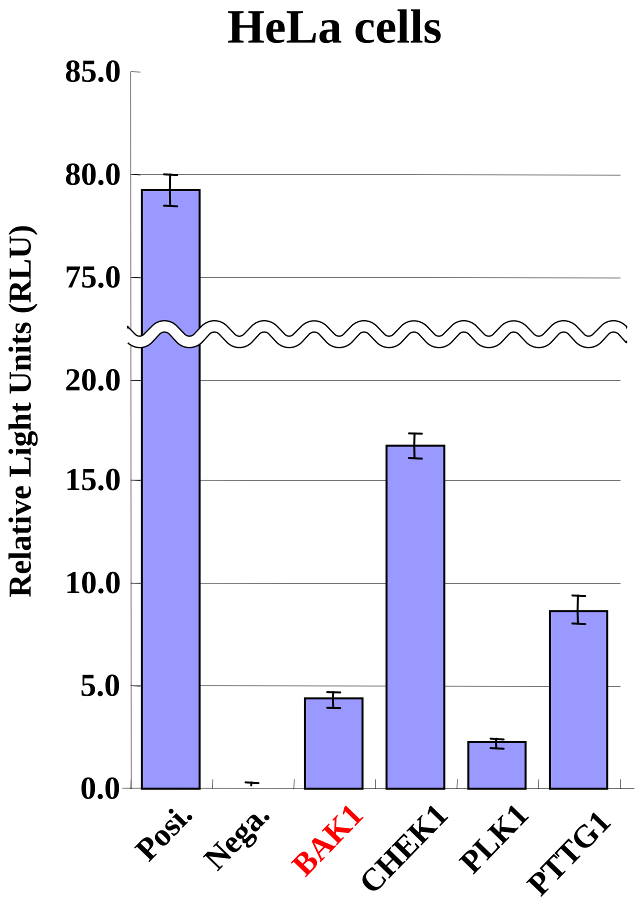
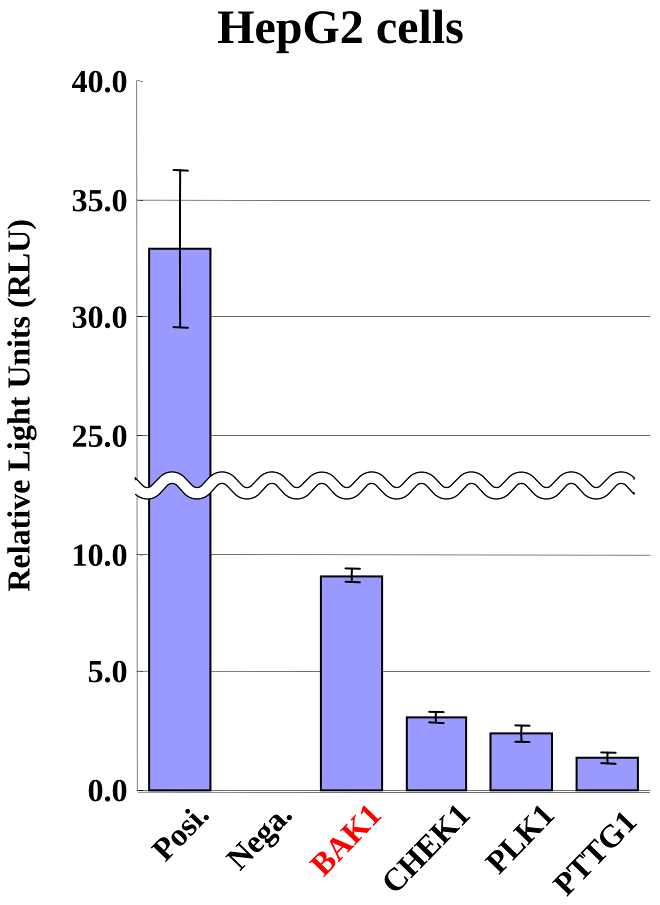
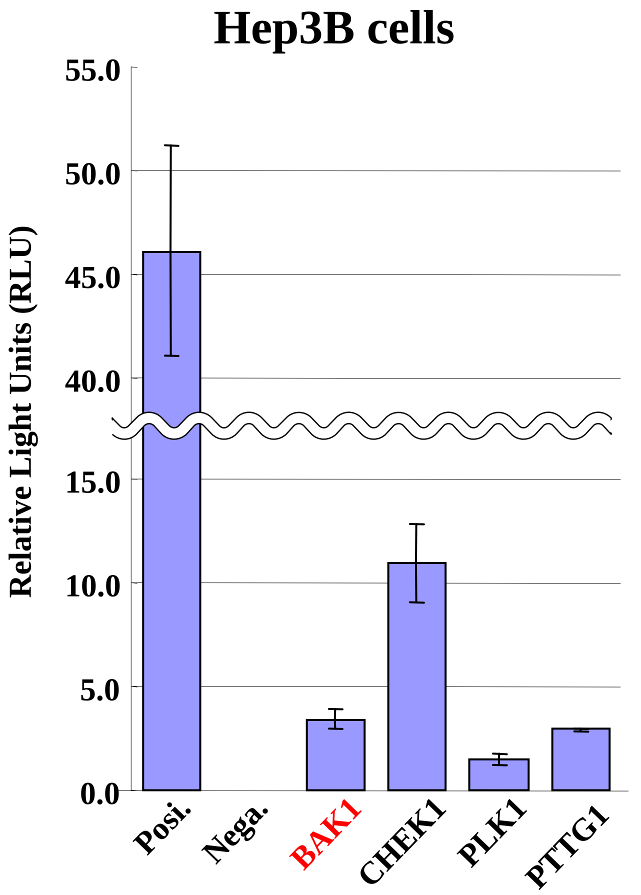
# The Promoter Activities of Reporter Constructs


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     : 5435

2nd Nucleotide Sequence
  File Name         : RDB7318F.fasta
  Sequence Size     : 660

  Unit Size to Compare = 1
  Pick up Location     = 1



[99.219% / 640 bp]     INT/OPT.Score : <   2468/  2513 >

    1’                   GG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATA
                         ** ********** ********** ********** **********
    1″ GTGCCAGAAC ATTTCTCTGG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATA

   43’ TGGGATTCTA GGCGTGACAC ACCGCAGCTG GCTGCCTTTT TTGTTGTTGT TGAGACAAGG
       ********** ********** ********** ********** ********** **********
   61″ TGGGATTCTA GGCGTGACAC ACCGCAGCTG GCTGCCTTTT TTGTTGTTGT TGAGACAAGG

  103’ TCTTGCTCTG TTGCCCAGGG CGGAATGCAG TGGTGCAAAC ATGGCTCACT GTGGCCTCGA
       ********** ********** ********** ********** ********** **********
  121″ TCTTGCTCTG TTGCCCAGGG CGGAATGCAG TGGTGCAAAC ATGGCTCACT GTGGCCTCGA

  163’ CTTCCTGTGC TCAGGTGATC CTCCTGCCTC AGCCTCCTAG GTAGCTGGGA CCACCAAATG
       ********** ********** ********** ********** ********** **********
  181″ CTTCCTGTGC TCAGGTGATC CTCCTGCCTC AGCCTCCTAG GTAGCTGGGA CCACCAAATG

  223’ CACAGGTGTG CACTACCATA CCCAGCTAAT TTCTAATTTT TTTTTGTAGA GACATGGTCT
       ********** ********** ********** ********** ********** **********
  241″ CACAGGTGTG CACTACCATA CCCAGCTAAT TTCTAATTTT TTTTTGTAGA GACATGGTCT
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283’ CACTTTGTTG CCCAGGCTGG TCTTGAACTC CTGGGCTCAA GCAATCCTCC CACCTCAGCC
     ********** ********** ********** ********** ********** **********
301″ CACTTTGTTG CCCAGGCTGG TCTTGAACTC CTGGGCTCAA GCAATCCTCC CACCTCAGCC

343’ TTCCAAAGTG TTGGGATTAC AGGCGTGAGC CACTGGGCCC AGCCTCTATT GAGTTTTAAT
     ********** ********** ********** ********** ********** **********
361″ TTCCAAAGTG TTGGGATTAC AGGCGTGAGC CACTGGGCCC AGCCTCTATT GAGTTTTAAT

403’ CTCCGTTTAC TTGACTATCA CCTTCAGGAT TTCAAACATC CAGAGACCAC CAAGGTGCAT
     ********** ********** ********** ********** ********** **********
421″ CTCCGTTTAC TTGACTATCA CCTTCAGGAT TTCAAACATC CAGAGACCAC CAAGGTGCAT

463’ GGTGCACAGG TCTAAATTGC AGGTTGAATC TCAATCTAGT ATTAGTATTC CCCAATGCGA
     ********** ******* ** ********** ********** ********** **********
481″ GGTGCACAGG TCTAAATAGC AGGTTGAATC TCAATCTAGT ATTAGTATTC CCCAATGCGA

523’ CTACAGAACT GATTATTACT ATTTATTTTT TTTGAGATGG AGTCTTGCAC TGTCACCAGG
     ********** ********** ********** ********** ********** **********
541″ CTACAGAACT GATTATTACT ATTTATTTTT TTTGAGATGG AGTCTTGCAC TGTCACCAGG

583’ GCTGGAGTGC AATGGCGCAA TCCTGGTTTA CTGC-AACCT CC-ACCTCCC AGGTTCAAGG
     ********** ********** ********** **** ***** ** ******* *.**** *
601″ GCTGGAGTGC AATGGCGCAA TCCTGGTTTA CTGCAAACCT CCAACCTCCC ANGTTCCAAA
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1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5435

2nd Nucleotide Sequence
  File Name         : RDB7318R.fasta (Complementary)
  Sequence Size     : 704

  Unit Size to Compare = 1
  Pick up Location     = 1
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[99.147% / 703 bp]     INT/OPT.Score : <   1372/  2756 >

 601' AATCCTGGTT TACTGCAACC TCCACCTCCC AGGTTCAAGG GATTCTCCTG CCTCAGCCTT
                        **   ******** * ******** ******* ** **********
   1″                  CCC CTCACCTCCC AAGTTCAAGG GATTCTCTTG CCTCAGCCTT

 661' CCAACTAGCT GGGATTACAG GCGCCCGCCA CCACACCCAG CTAATTTTTT GTATTTTTAG
      ********** ********** ********** ********** ********** **********
  44″ CCAACTAGCT GGGATTACAG GCGCCCGCCA CCACACCCAG CTAATTTTTT GTATTTTTAG

 721' TAGAGACGGG GTTTCACCAT GTTAGCCAGA ATGGTCTCGA TCTCTTGACC TCGTGATCTG
      ********** ********** ********** ********** ********** **********
 104″ TAGAGACGGG GTTTCACCAT GTTAGCCAGA ATGGTCTCGA TCTCTTGACC TCGTGATCTG

 781' CCTGCCTCAG CCTCCCAAGG TGCTGGGATT ATAGGCGTGA GCCACCGCGC CTGGCCCAGA
      ********** ********** ********** ********** ********** **********
 164″ CCTGCCTCAG CCTCCCAAGG TGCTGGGATT ATAGGCGTGA GCCACCGCGC CTGGCCCAGA

 841' ACTGATGATT AACCCAGCTG AGCCTCTGTT CATCTGAATG GGTATTGTCA ACAGCACTCA
      ********** ********** ********** ********** ********** **********
 224″ ACTGATGATT AACCCAGCTG AGCCTCTGTT CATCTGAATG GGTATTGTCA ACAGCACTCA

 901' CTTACAAGAG TTGCTGAGAA GATCCAATGA GACAAATAGT TGCTAAAGTG CCAGGCATGC
      ********** ********** ********** ********** ********** **********
 284″ CTTACAAGAG TTGCTGAGAA GATCCAATGA GACAAATAGT TGCTAAAGTG CCAGGCATGC

 961' AGCAGTG-CT TAAGAAACTT CTCACCCTGG GTTTTTTATT GGTATTGATT GATGTAGAGG
      ******* ** ********** ********** ********** ********** **********
 344″ AGCAGTGACT TAAGAAACTT CTCACCCTGG GTTTTTTATT GGTATTGATT GATGTAGAGG

1020' TGGGGGAGAA GATCAAAGAC AAGGATTGAG AATCAGGGAT GGGAAAAGCA GTGGGCCACT
      ********** ********** ********** ********** ********** **********
 404″ TGGGGGAGAA GATCAAAGAC AAGGATTGAG AATCAGGGAT GGGAAAAGCA GTGGGCCACT

1080' GACAGCCGCC CTGCCTGCCT GGGAGGTGGG GTGGGGAAAG TGGGCGGGAC ATGCTCCTGG
      ********** ********** ********** ********** ********** **********
 464″ GACAGCCGCC CTGCCTGCCT GGGAGGTGGG GTGGGGAAAG TGGGCGGGAC ATGCTCCTGG
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1140' GCCTGGCCCA CCCAGATCAC CCTACAGGCT GTCGGCCTGT GCGTCTGCAT CCGGTGGCCA
      ********** ********** ********** ********** ********** **********
 524" GCCTGGCCCA CCCAGATCAC CCTACAGGCT GTCGGCCTGT GCGTCTGCAT CCGGTGGCCA

1200' CAGAGCAACT TCCTCTAGAG GGAGCTGATT GGAGCATCAA GATCTGGCCT CGGCGGCCAA
      ********** ********** ********** ********** ********** **********
 584" CAGAGCAACT TCCTCTAGAG GGAGCTGATT GGAGCATCAA GATCTGGCCT CGGCGGCCAA

1260' GCTTGGCAAT CCGGTACTGT TGGTAAAG-C CACCATGGAA GATGCCAAAA ACATTAAGAA
      ********** ********** ******** * ********** ********** **********
 644" GCTTGGCAAT CCGGTACTGT TGGTAAAGAC CACCATGGAA GATGCCAAAA ACATTAAGAA

1319' GGGCCCAGCG CCATTCTACC CACTCGAAGA CGGGACCGCC GGCGAGCAGC TGCACAAAGC
      *
 704" G
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