

pMSCV-puro-GFP-miR-27a SPONGE

Absent Sites	0	AarI, AbsI, Accl, AflI, AflI', Apal, AsiSI, AvrII, BamHI, BarI, BarI', BbsI, BclI, BpI, BpI', BsaAI, BsaBI, BstBI, BstXI, BstZ17I, CspCI, CspCI', FseI, FspAI, HincII, HpaI, MauBI, MfeI, MluI, MreI, NruI, PacI, PflMI, PmeI, PmlI, PshAI, PstI, PspOMI, PspXI, PstI, PstI', Sall, SandI, SbfI, SfiI, SgrDI, SnaBI, SrfI, Swal, XcmI, XhoI
AfIII	1	4689
AjuI	1	2264
AjuI'	1	2296
ArsI	1	1732
ArsI'	1	1700
BglIII	1	1411
BpI	1	2719
BsiWI	1	3022
BsmI	1	2877
BspMI	1	2955
BtgZI	1	1559
Clal	1	3620
DraIII	1	3537
EcoRI	1	2436
HindIII	1	2957
NcoI	1	1436
NdeI	1	6753
NotI	1	2158
NsiI	1	3619
PciI	1	4689
RsrII	1	3082
SacII	1	3180
Scal	1	6062
SgrAI	1	7125

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5' TGAAAGACCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGAAGGCATGGAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGG
 100
 3' ACTTCTGTTGGGTGGACATCCAAACCGTTCGATCGAATTCATTGCGGTAAAACGTTCCGTACCTTTTATGTATTGACTCTTATCTCTTCAAGTCTAGTTCC
 5' pCMV LTR

5' TTAGGAACAGAGAGACAGCAGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCG
 200
 3' AATCCTTGTCTCTCTGTGCTTATACCCGGTTTGTCTTATAGACACCATTTCGTCAAGGACGGGGCCGAGTCCCGGTTCTTGTCTACCAGGGGTCTACGC
 5' pCMV LTR

5' GTCCCGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTC
 300
 3' CAGGGCCGGGAGTCGTCAAAGATCTCTTGGTAGTCTACAAAGTCCACGGGGTTCCTGGACTTTACTGGGACACGGAATAAACTTGATTGGTTAGTCAAG
 5' pCMV LTR

5' GCTTCTCGTCTCTGTTCGCGCCTTCTGCTCCCCGAGCTCAATAAAAAGAGCCACAAACCCCTCACTCGGCGCGCAGTCTCCGATAGACTGCGTCGCCC
 400
 3' CGAAGAGCGAAGACAAGCGCGGAAGACGAGGGGCTCGAGTTAATTTCTCGGGTGTGGGGAGTGAGCCGCGCGGTGAGGAGGCTATCTGACGCAGCGGG
 5' pCMV LTR

5' GGGTACCCGTATTCCCAATAAAGCCTCTTGCTGTTTGCATCCGAATCGTGGACTCGCTGATCCTTGGGAGGGTCTCCTCAGATTGATTGACTGCCACCT
 500
 3' CCCATGGGCATAAGGGTTAATTTGCGGAGAACGACAAACGTAGGCTTAGCACCTGAGCGACTAGGAACCCCTCCAGAGGAGTCTAACTAACTGACGGGTGGA
 5' pCMV LTR

5' CGGGGTCTTTTCAATTTGGAGGTTCCACCGAGATTGGAGACCCCTGCCAGGGACCACCGACCCCCCGCGGGAGGTAAGCTGGCCAGCGGTCTGTTTCG
 600
 3' GCCCCAGAAAGTAAACCTCCAAGGTGGCTCTAAACCTCTGGGGACGGGTCCCTGTTGGCTGGGGGGCGGCCCTCCATTCGACCGGTGCGCAGCAAAGC
 5' pCMV LTR

Pack Signal

5' TGTCTGTCTCTGTCTTGTGCGTGTGTGCGCCGCATCTAATGTTTGGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGG
 700
 3' ACAGACAGAGACAGAAACACGCACAAACACGGCCGTAGATTACAAACCGCGACGCAGACATGATCAATCGATTGATCGAGACATAGACCGCTGGGCACC
 Pack Signal

5' TGGAATGACGAGTTCTGAACACCCGGCCGCAACCTGGGAGACGTCCCAGGGACTTTGGGGCCGTTTGTGGCCCGACCTGAGGAAGGGAGTCGATG
 800
 3' ACCTTGACTGCTCAAGACTTGTGGGCCGGCGTTGGGACCTCTGCAGGGTCCCTGAAACCCCGGCAAAAACACCGGGCTGGACTCCTTCCTCAGCTAC
 Pack Signal

5' TGGAATCCGACCCCGTCAGGATATGTGGTTCTGGTAGGAGACGAGAACC TAAAACAGTTCCCGCCTCCGTCTGAATTTTGTCTTTCGGTTTGAACCGAA
 900
 3' ACCTTAGGCTGGGGCAGTCTTATACACCAAGACCATCCTCTGCTCTTGGATTTTGTCAAGGGCGGAGGCAGACTTAAAAACGAAAGCCAAACCTTGGCTT
 Pack Signal

5' GCCGCGCTCTGTCTGCTGCAGCGCTGCAGCATCGTTCGTGTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTAGGGCCAGACTGTCTAC
 1000
 3' CGGGCGCAGAAACAGACGACGTCGCGACGTCGTAGCAAGACACAAACAGAGACAGACTGACACAAAGACATAAACAGACTTTTAATCCCGGTCTGACAATG
 Pack Signal

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5' CACTCCCTTAAGTTTACCTTAGGTCACCTGGAAGATGTCGAGCGGATCGCTCACACCAGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTCTGC
 1100
 3' GTGAGGGAATCAAACTGGAATCCAGTGACCTTTCTACAGCTCGCCTAGCGAGTGTGGTCAGCCATCTACAGTTCTTCTCTGCAACCCAATGGAAGACG
 Pack Signal

5' TCTGCAGAATGGCCAACCTTTAACGTCGGATGGCCGCGAGACGGCACCTTTAACCGAGACCTCATCACCAGGTTAAGATCAAGGTCTTTTACCTGGCC
 1200
 3' AGACGCTTTACCGGTTGGAATTCAGCCTACCAGCGCTCTGCCGTGGAATTTGGCTCTGGAGTAGTGGGTCCAATTCTAGTTCCAGAAAAGTGGACCGG
 Pack Signal

5' CGCATGGACACCCAGACCAGGTCCCCTACATCGTGACCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACACCCTAAGCCTCC
 1300
 3' GCGTACCTGTGGGTCTGGTCCAGGGGATGTAGCACTGGACCTTCGGAACCGAAACTGGGGGAGGGACCCAGTTCGGGAAACATGTGGGATTCGGAGG
 Pack Signal

5' GCCTCTCTTCTCCATCCGCCCCGTCTCTCCCCTTGAACCTCCTCGTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCACTCCTTCTCTAGGC
 1400
 3' CGGAGGAGAAGGAGGTAGGCGGGGCGAGAGGGGGAACCTGGAGGAGCAAGCTGGGGCGGAGCTAGGAGGGAAATAGGTGGGAGTGAGGAAGAGATCCG
 Pack Signal

BglII NcoI
 5' GCCGGAATTAGATCTccagcgtgaccggtgcccaccatggtgagcaagggcgaggagctgttcaccggggtggtgcccatcctggtcgagctggacggcg
 1500
 3' CGGCCTTAATCTAGAggtcgactggccagcgtggtaccactcgttcccgtcctcgacaagtggccccaccacgggtaggaccagctcgacctgccgc
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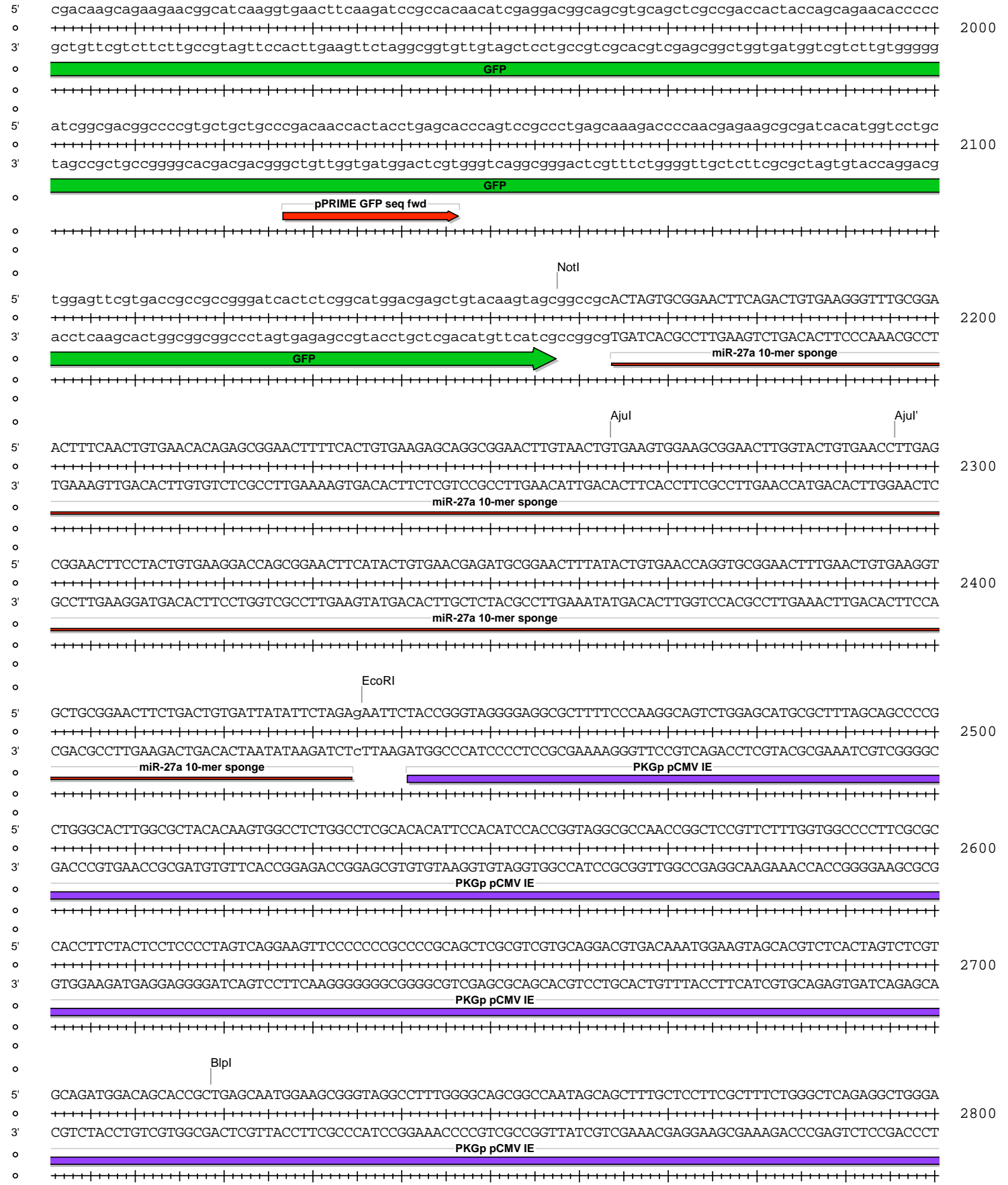
BtgZI
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 3' tgcatttgcgggtgttcaagtcgcacaggccgctcccgtcccgtacggtggatgcccgttcgactgggacttcaagtagacgtggtggcgttcgacgg
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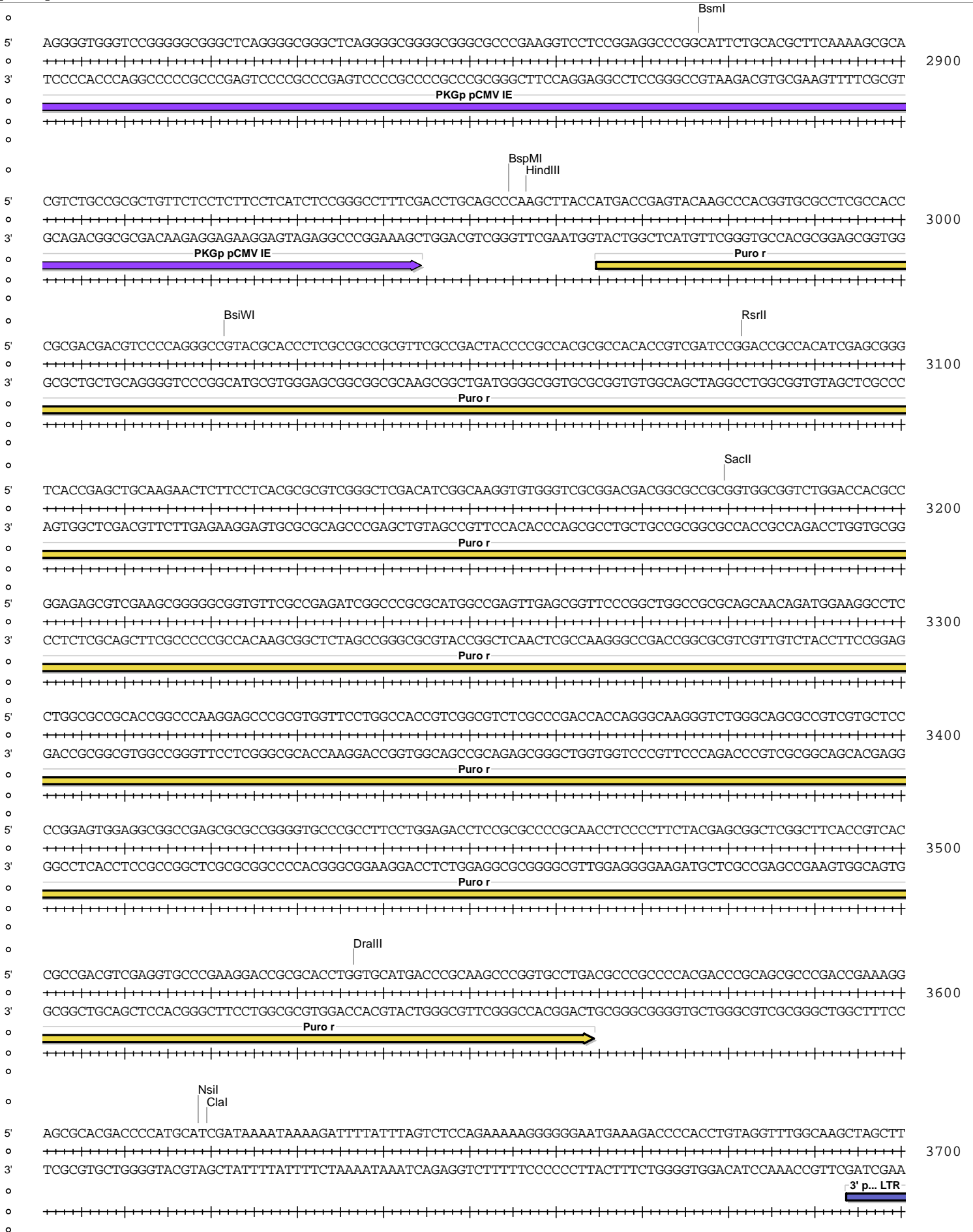
ArsI
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 1700
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 GFP

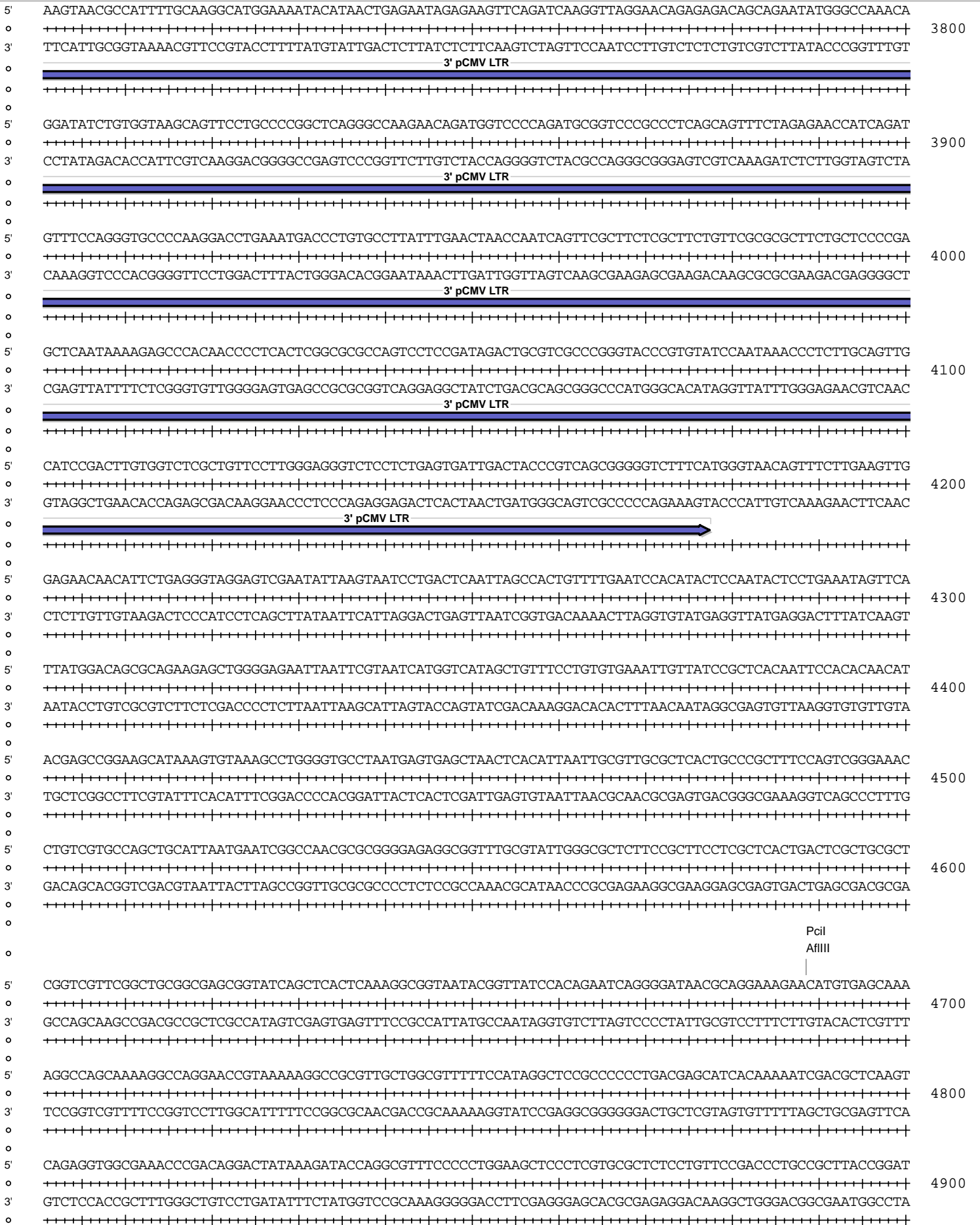
ArsI
 5' atgcccgaaggctacgtccaggagcgcaccatcttcttcaaggacgacggcaactacaagaccgcgccgaggtgaagttcgagggcgacaccctggtga
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 3' tacgggcttccgatgcaggtcctcgcgtggtagaagaagttcctgctgcccgtgatgttctgggcgaggctccacttcaagctcccgtgtgggaccact
 GFP

5' accgcatcgagctgaaggcatcgacttcaaggaggacggcaacatcctggggcacaagctggagtacaactacaacagccacaacgtctatatcatggc
 1900
 3' tggcgtagctcgacttcccgtagctgaagttcctcctgcccgtttaggaccccgtgttcgacctcatgtgatgttgcggtgtgcagatatagtaccg
 GFP

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5' ACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTG
+ + + + + 5000
3' TGGACAGGCGGAAAGAGGGAAGCCCTTCGCACCGCGAAAGAGTATCGAGTGCACATCCATAGAGTCAAGCCACATCCAGCAAGCGAGGTTTCGACCCGAC
+ + + + +
o
o
5' TGTGCACGAACCCCGTTCAGCCCAGCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCA
+ + + + + 5100
3' ACACGTGCTTGGGGGCAAGTCGGGCTGGCGACCGGAATAGGCCATTGATAGCAGAACTCAGGTTGGGCCATTCTGTGCTGAATAGCGGTGACCGTCGT
+ + + + +
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o
5' GCCACTGGTAAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTG
+ + + + + 5200
3' CGGTGACCATGTCTCTAATCGTCTCGCTCCATACATCCGCCACGATGTCTCAAGAACTTACCACCGGATTGATGCCGATGTGATCTTCTGTGCATAAAC
+ + + + +
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5' GTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTG
+ + + + + 5300
3' CATAGACGCGAGACGACTTCGGTCAATGGAAGCCTTTTCTCAACCATCGAGAACTAGGCCGTTTGGTTGGTGGCGACCATCGCCACCAAAAAACAAC
+ + + + +
o
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5' CAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGG
+ + + + + 5400
3' GTTCGTCGCTAATGCGCGTCTTTTTCTTAGAGTCTTCTAGGAACTAGAAAAGATGCCCCAGACTGCGAGTCACCTTGCTTTTGAAGTCAATTTCC
+ + + + +
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5' ATTTTGGTCAAGATATCAAAAAGGATCTTACCTAGATCCTTTTAAATTAATAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGT
+ + + + + 5500
3' TAAACAGTACTCTAATAGTTTTCTTAGAAGTGGATCTAGGAAATTTAATTTTACTTCAAAATTTAGTTAGATTTTCAATATACTCATTTGAACCA
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5' CTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCCATAGTTGCTGACTCCCGCTCGTGTAGATAACTAC
+ + + + + 5600
3' GACTGTCAATGGTTACGAATTAGTCACTCCGTGGATAGAGTCGCTAGACAGATAAAGCAAGTAGGTATCAACGGACTGAGGGGCAGCACATCTATTGATG
+ + + + +
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5' GATACGGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACAGCCAGCCGGA
+ + + + + 5700
3' CTATGCCCTCCCGAATGGTAGACCGGGTACAGACGTTACTATGCGCCTCTGGGTGCGAGTGGCCGAGGCTAAATAGTCGTATTGTGGTGGTGGCCCT
+ + + + +
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5' AGGGCCGAGCGCAGAAGTGGTCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTTGTTGCCGGGAAGCTAGAGTAAGTAGTTCCGCAAGTAAAGTT
+ + + + + 5800
3' TCCCGGCTCGCGTCTTACCAGGACGTTGAAATAGCGGAGGTTAGGTGAGATAAATAACAACGGCCCTTCGATCTCATTCAAGCGGTCAATTATCAA
+ + + + +
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5' TGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTACGCTCGTCTGTTGGTATGGCTTCATTAGCTCCGGTTCCAACGATCAAGGCGAGTTAC
+ + + + + 5900
3' ACGGTTGCAACAACGGTAACGATGTCCGTAGCACCACAGTGCAGCAGCAAAACCATACCGAAGTAAGTTCGAGGCCAAGGGTTGCTAGTTCCGCTCAATG
+ + + + +
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5' ATGATCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCCCTCCGATCGTTGTCAGAAAGTAAGTTGGCCGAGTGTATCACTCATGGTTATGGCA
+ + + + + 6000
3' TACTAGGGGTACAACACGTTTTTTCGCCAATCGAGGAAGCCAGGAGGCTAGCAACAGTCTTCAATTCACCGGCGTCACAATAGTGAGTACCAATACCGT
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