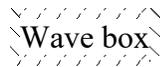


CCCGGCGTGCCTCATGCACGGCGCCGGCAGGCCTGCAGGTTCCCTCCCGTTTCCATTGAAA**GGACTACACA**ATGACT
GACGTTGTCATCGTATCCGCCGCCCGCACCCGCGTTCGGCAAGTTTGGCGGCTCGCTGGCCAAGATCCCGGCACCGGA
ACTGGGTGCCGTGGTTCATCAAGGCCGCGCTGGAGCGCGCCGGCGTCAAGCCGGAGCAGGTGAGCGAAGTCATCATGG
GCCAGGTGCTGACCGCCGGTTTCGGGCCAGAACCCCGCACGCCAGGCCGCGATCAAGGCCGGCCTGCCGGCGATGGTG
CCGGCCATGACCATCAACAAGGTGTGCGGCTCGGGCCTGAAGGCCGTGATGCTGGCCGCCAACGCGATCATGGCGGG
CG

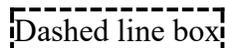
Pink highlighted: Coding Sequence (CDS) of *phbC* gene. Parts encoding start and stop codons, are shown in boxes at the beginning and the end of pink region.

 **Wave box**: Ribosome binding site.

Bold bases: Attachment sites for forward and reverse cloning primers.

Underlined sequences: Attachment sites for forward and reverse internal primers.

Boxes with two colored ends: Promoter sequences.

 **Dashed line box**: Sequence encoding start codon of next gene (*phbA* gene).

Blue part: Sequence encoding stop codon of prior gene.

Yellow highlighted: Terminator

Also according to NCBI database information, translation of the CDS part (pink in the region above) results in PHB synthase (polymerase) enzyme production. This protein sequence is as below and includes 589 amino acid residues.

```
/product="poly-beta-hydroxybuterate polymerase"  
/protein_id="AAA21975.1"  
  
/translation="MATGKGAAASTQEGKSQPFKVTGPFDPATWLEWSRQWQGTEGN  
GHAAASGIPGLDALAGVKIAPAQLGDIQORYMKDFSALWQAMAEGKAEATGPLHDRRF  
AGDAWRTNLPYRFAAAFYLLNARALTELADAVEADAKTRQIRIFAISQWVDAMSPANF  
LATNPEAQRLLES GGESLRAGVRNMEDLTRGKISQTDESAFEVGRNVAVTEGAVVF  
ENEYFQLLQYKPLTDKVHARPLLMVPPCINKYYILDLPESLVRHVVEQGHTVFLVS  
WRNPDASMAGSTWDDYIEHAAIRAIEVARDISGQDKINVLGFCVGGTIVSTALAVLAA  
RGEHPAASVTLTLLDFADTGILDVVFVDEGHVQLREATLGGGAGAPCALLRGLLELAN  
TFSFLRPNDLVWNYVVDNYLKGNTVPFDFLLFWNGDATNLPGPWYCWYLRHTYLQNEL  
KVPGKLTVCVGPVDLASIDVPTYIYGSREDHIVPWTAAAYASTALLANKLRFVLGASGH  
IAGVINPPAKNKRSHWTNDALPESPQQLAGAI EHHGSWWPDWTAWLAGQAGAKRAAP  
ANYGNARYRAIEPAPGRYVKAKA"
```

