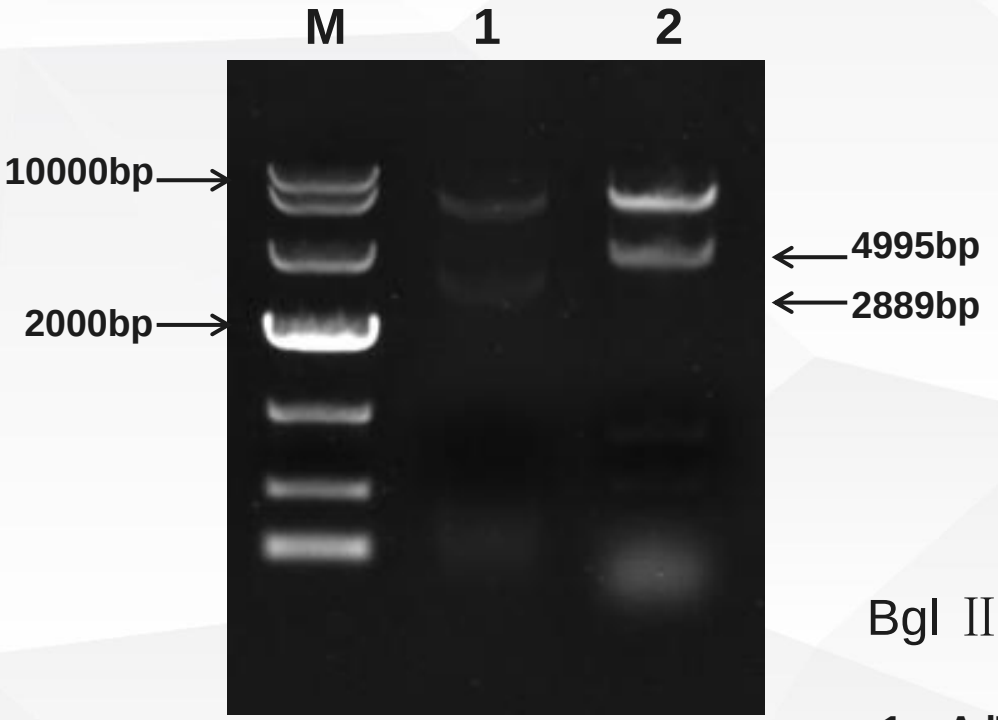
Primer sequence

ATG5-F(正向)
5’ GTCAGATCCGCTAGAGATCTGCTTACTAAGTTTGGCTTTGGTT 3’
ATG5-R(反向)
5’ GATATCTTATCTAGAAGCTTAAGGGTGACATGCTCTGATAAAT 3’
ATG7-F(正向)
5’-GTCAGATCCGCTAGAGATCTAAATAATGGCGGCAGCTACGG -3’
ATG7-R(反向)
5’-GATATCTTATCTAGAAGCTTGGGCCATCTCAGATGGTCTCATC-3’

Enzyme site: BglⅡ、HindⅢ

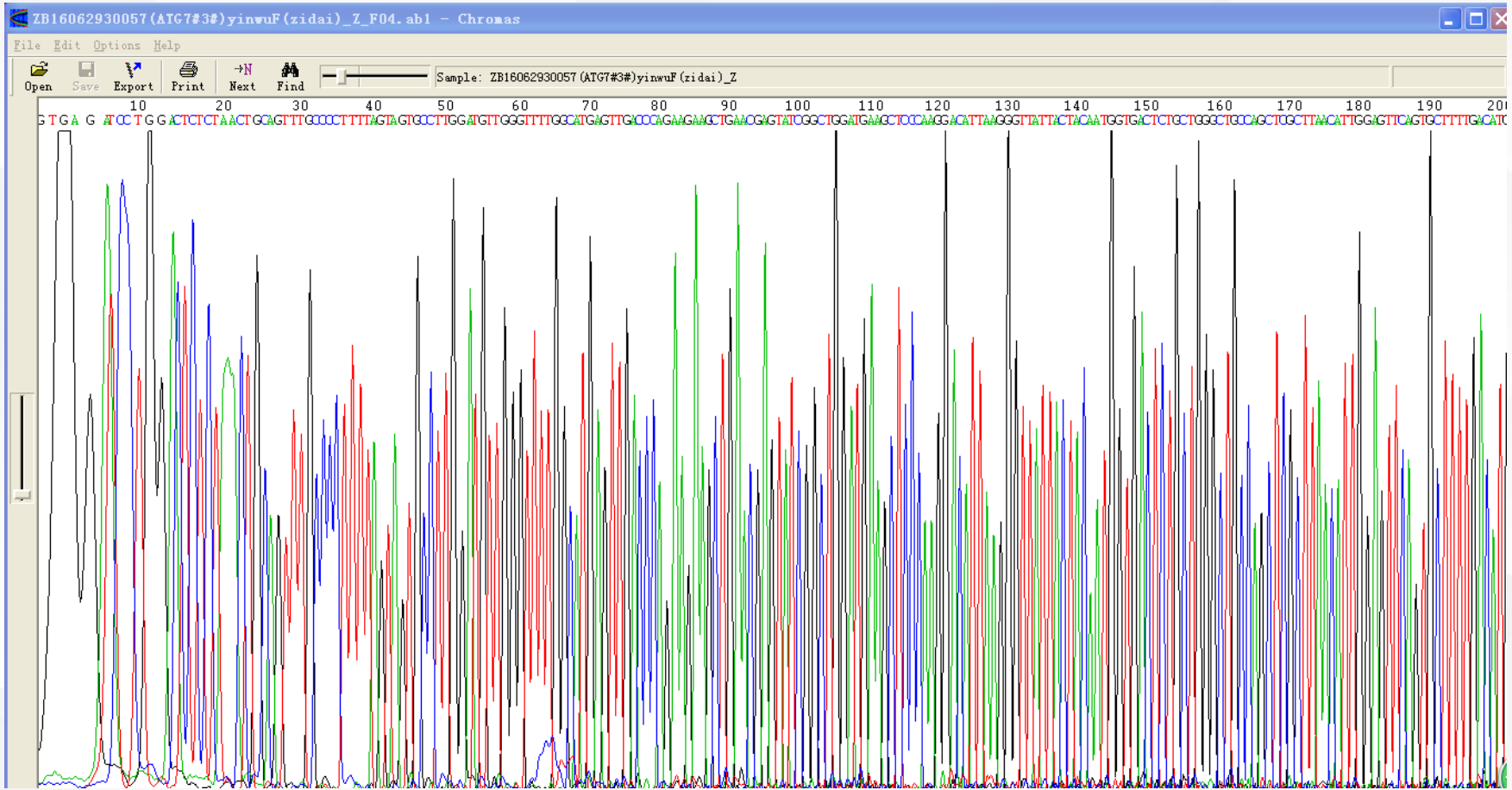
pAdTrack-ATG7 plasmid endonuclease digesting and DNA sequencing



Bgl Ⅱ、Hind Ⅲ(pAdTrack-ATG7)

1: pAdTrack-CMV; 2: pAdTrack-ATG7

ATG7 sequencing



ATG7 sequencing

GTGAGATCCTGGACTCTCTAACTGCAGTTTGCCCCTTTTAGTAGTGCCTTGGATGTTGGGTTTT
GGCATGAGTTGACCCAGAAGAAGCTGAACGAGTATCGGCTGGATGAAGCTCCCAAGGACATT
AAGGGTTATTACTACAATGGTGACTCTGCTGGGCTGCCAGCTCGCTTAACATTGGAGTTCAGT
GCTTTTGACATGAGTGCTCCCACCCCAGCCCGTTGCTGCCCAGCTATTGGAACACTGTATAAC
ACCAACACACTCGAGTCTTTCAAGACTGCAGATAAGAAGCTCCTTTTGGAACAAGCAGCAAAT
GAGATATGGGAATCCATAAAATCAGGCACTGCTCTTGAAAACCCTGTACTCCTCATCAAGTTCC
TCCTCTTGACATTTGCAGATCTAAAGAAGCACCACTTCTACTATTGGTTTTGCTATCCTGCCCTC
TGTCTTCCAGAGAGTTTACCTCTCATTCAGGGGCCAGTGGGTTTGGATCAAAGGTTTTCACTA
AAACAGATTGAAGCACTAGAGTGTGCATATGATAATCTTTGTCAAACAGAAGGAGTCACAGCTC
TTCCTTACTTCTTAATCAAGTATGATGAGAACATGGTGCTGGTTTCCTTGCTTAAACACTACAGT
GATTTCTTCCAAGGTCAAAGGACGAAGATAACAATTGGTGTATATGATCCCTGTAACTTAGCCC
AGTACCCTGGATGGCCTTTGAGGAATTTTTTGGTCCTAGCAGCCCACAGATGGAGTAGCAGTT
TCCAGTCTGTTGAAGTTGTTTGCTTCCGTGACCGTACCATGCAGGGGGCGAGAGACGTTGCC
CACAGCATCATCTTCGAAGTGAAGCTTCCAGAAATGGCATTTAGCCCAGATTGTCCTAAAGCA
GTTGGGATGGGAAAAGAACCAGAAAGGAGGCATGGACCAAGATGGTGAACCTCAGTGATGTA
TGGACCCTAAAGTTAGCTGAGTCATCAGTGGATCTAATCTCAACTGATGTGTGAGATGGCTACT
TTAGACTGACAGTGTGTCTGTCAATGTCTGCTGCTGAGCGCACTGGAGCATGTAGCTAGACGT
GATGGATGGGGCGTGGACCAATCACGGTTGTGGACAATGCCCAGATTCTCTAACTCCGATCTT
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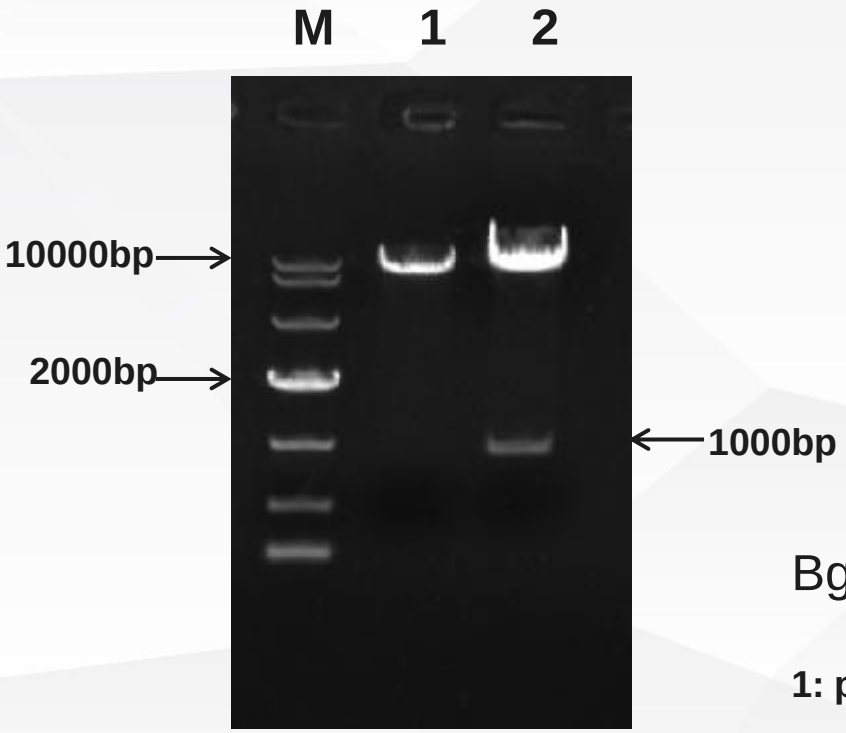
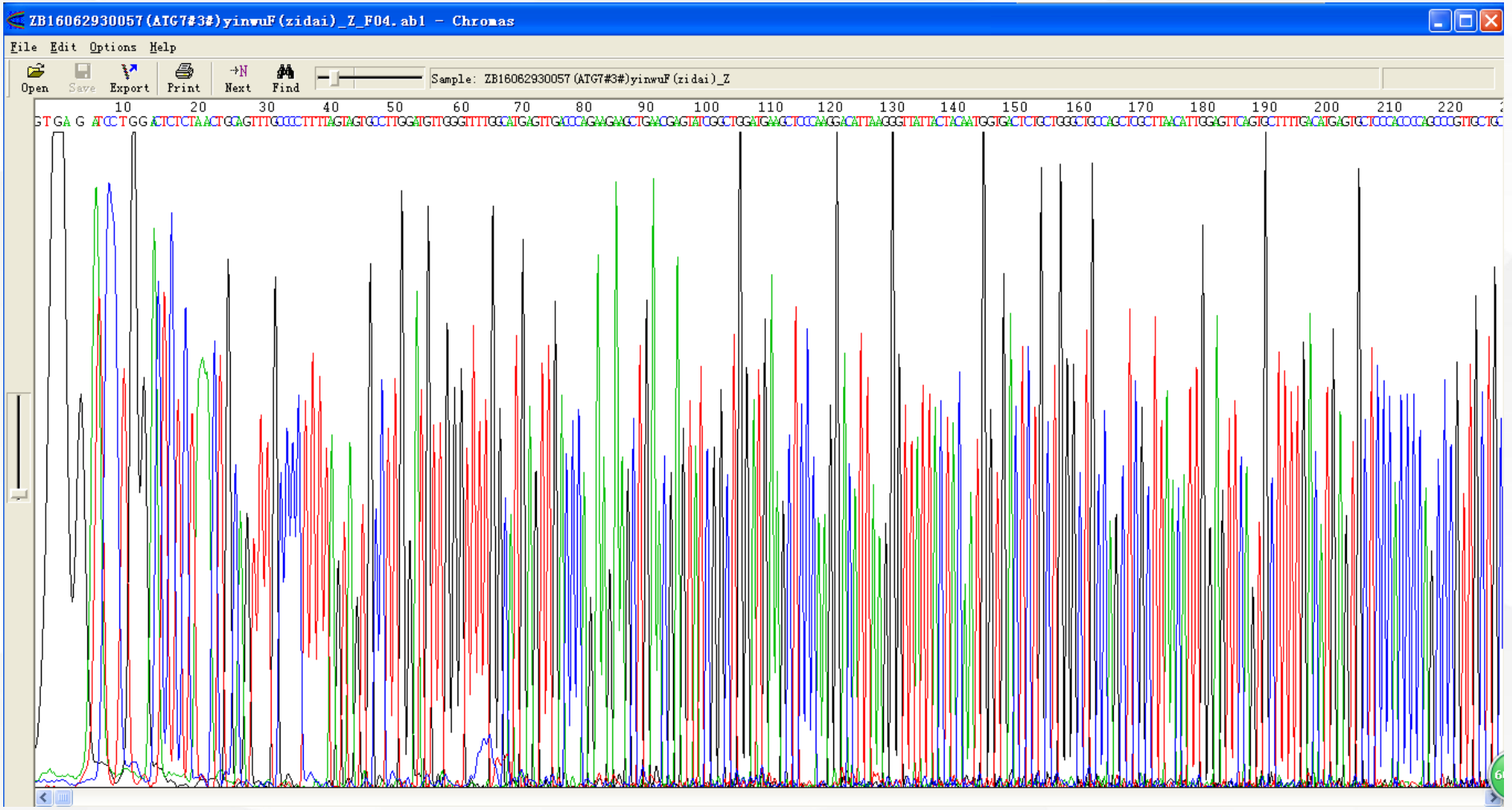
pAdTrack-ATG5 plasmid endonuclease digesting and DNA sequencing



Bgl Ⅱ、Hind Ⅲ(pAdTrack-ATG5)

1: pAdTrack-CMV; 2: pAdTrack-ATG5

ATG5 sequencing



ATG5 sequencing

AAGGAATAAAGAATTTAGCCTGTATGTACTGCTTTAACTCCTGGAAGAATGACAGATGACAAAGAT
GTGCTTCGAGATGTGTGGTTTGGACGAATTCCAACTTGTTTCACGCTATATCAGGATGAGATAAC
TGAAAGGGAAGCAGAACCATACTATTTGCTTTTGCCAAGAGTAAGTTATTTGACGTTGGTAACTG
ACAAAGTGAAAAAGCACTTTCAGAAGGTTATGAGACAAGAAGACATTAGTGAGATATGGTTTGAA
TATGAAGGCACACCACTGAAATGGCATTATCCAATTGGTTTGCTATTTGATCTCCTTGCATCAAGT
TCAGCTCTTCCTTGGAACATCACAGTACATTTTAAGAGTTTTCCAGAAAAAGACCTTCTGCACTG
TCCATCTAAGGATGCAATTGAAGCTCATTTTATGTCATGTATGAAAGAAGCTGATGCTTTAAAACAT
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TGACAGATTTGACCAGTTTTGGGCCATCAATCGGAAACTCATGGAATATCCTGCAGAAGAAAATG
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TTCGTCCTGTGGCTGCAGATGGACAGTTGCACACACTAGGAGATCTCCTCAAAGAAGTTTGTCC
TTCTGCTATTGATCCTGAAGATGGGGAAAAAAAGAATCAAGTGATGATTCATGGAATTGAGCCAA
CGTTGGAAACACCTCTGCAGTGGCTGAGTGAACATCTGAGCTACCCGGATAATTTTCTTCATATT
AGTATCATCCCACAGCCAACAGATTGAAGGATCAACTATTTGCCTGAACAGAATCATCCTTAAATG
GGATTTATCAGAGCATGTCACCCTTAAGCTTCTAGATAAGATATCCGATCCACCGGATCTAGATAA
CTGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAACCTCCCACACCTCC
CCTGAACCTGAAACATAAATGATGCATTGTGTGTTAACTTGTTTTATTGCAGCTATATGGTACAAAT
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CAACTATCATGATCCTAACGCGGAGGTTTATCGACGACTGTCTAGTGATTATTAGGTTAATTC