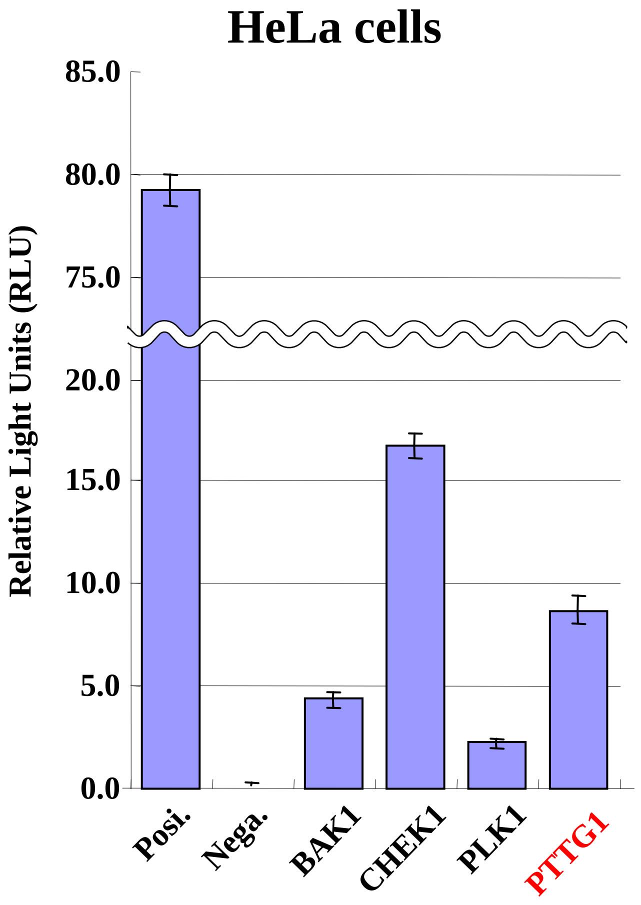
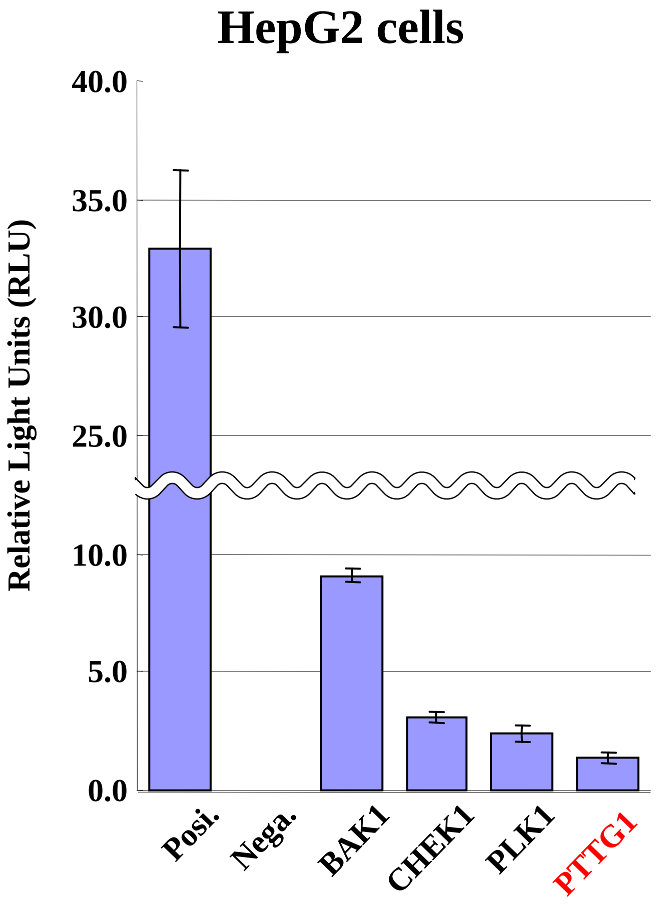
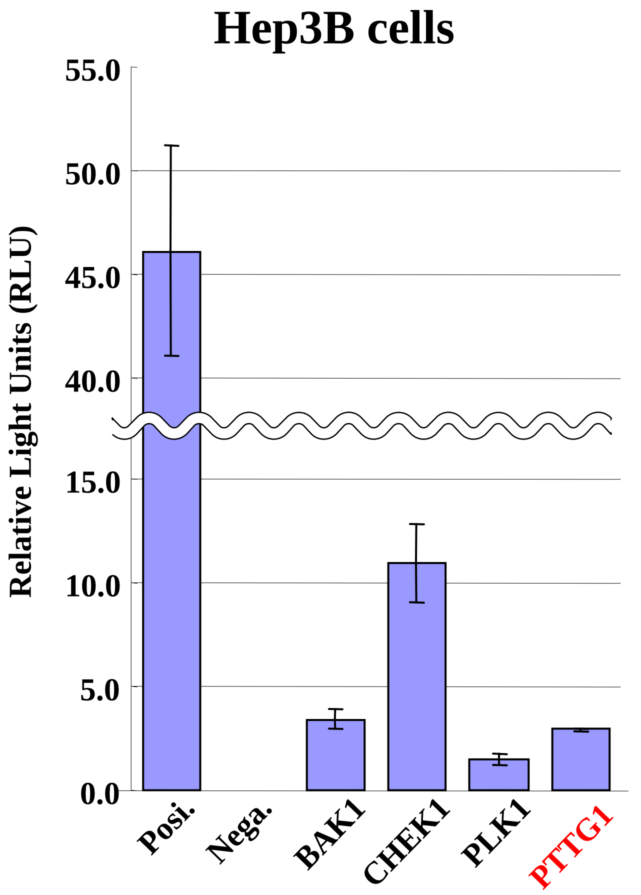
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

Posi.: pGL3 Control Vector
(SV40 promoter)
Nega.: Empty Vector

BAK1: pGL4-phBAK1 (RDB# 7318)
CHEK1: pGL4-CHEK1 (RDB# 7319)
PLK1: pGL4-phPLk1 (RDB# 7327)
PTTG1: pGL4-phPTTG1 (RDB#7329)

2009, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.03.02

1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5464

2nd Nucleotide Sequence
  File Name         : RDB7329F.fasta
  Sequence Size     : 683

  Unit Size to Compare = 1
  Pick up Location     = 1



[98.343% / 664 bp]     INT/OPT.Score : <   1784/  2560 >

     1’                      G GCCTAAC-TG GCCGGTACCT GAGCTCGCTA GCCTCGAGGA
                             * ******* ** ********** ********** **********
     1″ GTGCCAGAAC ATTATCTCTG GCCTAACTTG GCCGGTACCT GAGCTCGCTA GCCTCGAGGA

    41’ TTCTGTCTTT CCTCTTTTCT TCACCTTAAG TTAGGCTCTT TTCTTATAAC CTAGTATAAT
        ********** ********** ********** ********** ********** **********
    61″ TTCTGTCTTT CCTCTTTTCT TCACCTTAAG TTAGGCTCTT TTCTTATAAC CTAGTATAAT

   101’ GTCCAGCATT TAATAGGTAT TCAATAAATA TTTGTGAATG AATGAATCAT TCAATCAATA
        ********** ********** ********** ********** ********** **********
   121″ GTCCAGCATT TAATAGGTAT TCAATAAATA TTTGTGAATG AATGAATCAT TCAATCAATA

   161’ TTGGTCCTGA AATGCCAGGG AAAAAGAGAT GATGAACTGG CATATATTGA GAACCATGTC
        ********** ********** ********** ********** ********** **********
   181″ TTGGTCCTGA AATGCCAGGG AAAAAGAGAT GATGAACTGG CATATATTGA GAACCATGTC

   221’ TATGTCAGGT ATAGTGTCAA GCCTTTCGTG AAAGAGTAAT ATGGAATCAA CTCCTCTCTC
        ********** ********** ********** ********** ********** **********
   241″ TATGTCAGGT ATAGTGTCAA GCCTTTCGTG AAAGAGTAAT ATGGAATCAA CTCCTCTCTC
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281' TCAGCTGATC TGCAGCTTAA AATGCATATA TGGTGAACTG TGGGAAGCGG AGTTTGAATG
     ********** ********** ********** ********** ********** **********
301" TCAGCTGATC TGCAGCTTAA AATGCATATA TGGTGAACTG TGGGAAGCGG AGTTTGAATG

341' ACACAGGTCA GCCTTATGTT TTAATTTATA TCTTCATCTT GTAGTTGTTC AATGTATTCC
     ********** ********** ********** ********** ********** **********
361" ACACAGGTCA GCCTTATGTT TTAATTTATA TCTTCATCTT GTAGTTGTTC AATGTATTCC

401' ATTTTACTAT AGAAACAGGA AAAGGTCGTC AACTTTTTC- AAGCAAAATT TCTTTTCATA
     ********** ********** ********** *********  ********** **********
421" ATTTTACTAT AGAAACAGGA AAAGGTCGTC AACTTTTTCA AAGCAAAATT TCTTTTCATA

460' TCTGGGAAAT TGGAATTCCT TTTTTATATC TTTATTATCT CTCTGATATT CTCTTGCTCC
     ********** ****** *** ********** ********** ********** **********
481" TCTGGGAAAT TGGAATCCCT TTTTTATATC TTTATTATCT CTCTGATATT CTCTTGCTCC

520' CTGGCCAAGC CCTTCCAGGC AACTTTGGTT AATATATTAT TGAGATGTTA GAGGTTTAAA
     ****** *** ********** ********** *********  ******** * **********
541" CTGGCCCAGC CCTTCCAGGC AACTTTGGTT AATATATTAA TGAGATGTAA GAGGTTTAAA

580' ATAAATCACT ATCAAAGGAT AGAATTTTAA GGGAAGACTA AATTATGTAT TCATTAGAAT
     ********** ****** *** * ******** *********  **********  *********
601" ATAAATCACT ATCAAAAGAT AAAATTTTAA GGGAAGACT- AATTATGTAT CCATTAGAAT

640' CATAATTTTG TTCCTAAGAC AGATTCGTGA TGGTATAATA GAAACAGTGT CTTAGCCTGA
     ********** * ******** ***
660" CATAATTTTG TCCCTAAGAC AGAA
```

1st Nucleotide Sequence
File Name : Reference Seq.gnu
Sequence Size : 5464

2nd Nucleotide Sequence
File Name : RDB7329R.fasta (Complementary)
Sequence Size : 696

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Unit Size to Compare = 1
Pick up Location     = 1



[99.139% / 697 bp]     INT/OPT.Score : <   2584/  2742 >

   601' GAATTTTAAG GGAAGACTAA ATTATGTATT CATTAGAATC ATAATTTTGT TCCTAAGACA
                                                                *** *****
     1″                                                          CCTTAGACA

   661' GATTCGTGAT GGTATAATAG AAACAGTGTC TTAGCCTGAA GTATTGAGGA TAGTCCTAAG
        *********  **********  ********* ******** * ********** **********
    10″ GATTCGTGAG GGTATAATAG GAACAGTGTC TTAGCCTG-A GTATTGAGGA TAGTCCTAAG

   721' ATTAGGGAAC GATCAGTTCG TTCTTAATCA TAAGCATAAG AGAATGACTC AAACGCTGCT
        ******* ** ********** ********** ********** ********** **********
    69″ ATTAGGGGAC GATCAGTTCG TTCTTAATCA TAAGCATAAG AGAATGACTC AAACGCTGCT

   781' GTTTGATCTA CCTGTACTTA CATTTCTTCT TAATTTTAAA TTCTTCTCTG CTAGTATTCT
        ********** ********** ********** ********** ********** ** *******
   129″ GTTTGATCTA CCTGTACTTA CATTTCTTCT TAATTTTAAA TTCTTCTCTG CTCGTATTCT

   841' TTAGACCCAA CATTGGTTGT TTCCCCTATT TCTTCAATAT TTCTATTTAT TTTCCATCCT
        ********** ********** ********** ********** ********** **********
   189″ TTAGACCCAA CATTGGTTGT TTCCCCTATT TCTTCAATAT TTCTATTTAT TTTCCATCCT

   901' TTTTACAGGG TCATCTAAAT AAAAATATCT TAAAGCAATA AACCATTGTT ATTGAGTCAG
        ********** ********** ********** ********** ********** **********
   249″ TTTTACAGGG TCATCTAAAT AAAAATATCT TAAAGCAATA AACCATTGTT ATTGAGTCAG

   961' TACCTCAGTC CATGCAGCTT AATAATATGG AGAGCAAAAA AAAAAAGCCT CTCGATTTAT
        ********** ********** ********** ********** ********** **********
   309″ TACCTCAGTC CATGCAGCTT AATAATATGG AGAGCAAAAA AAAAAAGCCT CTCGATTTAT

  1021' TTTTTAATAT TACACGATCC TAGTTTTTTC TTCCCAGAAA ACGTGCCACA AAGTTTGCAA
        ********** ********** ********** ********** ********** **********
   369″ TTTTTAATAT TACACGATCC TAGTTTTTTC TTCCCAGAAA ACGTGCCACA AAGTTTGCAA
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1081’ GAAAGAGCTT TTGGGGCGGA GCCCTGGCTG CTTAGGTCCT TTCCATTGGT TCTACTTGGT
      ********** ********** ********** ********** ********** **********
 429″ GAAAGAGCTT TTGGGGCGGA GCCCTGGCTG CTTAGGTCCT TTCCATTGGT TCTACTTGGT

1141’ GACCACGCCC ACGGCCCCGC CTCCTGGGCG GAAGAGCCAA TTGGGCCGCG AGTTGTGGTT
      ********** ********** ********** ********** ********** **********
 489″ GACCACGCCC ACGGCCCCGC CTCCTGGGCG GAAGAGCCAA TTGGGCCGCG AGTTGTGGTT

1201’ TAAACCAGGA GTGCGCCGCG TCCGTTCACC GCGGCCTCAG ATGAATGCGG CTGTTAAGAC
      ********** ********** ********** ********** ********** **********
 549″ TAAACCAGGA GTGCGCCGCG TCCGTTCACC GCGGCCTCAG ATGAATGCGG CTGTTAAGAC

1261’ CTGATCAAGA TCTGGCCTCG GCGGCCAAGC TTGGCAATCC GGTACTGTTG GTAAAGCCAC
      ********** ********** ********** ********** ********** **********
 609″ CTGATCAAGA TCTGGCCTCG GCGGCCAAGC TTGGCAATCC GGTACTGTTG GTAAAGCCAC

1321’ CATGGAAGAT GCCAAAAACA TTAAGAAGGG CCCAGCGCCA TTCTACCCAC TCGAAGACGG
      ********** ********** ********
 669″ CATGGAAGAT GCCAAAAACA TTAAGAAG
```