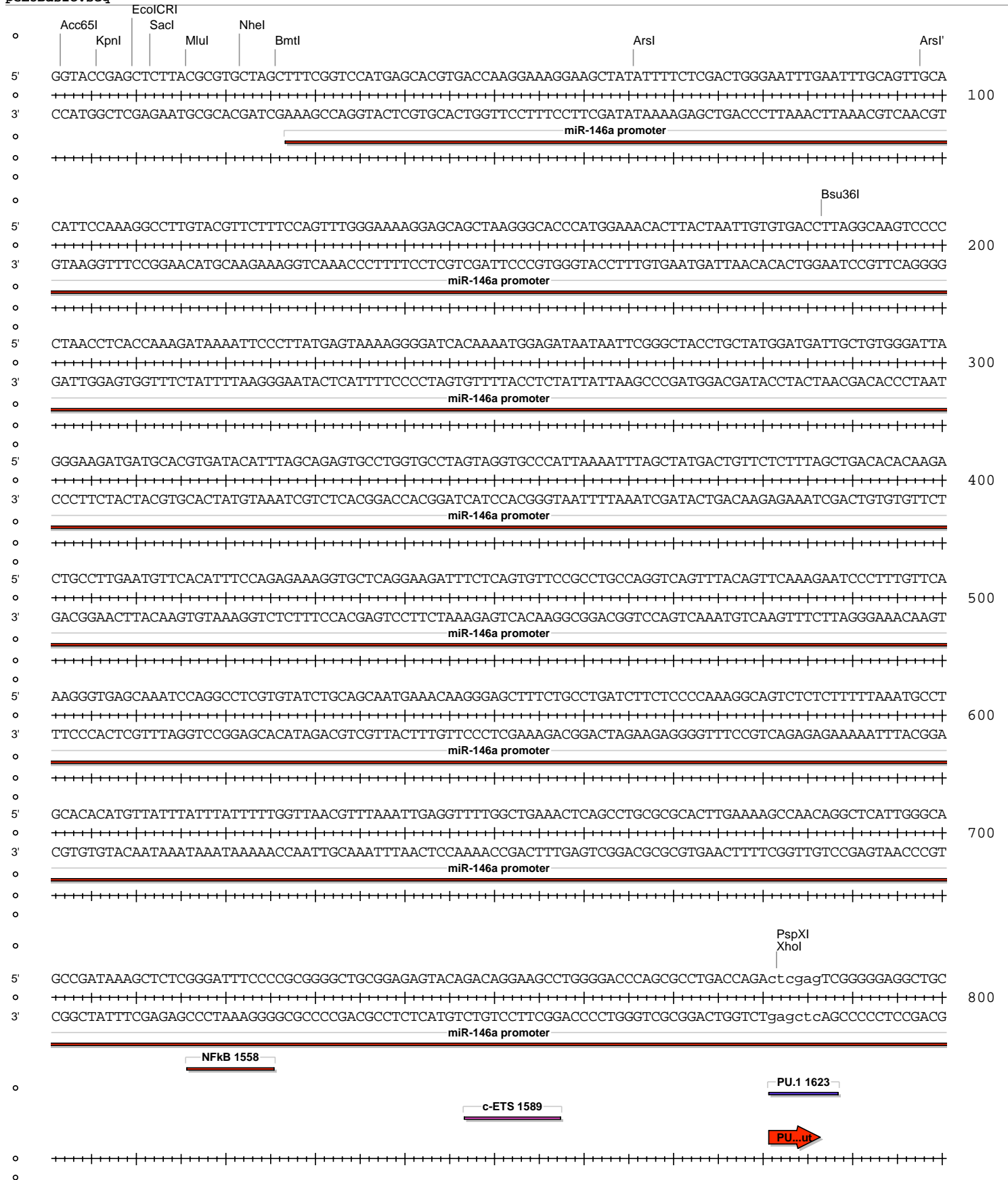
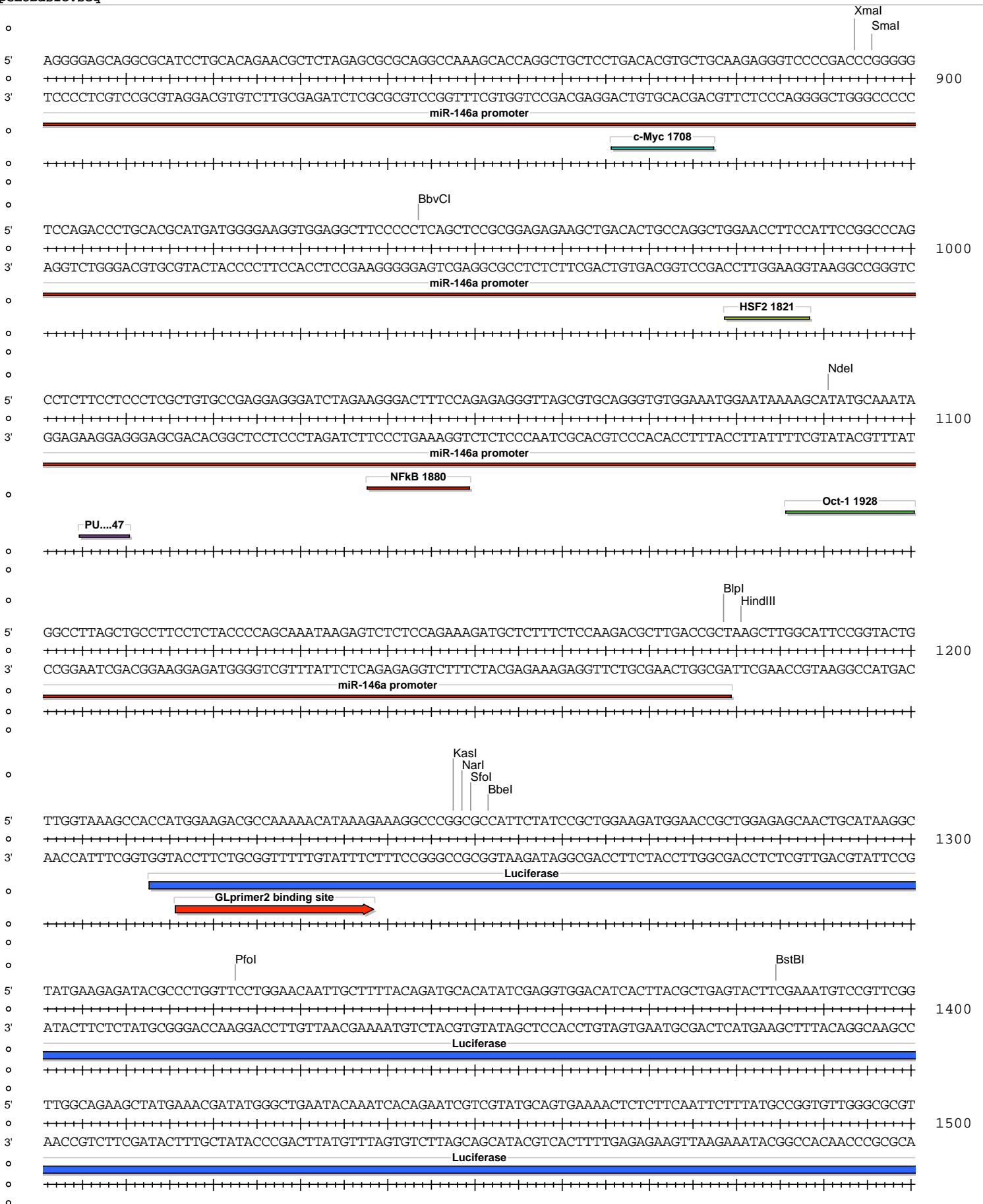


## pGL3Basic.seq

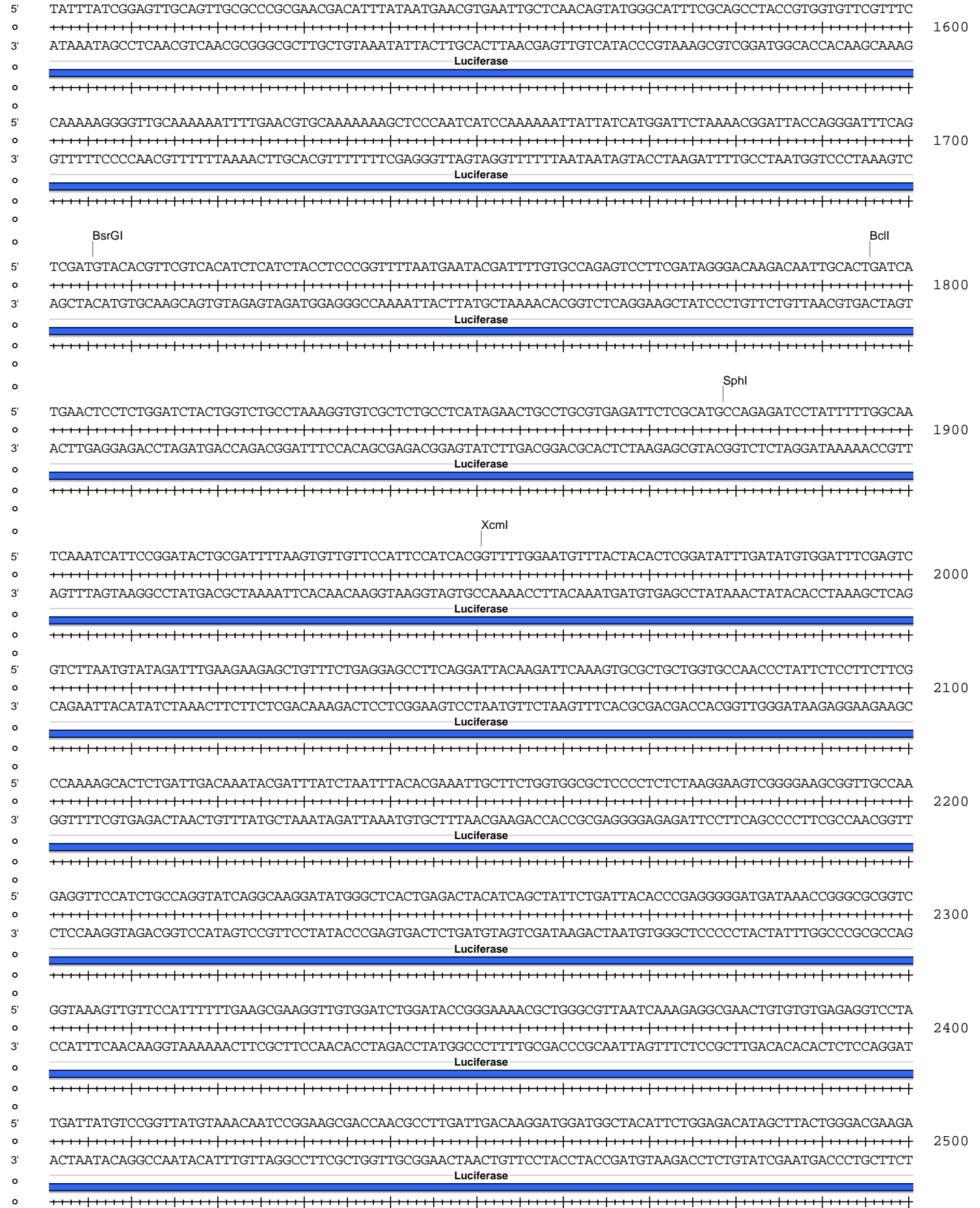
Absent Sites	0	AatII,AbSI,AfIII,Agel,Ajul,Ajul',AleI,Apal,AscI,AsiSI,AvrII,BaeI,BaeI',BamHI,BglII,BmgBI,BsiWI,BsmBI,BstAPI,BstEII,BstXI,BstZ171,CspCI,CspCI',EcoRI,EcoRV,FspAI,MauBI,MreI,MscI,NruI,NsiI,Pacl,Pacl',PflMI,PmeI,PspOMI,Psrl,Psrl',PvuII,RsrII,SbfI,SexAI,SfiI,SgrDI,SnaBI,SpeI,SrfI,Swal,Tth111I,ZraI
Acc65I	1	2 (5945)
Accl	1	3139 (5945)
Afel	1	3264 (5945)
AhdI	1	4281 (5945)
Alol	1	5501 (5945)
Alol'	1	5469 (5945)
Arsl	1	66 (5945)
Arsl'	1	98 (5945)
Asel	1	4453 (5945)
BamHI	1	3132 (5945)
BbeI	1	1252 (5945)
BbvCI	1	944 (5945)
BclI	1	1796 (5945)
BplI	1	1179 (5945)
BmtI	1	26 (5945)
BsaBI	1	3131 (5945)
Bsal	1	4342 (5945)
BsrGI	1	1706 (5945)
BstBI	1	1385 (5945)
Bsu36I	1	187 (5945)
BtgZI	1	5425 (5945)
DrallI	1	5433 (5945)
EcoICRI	1	10 (5945)
FseI	1	2889 (5945)
HindIII	1	1181 (5945)
KasI	1	1248 (5945)
KpnI	1	6 (5945)
MluI	1	16 (5945)
NarI	1	1249 (5945)
NdeI	1	1091 (5945)
NheI	1	22 (5945)
NotI	1	5779 (5945)
PfoI	1	1323 (5945)
PspXI	1	782 (5945)
SacI	1	12 (5945)
Sall	1	3138 (5945)
SfoI	1	1250 (5945)
SgrAI	1	2644 (5945)
SmaI	1	896 (5945)
SphI	1	1879 (5945)
TstI	1	2779 (5945)
TstI'	1	2747 (5945)
XcmI	1	1951 (5945)
XhoI	1	782 (5945)
XmaI	1	894 (5945)
XmnI	1	4880 (5945)

pGL3Basic.seq

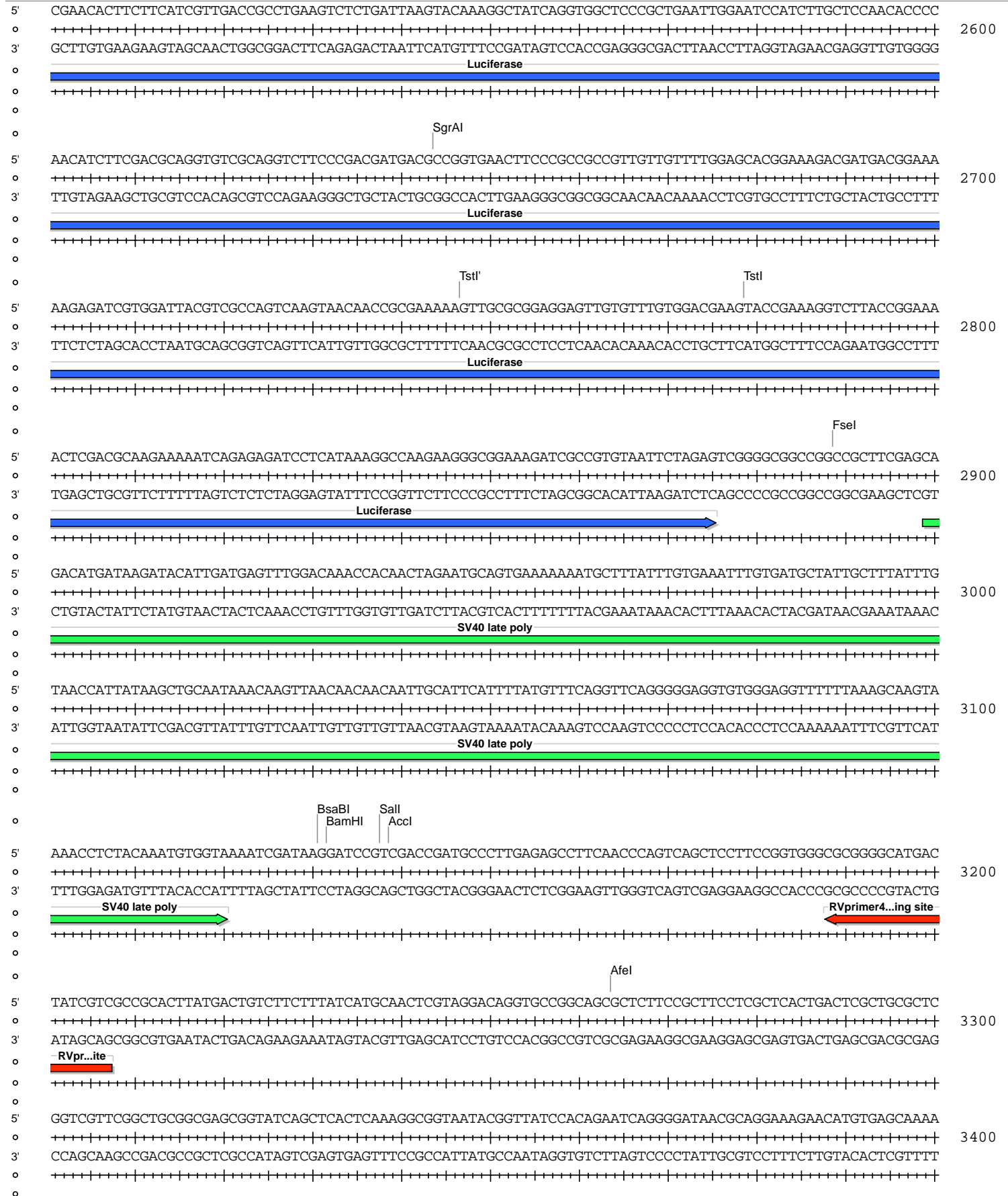




pGL3Basic.seq

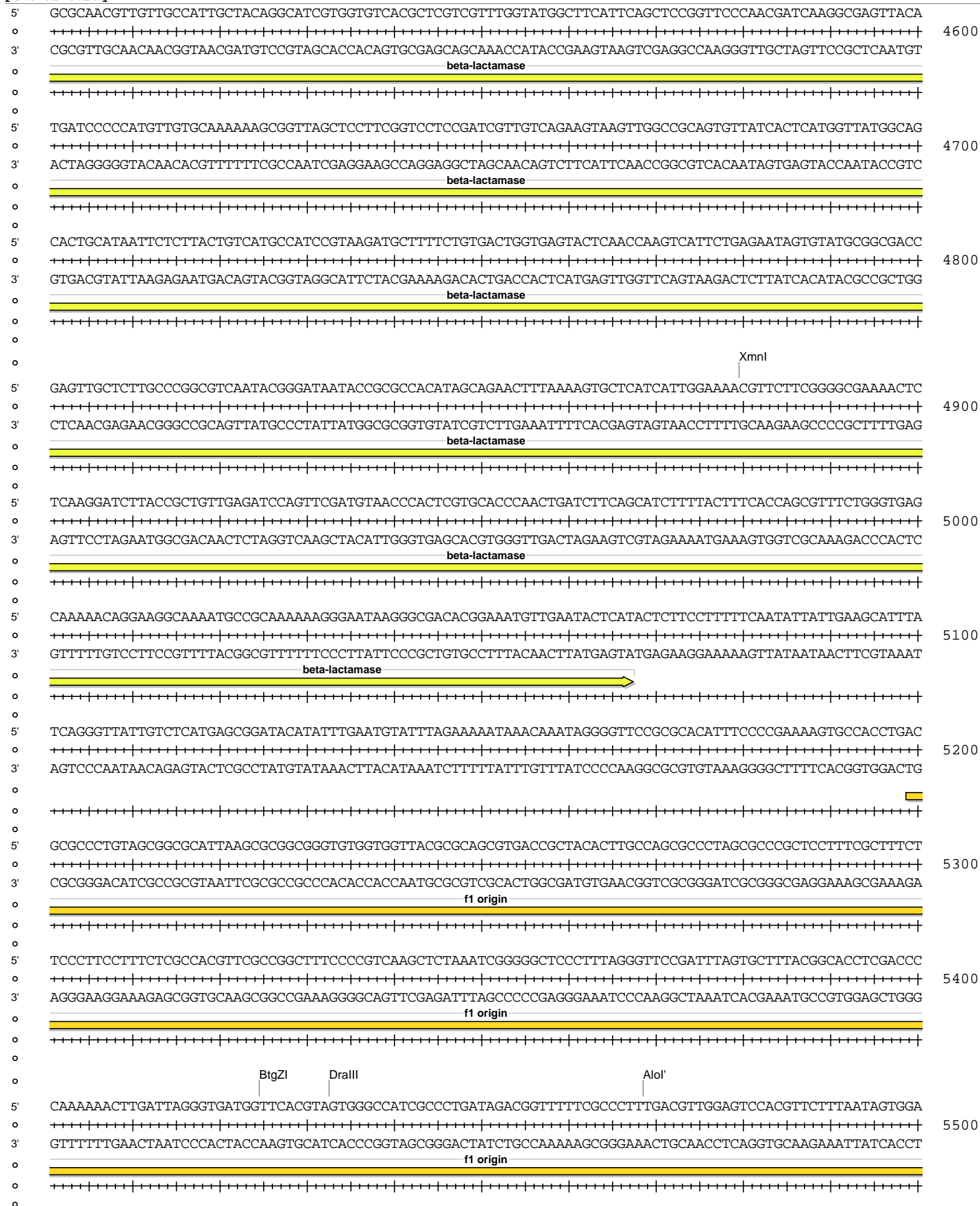


pGL3Basic.seq



```
5'  GGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCGTTTGTGCGCTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTC
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  3500
3'  CCGGTCTGTTTCCGGTCTTGGCATTTCCTCGGCGCAACGACCGCAAAAGGTATCCGAGGCCGGGGGACTGCTCGTAGTGTTTTAGCTGCGAGTTCAG
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
5'  AGAGGTGGCGAAACCCGACAGGACTATAAAGATAACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGGCGTCTCTGTTCGACCCCTGCCGTTACCGGATA
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  3600
3'  TCTCCACCGCTTTGGGCTGTCTGATATTTCTATGGTCCGCAAAGGGGACTTCGAGGAGCACCGGAGAGACAAGGCTGGGACGGCGAATGGCCTAT
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
5'  CCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGT
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  3700
3'  GGACAGGCGGAAAGAGGGAAGCCTTCGCACCGCGAAAGAGTATCGAGTGCACATCCATAGAGTCAAGCCACATCCAGCAAGCAGGTTCCGACCCGACA
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
5'  GTGCACGAACCCCCGTTAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAG
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  3800
3'  CACGTGCTTGGGGGCAAGTCGGCTGGCGACCGGAATAGGCCATTGATAGCAGAACTCAGGTTGGGCGATTTCTGTGCTGAATAGCGGTGACCGTCGTC
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
5'  CCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCCTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGG
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  3900
3'  GGTGACCAATGTCCTAATCGTCTCGCTCCATACATCCGCCACGATGTCTCAAGAACTTCACCACCGGATTGATGCCGATGTGATCTTCTTGCATAAACC
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
5'  TATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCCGCTGGTAGCGGTGGTTTTTTTGTGTTGC
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  4000
3'  ATAGACGCGAGACGACTTCGGTCAATGGAAGCCTTTTTCTCAACCATCGAGAACTAGGCCGTTTGTTTGGTGGCGACCATCGCCACCAAAAAAACAACG
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
5'  AAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGA
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  4100
3'  TTCGTGCTCTAATGCGCGTCTTTTTTCTAGAGTTCTTCTAGGAACTAGAAAAGATGCCCCAGACTGCGAGTCACCTTGCTTTTGTAGTGCAATTCCCT
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
5'  TTTTGGTCAATGAGATTATCAAAAAGGATCTTACCTTAGATCTTTTAAATTA AAAATGAAGTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTC
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  4200
3'  AAAACCAGTACTCTAATAGTTTTCTAGAAAGTGGATCTAGGAAAATTAATTTTTACTTCAAATTTAGTTAGATTTCATATATACTCATTGTAACCAG
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
                    AhdI
                    |
5'  TGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCCATAGTTGCCCTGACTCCCCGTCGTGTAGATAACTACG
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  4300
3'  ACTGTCAATGGTTACGAATTAGTCACTCCGTGGATAGAGTCGCTAGACAGATAAAGCAAGTAGGTATCAACGGACTGAGGGGCAGCACATCTATTGATGC
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
                    beta-lactamase
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
                    Bsal
                    |
5'  ATACGGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACAGCCAGCCGGAA
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  4400
3'  TATGCCCTCCGGAATGGTAGACCGGGGTCACGACGTACTATGGCGCTCTGGGTGCGAGTGGCCGAGGCTAAATAGTCTTATTGGTGGTTCGGCCTT
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
                    beta-lactamase
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
                    AseI
                    |
5'  GGGCCGAGCGCAGAAGTGGTCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCCGCCAGTTAATAGTTT
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  4500
3'  CCGGCTCGCGTCTTCAACAGACGTTGAAATAGGCGGAGGTAGGTGAGATAAATAACAACGCCCTTCGATCTCATTCATCAAGCGGTC AATTATCAAA
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
                    beta-lactamase
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
```

pGL3Basic.seq





pGL3Basic.seq

