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**AcCANDI N-term FINISHED - DNA DEST SEQUENCE VERIFIED**

The figure displays a genomic map with two main horizontal lines representing DNA strands. The top strand shows the PH promoter region, which includes a blue box labeled "PH promoter" and a blue arrow pointing upwards. A blue triangle marks the transcription start site. The bottom strand shows the TK gene region, which includes a blue box labeled "TK gene" and a blue arrow pointing downwards. Several restriction sites are indicated by colored boxes: an orange box labeled "m..." at position 1560, a yellow box labeled "K...C" at position 1820, and red boxes labeled "8XHis", "StrepTagII", and "attR1" at positions 1690, 1750, and 1820 respectively. The map also features a series of tick marks along both strands.

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The figure displays a genomic map of a DNA sequence, likely from *Phytophthora*, focusing on the **Pp10 promoter**. The sequence is shown as a series of horizontal lines with vertical tick marks indicating nucleotide positions. Key features include:

- TK gene:** Located at approximately position 3120.
- Promoters:** Several promoters are indicated by blue bars above the sequence:
  - PIE-1(0) promoter:** Located between positions 3250 and 3380.
  - PIE-1(0) promoter:** Located between positions 3510 and 3640.
  - PIE-1(0) promoter:** Located between positions 3770 and 3900.
  - Pp10 promoter:** Located between positions 4030 and 4290.
  - LacZ:** Indicated by a blue bar spanning the region from approximately 4290 to 4550.
  - LacZ:** Indicated by a blue bar spanning the region from approximately 4550 to 4680.
  - LacZ:** Indicated by a blue bar spanning the region from approximately 4680 to 4810.
  - LacZ:** Indicated by a blue bar spanning the region from approximately 4810 to 4940.
  - LacZ:** Indicated by a blue bar spanning the region from approximately 4940 to 5070.
  - LacZ:** Indicated by a blue bar spanning the region from approximately 5070 to 5200.
  - LacZ:** Indicated by a blue bar spanning the region from approximately 5200 to 5330.
  - LacZ:** Indicated by a blue bar spanning the region from approximately 5330 to 5460.
- Restriction Enzyme Sites:**
  - SbfI:** Located at position 3250.
  - SrfI:** Located at position 3380.
  - Bsu36I:** Located at position 4160.
  - MauBl:** Located at position 5460.
- Transcription Start Sites:** Indicated by arrows pointing to the left of the sequence line.

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The diagram illustrates the lambda phage genome, which consists of approximately 58,000 base pairs. The genome is represented by a horizontal blue line with vertical tick marks indicating nucleotide positions. Several key features are highlighted:

- LacZ Gene:** Located at approximately position 5590, this gene encodes beta-galactosidase. It is flanked by two PstI restriction sites.
- attR2 Site:** A red arrow pointing left is located at approximately position 7020, representing the right attachment site for lambda phage integration.
- attL2 Site:** A red arrow pointing right is located at approximately position 7150, representing the left attachment site for lambda phage integration.
- attR2 and attL2 Regions:** These regions are shown as red arrows spanning from approximately position 7020 to 7280 and 7150 to 7280 respectively, indicating the sites where the phage genome is integrated into the host bacterial chromosome.
- Other Genes:** Other genes are indicated by blue arrows, including the *cro* gene (position 5720-5850), *q<sub>pro</sub>* gene (position 5980-6110), and *q<sub>rel</sub>* gene (position 6240-6370).
- Regulatory Elements:** The *lacO* operator site is marked with an orange box at approximately position 7280.
- Start and Stop Codons:** The start codon (ATG) is at position 7410, and the stop codon (TAA) is at position 8450.

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**ACGANDI N-term FINISHED - DNA DEST. SEQUENCE VERIFIED**

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5'	tatttcaactaaatgcctagcgtcgatctttgaattgattgtcgcttcgtcgaaaatggccaaaccatttgacatttacgttttatgagggttgttgc当地	78910
o	+	+
5'	atgatacgcgtcgccgaaacacggcgatttgtatgttatgcacgcgtcgacgacacatggccggatcgacgttacttcattgtcgccgc当地	79040
o	+	+
5'	ttgcgttataaatatggactacggcgatttgtgattgagaagaatcttattcaataatggcaagatttgttataattttatgttccattattcgctgg当地	79170
o	+	+
5'	acaatattcgattgtacgacgaaaacggcttcgactcgatatacttgcacgcgttgc当地	79300
o	+	+
5'	gataccaacgcgttggtgccgttggtggagagaagcaaagaaatcaactgc当地	79430
o	+	+
5'	aatttgaacatgtatattttcgaaaagtgcattgtatattgc当地	79560
o	+	+
5'	ggcagcgtgaaatttggccgc当地	79690
o	+	+
5'	atatcaccgttgc当地	79820
o	+	+
5'	tggcggatgc当地	79950
o	+	+
5'	ggttatggacaaaacaaaagatttacattacagattgtcgatgtt当地	80080
o	+	+
5'	tgtataactacatgc当地	80210
o	+	+
5'	acgggtatgtcgctgc当地	80340
o	+	+
5'	ttaaccgacttgc当地	80470
o	+	+
5'	ggcagtc当地	80600
o	+	+
5'	cagcgtatgtcgacttgc当地	80730
o	+	+
5'	aggtaggtgttaggagaataggc当地	80860
o	+	+
5'	ggaggtataagggtgttaggtgttaggtgttaggtgt当地	80990
o	+	+
5'	taggtgtgtacaattgggatgttaggtgt当地	81120
o	+	+
5'	gttgcttaatataaaatggatgtt当地	81250
o	+	+
5'	gttaatgtggaaaatctactgc当地	81380
o	+	+
5'	cgatgttgc当地	81510
o	+	+
5'	tcattgtttcaactgtcgat当地	81640
o	+	+
5'	ggctggcacgcaatgtgtgt当地	81770
o	+	+
5'	tctttgtatttcatcaacacgc当地	81900
o	+	+
5'	ctttgtacggaaaaacggcgctcgat当地	82030
o	+	+
5'	tattttcgaaaatattacacgc当地	82160
o	+	+
5'	gaggggttttacaaacaccacgttgc当地	82290
o	+	+
5'	ttttgaattttcgctc当地	82420
o	+	+
5'	aaacaaatcatgtgggatgtgt当地	82550
o	+	+
5'	tggaaattagacgagaacaacaatgc当地	82680
o	+	+

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AcCANDI N-term FINISHED - DNA DEST SEQUENCE VERIFIED

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I - SANDBY N/A FINISHED BYA BEST SEQUENCE VERIFIED

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1 SAMPLE NUMBER FINISHED RNA PROF SEQUENCE VERIFIED

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AcCANDI	N-term FINISHED - DNA DEST	SEQUENCE	VERIFIED
5'	ttctatataattttaataaaacgataaccgcgttgttttagaggcataataaaaagaaatattgttatcggttcgcattagggcagtataaaattgacgttcatgttgatattgttcagtt		129610
0			
5'	gcaagttgacactggccgacaagatcgtaacaaccaagtgactatgacgcaaattaatttaacgcgtcgacaccagcgcttcgcacgcccggcagcgtcgacaacagctattcagagtt		129740
0			
5'	tgtgataaacaaccaacgactatattaagtattataaccatcccacccggatggagccgacacggtgatctgcacagcgagactcgccgagcttcaaacttttggcaagcgtcaactcgtaact		129870
0			
5'	ataatgatTTtagtggaatgttgcataagaccactgataatctcgaaAGAAGCAGTTAGTCTGTTATTATCGGAATCCCTGAGCAGCTGTGGAGCAACCACGCCAGTTCTGTTATCATGC		130000
0			
5'	ggaatctttgagattctgctgggtgaaccacatcgcaactggaaACTACCGGAAGCTGGACGAATACTGGACAATTCCAAAGGTGTGGCCAGTTAACAAAATTGAGGCCTAA		130130
0			
5'	tacaagaaaAGCACAATTCAAAGCTGTCAACCCCTGAACAGACAATTACACACGAAACATTGACCGTCGCTCAACTCAAGAAATTACGCATTATTTACTAATGATTTGCCGTATTTAA		130260
0			
5'	tgcgttgcacgacaacgactacaattccaaACAGTTCTCGACCATAATGTCGAAACTGGTTATTACATGTTGGTTAAAAAAGTGAAGTGAAGCGTTGAAATTATATTGCAAGTACGTGAG		130390
0			
5'	caatgtggTTTACAATAACAAATTATTACATGGTAGATAATCGCGTTGGTAACCTTGATAAAATTAGGTTATGTTGACAATTGGTTAAAGAACCGGCATAGAAATTCTCAT		130520
0			
5'	tctcaagatgtgtcaacgacgagacggctgcacaaaATTGTTAAAGCCTTCGATGTGCACCCACGTTAAAGCTGCTCTGACTTCATATTAAATTAGATATGTTACCGCAGAACCA		130650
0			
5'	catttgcactttttacaatcgtggcgaaAGAAATGTGGTTTTGAGCAAGTTGACAAATTACTTGCTTATTGCTTAGTCGAAAGAGATAATGTTACATGTTACATGTTACATGTTACAGAGAATG		130780
0			
5'	aatttagactgcataataattttttgtatcgccgtatgtgagtcataattaaAGTATTCCGAAAGTGTGCAAGTTCCCACAAATATGTTGGACAATTAAATTGTT		130910
0			
5'	aacaaaaaaAGTACGCTCACGTACAAACAGCAGCGCTGCTAACTTTTTGTTAAATTATAATCATGACAATTGCGAGATAATAACGAGAAAATTAAAAAGGTTAAGAAGGAGGACG		131040
0			
5'	gcagcatgcacattgtcgAACAGTATTGACTCAGAATGTAAGGGTACAATTGTTAGTATTGTTCAAAACGAGGAGCGATTGACTAGCTAAGAAAACAAGAGTTTATTG		131170
0			
5'	gatttctggcgaaATTAAAGATGTAGCGTTAGTCAGTAATTCAAAATATAATAGATTAAAGCATCACATGTTGTAATCGTTAAAGTGAACCAGAGAGAGCCTACATTGCAAAATTTGTTA		131300
0			
5'	aaattgttagTTTAAATTACAGGGTCTGGTCCGACGCTATAACGTTGCGGAACAAAACTAAATTGTTAAATTAAATTGCAATTAAATTATAATTTGAAATTAAATT		131430
0			
5'	aattatacatatatTTTATTTGTTTATTATCGAGGGGCCGTTGGTGTGGGTTTGCTAGAAATAACATGGAGTTGGCAGCTGCTGCACACCCACCTCTCTCTCT		131560
0			
5'	ttcatcatgtatctgtAGATAAAATTAACCTAAAACAGCCGCCTATCAACAAATGATAGGCATTAACCTGGCGTCGACTGTCACTAACGTTGACGATTGCGACTAACCTT		131690
0			
5'	catccccAGTAACCAACTAGCAGCAACTAAACCGAGTAAGGTTGATGACATGAGTTGGCCCGAGGAAGTCGCTAAATATCTACGTATTGAGGCGAATCTGGTCCG		131820
0			
5'	ggacggatcgctggcgacAAACTGTTTCTACTTCATAGTTGAATCCTGGCACATGTTGTTAGTCGGCGATTGTTAGGCAACAGGGTCAATGGCAACATCCGACTGATT		131950
0			
5'	agattgggtcttgcgacaAGTGCCTGCAATAACAGCAGGCCCGATTTCCCGCTTACCTGACATAATAACTCCGCCGTGTTATTGATGGCGTTGATTATCTGTACTAGT		132080
0			
5'	tggccgcgtAAACAGAAATAGCCCGGTGGCAGAGTATGCCGTTCTCTACTTTAAGCTTGTGATGTAACTATGTTAGACGGGGTTTGTGCGAGTGCCTTGAACACCTTCGGCGTGC		132210
0			
5'	cacgttggTTCCGGGAAGTTTTGTTGACTGCATTGGATCGCTCTGTTGGTGTGTTAATTAAAGTCTGGCACGTTGTCACCGCCGCAATTGGCTCAATGAGTTATTGAGGGCTGAAATGCC		132340
0			
5'	tgaAAATACTCCCGCTATGTTGGGGACATCATTGTTACGAGTAATTCTGTTATGTCAGTGTGAACTGCTCAACAAACTGGTTGTTAGATGTTGAGTGCCTGCTGAAATCTGTTCAATGTTGCGTACAC		132470
0			
5'	tggcgcgTTGAGCACATTGTTGAAACAGCGCGGAGTGCTGTTAAAAGACGCGTATTATCGATAATAAAACTGGCTGATTAGGATAACATTGACTGCGCAAGATTGAAAAAAACTCATTT		132600
0			
5'	aaAGCAAACTTATAATAATACAGTAAGGTTGCAAAACTGCCGTCGTAATACAACACGGCAGCGCGTCATGTTGTTAAATCTAACTTCTCCTGCTTAAATTCTGGCGAGAAG		132730
0			
5'	cgcattttgtgtAAAGTTCTGACGTCTGCATTGTTGTTGTAAGGTATCTCGACGTATGAGCAACTTAACATTGTTATAATTGATGCGCTCCACGGCGCGCGTGTACAT		132860
0			
5'	ggatgatATCTCTCATTGTTGATCGCTAAATTATACCGTTCAATAAAATGTTAAACCCAACATGTTAATTATAATATTCTATAATAGTTGTTGTTCAATAATTATTTACTGTTG		132990
0			
5'	aacttAAAAGAGGTGACGATGACGAATCAGACGACGGGTCAGTTGCTATAACAAACCAATTGGAGTAATTTCGCGATCTACTAGATGTCAGCTTCTACATGTTGTCGGTTAAATCAAAATT		133120
0			
5'	agagttaatCTGCCCTGAAGGATTGATCCAGATGTTAAAGACGCGTATTATCGAGATTGATGGATGACCGCTAACAAAACAAAAATAAAATTATAGATAATGAAATAAA		133250
0			
5'	atttatataGATTAATAAAATAATTATACATTATTTACACACTAACACTAACGTCAGACATAACAGTTGTAACCTAGAAACTACAGTTACTGCGCTCAAACCTG		133380
0			

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