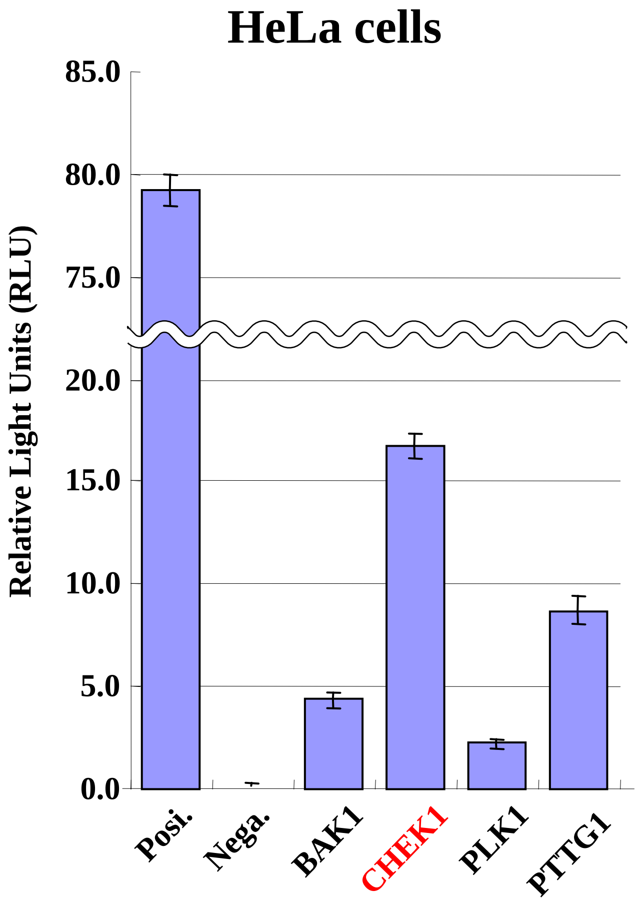
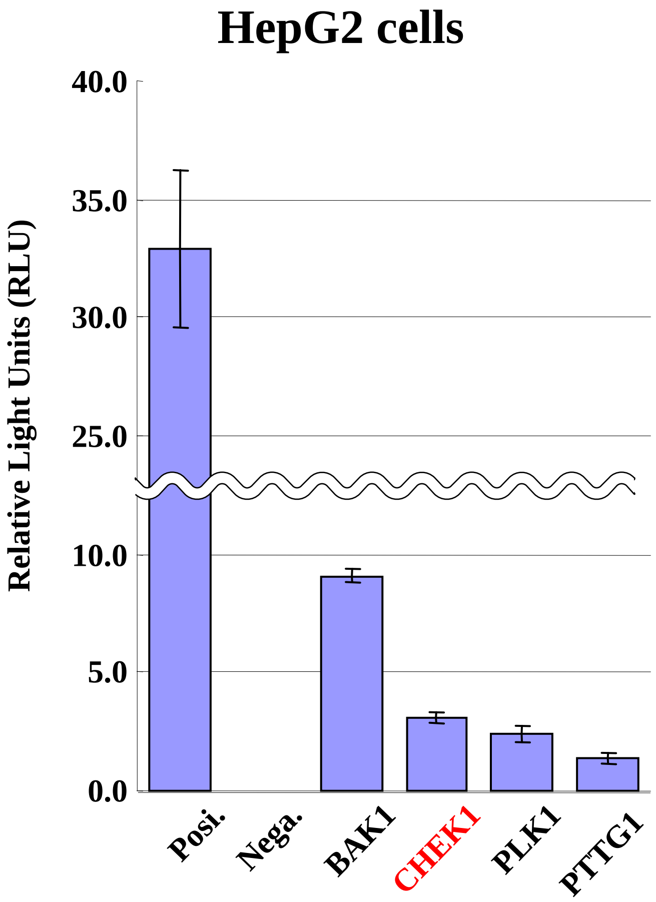
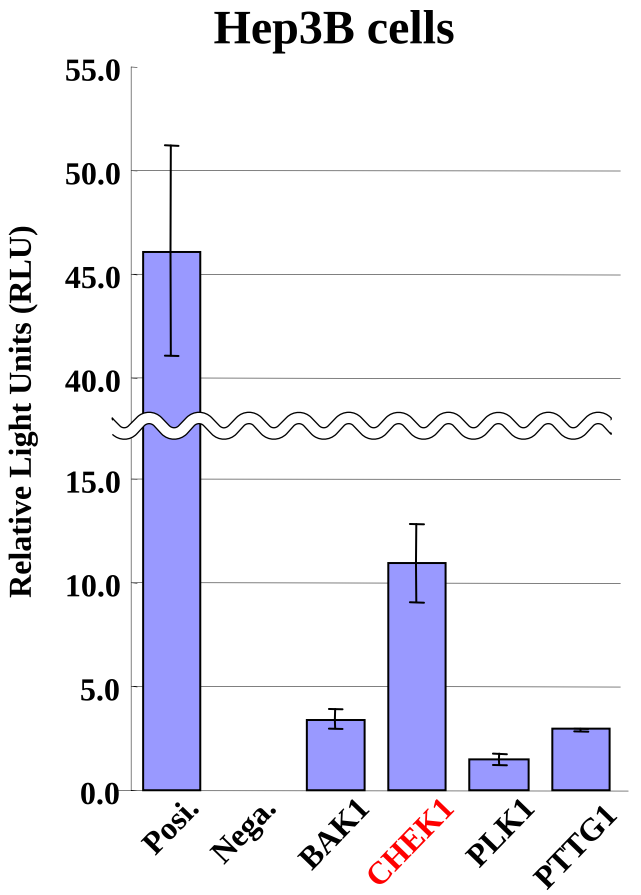
The Promoter Activities of Reporter Constructs


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 : 2010.03.01

1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5451

2nd Nucleotide Sequence
  File Name         : RDB7319F.fasta
  Sequence Size     : 688

  Unit Size to Compare = 1
  Pick up Location     = 1



[98.190% / 663 bp]     INT/OPT.Score : <    2184/  2460 >

   1'                                       GGCCT AAC-TGGCCG GTACCTGAGC
                                            ***** *** ****** **********
   1" GAGATGCTAG TCCAGGTGCG CAGAACATTA TCTCTGGCCT AACTTGGCCG GTACCTGAGC

  25' TCGCTAGCCT CGAGGATTGT TTTGGAGCTG GTTCACAGAA AAAAGGCAAA ACTGGTTATC
      ********** ********** ********** ********** ********** **********
  61" TCGCTAGCCT CGAGGATTGT TTTGGAGCTG GTTCACAGAA AAAAGGCAAA ACTGGTTATC

  85' CTGACTTCAA GCTCCAACAT AAACTGCTCG CTTTCTCCGG GAAACTTGCC CCGCCACACA
      ********** ********** ********** ********** ********** **********
 121" CTGACTTCAA GCTCCAACAT AAACTGCTCG CTTTCTCCGG GAAACTTGCC CCGCCACACA

 145' CACTTGACTG CGTGGCCAGT TCTTTCGAAG CCTCTCGCTC CCAACACGGA GTTCCTCCCA
      ********** ********** ********** ********** ********** **********
 181" CACTTGACTG CGTGGCCAGT TCTTTCGAAG CCTCTCGCTC CCAACACGGA GTTCCTCCCA

 205' TTTCTTCACA GTCGGCTCTC AGCAGCTGCT GCTGGTTTCT CGGCTCCAGC ACCACGAGTA
      ********** ********** ********** ********** ********** **********
 241" TTTCTTCACA GTCGGCTCTC AGCAGCTGCT GCTGGTTTCT CGGCTCCAGC ACCACGAGTA
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265’ CCGCACTCTG AGGTTTACAA AGCACTCTGC TTCACCGACT GTGATCCTCA CAGTCCTGTC
     ********** ********** ********** ********** ********** **********
301″ CCGCACTCTG AGGTTTACAA AGCACTCTGC TTCACCGACT GTGATCCTCA CAGTCCTGTC

325’ CGGTGGCCTC ACGCAGGTGG CGGTGCAGCC TTTCAGGCCC AGAGCGGCCA GGAGCGAAGC
     ********** ********** ********** ********** ********** **********
361″ CGGTGGCCTC ACGCAGGTGG CGGTGCAGCC TTTCAGGCCC AGAGCGGCCA GGAGCGAAGC

385’ CCGCAGCCCC GCCTGGAAGC GCAGCGCGGT CGGTCGCGCG CCCCTGAGGC TTGGAGGCCT
     ********** ********** ********** ********** ********** **********
421″ CCGCAGCCCC GCCTGGAAGC GCAGCGCGGT CGGTCGCGCG CCCCTGAGGC TTGGAGGCCT

445’ GGGCTTCCCC CAGCAGCGCT CGAGCACCGC CCAGTCGAGC CTCACACCGG ATGCCACTTC
     ********** ********** ********** ********** ********** **********
481″ GGGCTTCCCC CAGCAGCGCT CGAGCACCGC CCAGTCGAGC CTCACACCGG ATGCCACTTC

505’ ATATTTGGGC CCAGAGCTCA ATTCGCGCCG ATGCGGTCCG CCGTCCTTAA ATCTCTTCAG
     ********** ********** ********** ********** ******** * **********
541″ ATATTTGGGC CCAGAGCTCA ATTCGCGCCG ATGCGGTCCG CCGTCCTT-A ATCTCTTCAG

565’ CCAGGATCTC TCCCCGACTG CAAAGCAGCC CTGGGCGGGA GCGGCAACAT CTCCACGTCA
     ********** * ******** * ****** * ****** *** ***** **** ** *******
600″ CCAGGATCTC T-CCCGACTG C-AAGCAG-C CTGGGC-GGA GCGGC-ACAT CT-CACGTCA

625’ CCCTTTTGGA GCCGCCGACA TTCAGAGGGG CAGGACACGG GAACGCGCGC TGTCTTGCTT
     ******* ** **** *****  ***** *** ********
654″ CCCTTTT-GA GCCG-CGACA -TCAGA-GGG CAGGACACC
```

1st Nucleotide Sequence
File Name : Reference Seq.gnu
Sequence Size : 5451

2nd Nucleotide Sequence
File Name : RDB7319R.fasta (Complementary)
Sequence Size : 600

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Unit Size to Compare = 1
Pick up Location     = 1



[99.667% / 600 bp]     INT/OPT.Score : <   2162/  2368 >

  721’ CCCTCAAGTT TTGGCGGGAA AAGCGCTGCA TTTGGATTCC TGCAGTGGTG GGCAAAGGAC
                       ***** ********** ********** ********** **********
    1″                GGGGAA AAGCGCTGCA TTTGGATTCC TGCAGTGGTG GGCAAAGGAC

  781’ AGTCCGGTGA GGAAGGGCGG CCGGTAGAGT AGGGAAGGTT TCTAAAGAAG GAGTTCGGGG
       ********** ********** ********** ********** ********** **********
   47″ AGTCCGGTGA GGAAGGGCGG CCGGTAGAGT AGGGAAGGTT TCTAAAGAAG GAGTTCGGGG

  841’ TCTAGATTAG TGAGGGAGGG CATGGTGGGA GAAAGTTAGC ATTGACTAGC GCAGGGGATT
       ********** ********** ********** ********** ********** **********
  107″ TCTAGATTAG TGAGGGAGGG CATGGTGGGA GAAAGTTAGC ATTGACTAGC GCAGGGGATT

  901’ GGAGAGACTC CTGCGGAGGG GCGGTTTCGG AGGGTGGAGG AATGGTACCA GGAGGTTCCC
       ********** ********** ********** ********** ********** **********
  167″ GGAGAGACTC CTGCGGAGGG GCGGTTTCGG AGGGTGGAGG AATGGTACCA GGAGGTTCCC

  961’ GTTGTGGGGG CGGGGGCAGG AGGGACTAAC CCGCTGCTAG CTAAGAACCC CAAGGAAGAG
       ********** ********** ********** ********** ********** **********
  227″ GTTGTGGGGG CGGGGGCAGG AGGGACTAAC CCGCTGCTAG CTAAGAACCC CAAGGAAGAG

 1021’ TCCCAGCCCT TCCTTTCGCC TCTGGGGGCA GTTTGGCCCC GCCCCGGCCT TTGGGACGGG
       ********** ********** ********** ********** ********** **********
  287″ TCCCAGCCCT TCCTTTCGCC TCTGGGGGCA GTTTGGCCCC GCCCCGGCCT TTGGGACGGG

 1081’ TGGGGCTGTG GATGGGGATG GGAATTGGAA TTGAGCAATT GGGAGGAGGC GCTGCCGCAG
       ********** ********** ********** ********** ********** **********
  347″ TGGGGCTGTG GATGGGGATG GGAATTGGAA TTGAGCAATT GGGAGGAGGC GCTGCCGCAG

 1141’ GCGTTTTCTG CCCCATACCG CTCCCTATAT CCTCTTCCTC TCTTCCCCAG ACCCCCACCT
       ********** ********** ********** ********** ********** **********
  407″ GCGTTTTCTG CCCCATACCG CTCCCTATAT CCTCTTCCTC TCTTCCCCAG ACCCCCACCT
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1201' CTCCCTCCTC CTTCCCCAGT CGTTCGCCGG AAAGCATTTG TCTCCCACCT ATCAAGATCT
      ********** ********** ********** ********** *********  **********
 467″ CTCCCTCCTC CTTCCCCAGT CGTTCGCCGG AAAGCATTTG TCTCCCACC- ATCAAGATCT

1261' GGCCTCGGCG GCCAAGCTTG GCAATCCGGT ACTGTTGGTA AAGC-CACCA TGGAAGATGC
      ********** ********** ********** ********** **** ***** **********
 526″ GGCCTCGGCG GCCAAGCTTG GCAATCCGGT ACTGTTGGTA AAGCACACCA TGGAAGATGC

1320' CAAAAACATT AAGAAGGGCC CAGCGCCATT CTACCCACTC GAAGACGGGA CCGCCGGCGA
      ********** *****
 586″ CAAAAACATT AAGAA
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