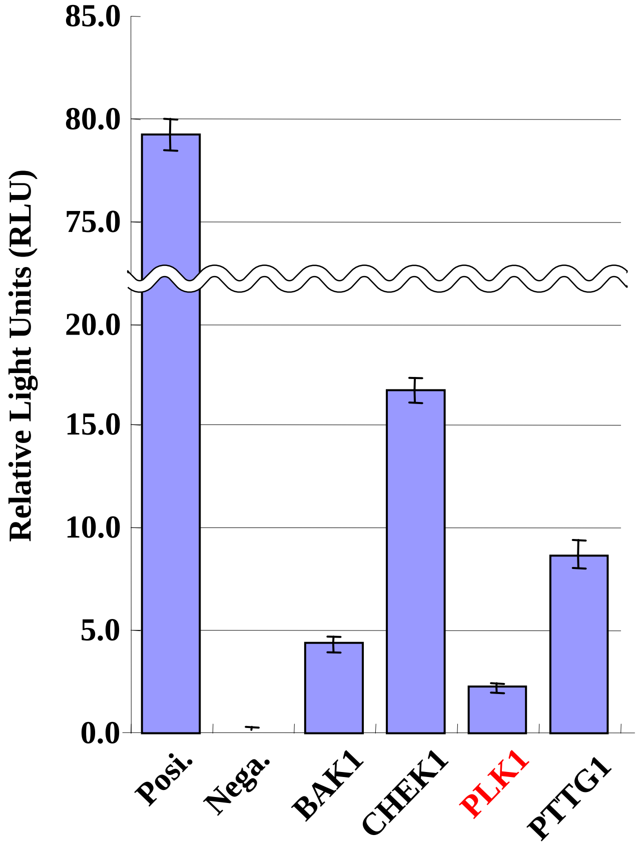
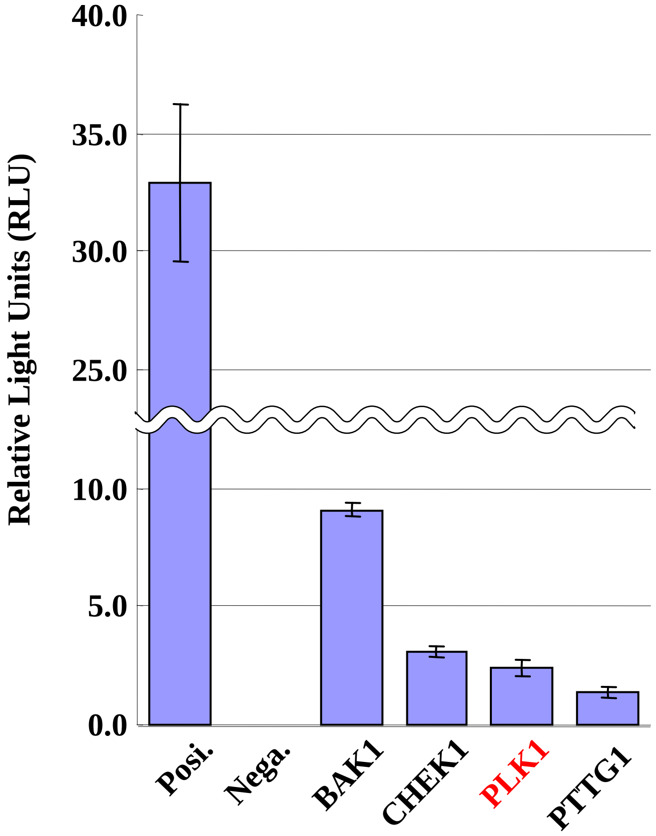
The Promoter Activities of Reporter Constructs

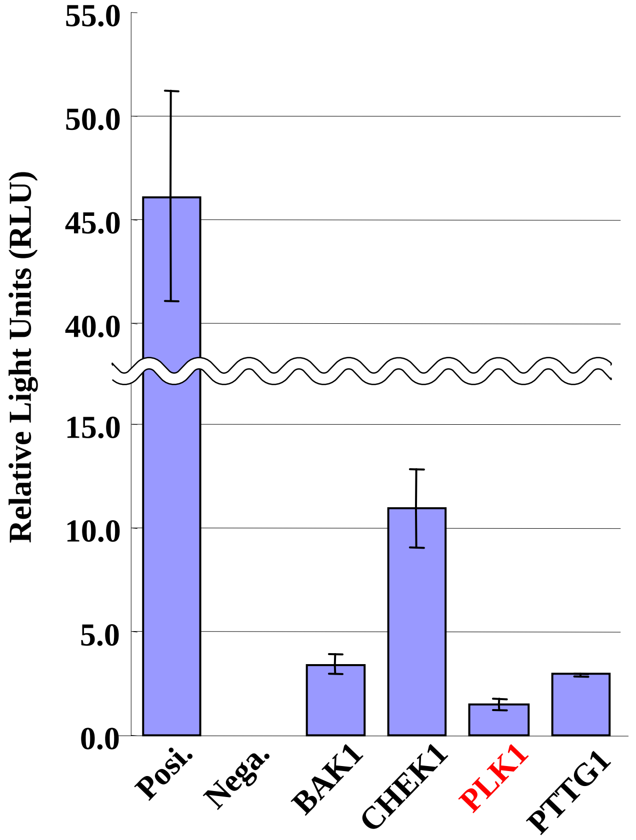
HeLa cells



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     : 5463

2nd Nucleotide Sequence
  File Name         : RDB7327F.fasta
  Sequence Size     : 684

  Unit Size to Compare = 1
  Pick up Location     = 1



[96.313% / 651 bp]     INT/OPT.Score : <   1496/  2290 >

    1’                                    GGCCTAAC TGGCCGGTAC CTGAGCTCGC
                                          ******** ********** **********
    1″ TATGCAATGT GCAGGTGCCA GAACATTTCT CTGGCCTAAC TGGCCGGTAC CTGAGCTCGC

   29’ TAGCCTCGAG GATAGGGTTG CCACTCAAGT ACCTACAGAA CAAACGGGTG TAGCTGTAAA
       ********** ********** ********** ********** ********** **********
   61″ TAGCCTCGAG GATAGGGTTG CCACTCAAGT ACCTACAGAA CAAACGGGTG TAGCTGTAAA

   89’ CTGTGGCAAA CTGAAAGCAT GTAGGCACAG AGTAAGTAGC TAGAGCTGAT TTTTTTCAGG
       ********** ********** ********** ********** ********** **********
  121″ CTGTGGCAAA CTGAAAGCAT GTAGGCACAG AGTAAGTAGC TAGAGCTGAT TTTTTTCAGG

  149’ AAAGGCCACA AATCCCAACT TTTATGAGCT CCTCTTTTAA ATGCTGTAAA TGTTTTACAA
       ********** ********** ********** ********** ********** **********
  181″ AAAGGCCACA AATCCCAACT TTTATGAGCT CCTCTTTTAA ATGCTGTAAA TGTTTTACAA

  209’ TGGCGGGGCG CGGTGGCTCA CGCCTGTAAT CCCAGCATTT GGGAGGCCGA GGGGCAGATC
       ********** ********** ********** ********** ********** **********
  241″ TGGCGGGGCG CGGTGGCTCA CGCCTGTAAT CCCAGCATTT GGGAGGCCGA GGGGCAGATC
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269’ ACTTGAGGTC AGGAGTTCAA GACCAGCCTG GCCAACATGG TGAAACCTCT TCTCTACTAA
     ********** ********** ********** ********** ********** **********
301″ ACTTGAGGTC AGGAGTTCAA GACCAGCCTG GCCAACATGG TGAAACCTCT TCTCTACTAA

329’ AATTACAAAA ATTAGCCGGG CATGGTGGTG CATGCTTGTA ATTCC-AGCT GCTAGGGAGG
     ********** ********** ********** ********** ***** **** **********
361″ AATTACAAAA ATTAGCCGGG CATGGTGGTG CATGCTTGTA ATTCCAAGCT GCTAGGGAGG

388’ CCGAGGCGGG AGGATTGCTT GAACCCGGGA AGCAGAGGTT GCAGTGAGCT GAGATCGTGC
     ********** ********** ********** ********** ********** **********
421″ CCGAGGCGGG AGGATTGCTT GAACCCGGGA AGCAGAGGTT GCAGTGAGCT GAGATCGTGC

448’ CACTGCACTC CAGCCTGGGC GACAGAGCAA GATTCCGTCA CACACACAAA AAAAAGGCGT
     ********** ********** ********** ********** ***** **** **********
481″ CACTGCACTC CAGCCTGGGC GACAGAGCAA GATTCCGTCA CACACCCAAA AAAAAGGCGT

508’ GGGGGGAGGC C-AAAC-AAA ACCCCGC-AA GACACATTT- GGCTATGA-C CTG-CCAG-T
     ********** * **** *** ******* ** ***** ***  ******** * *** **** *
541″ GGGGGGAGGC CAAAACAAAA ACCCCGCAAA GACACCTTTG GGCTATGACC CTGCCCAGTT

561’ TTG-CTAGG- CATTCTT-CC AACC-TTCCC T-CCCTCTGA -CCAA-GAAA CTGAGTGTCC
     *** *****  * ***** ** * ** ***** * ********  **** ***  **********
601″ TTGCCTAGGC CTTTCTTCCC ACCCTTTCCC TCCCCTCTGA CCCAAGGAAC CTGAGTGTCC

614’ AC-TATTTTA -GGCCCTGGG AAATTCAGTA GCGAGGAGGC CAGACAGCTT CGTTGCATCA
      * ** ****  ********* ***
661″ CCTTAATTTA GGGCCCTGGG AAAA
```

1st Nucleotide Sequence

File Name : Reference Seq.gnu

Sequence Size : 5463

2nd Nucleotide Sequence

File Name : RDB7327R.fasta (Complementary)

Sequence Size : 748

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 Unit Size to Compare = 1
 Pick up Location     = 1



[92.867% / 729 bp]     INT/OPT.Score : <   2494/  2545 >

  601' AAACTGAGTG TCCACTATTT TAGGCCCTGG GAAATTCAGT AGCGAGGAGG CCAGACAGCT
                              **.**    ***      *   ** *  **  **  **   
    1"   TTCAGGTA GGCGGAGGGG AGGGNCCCAA GAACAAGGCT TTCG-GTTGG GCATTCAATG

  661' TCGTTGCATC -ATGGGGGGC TCTGGTACTG TGCTTCTCCA ACTTCA--GG ATGT-GTAGG
         *  *   *    * **     ****  ** * * **   *   ****  *  **** *****
   58" GGGGGGGGGC TCCGTGGTAA CCTGGGGCT- TTCCTCCAAA CTTTCAGGGA ATGTGGTAGG

  717' AATCA-CCTG AGCAGTCTTG TTGAGAGGCG GACACTGACT CGGGAGGTCT GGGGTAGGGC
       ***** **** ********** ********** ********** ********** **********
  117" AATCACCCTG AGCAGTCTTG TTGAGAGGCG GACACTGACT CGGGAGGTCT GGGGTAGGGC

  776' CTGAACGTTT GCCTTTGCGG TTCTAACAAG CTCTCAGGTG ATGGCGATGC TACTGTTCCC
       ********** ** ******* ********** ********** ********** **********
  177" CTGAACGTTT GCTTTTGCGG TTCTAACAAG CTCTCAGGTG ATGGCGATGC TACTGTTCCC

  836' TGGCCCCGAG GTAGAGGAAG ATTTAAGTAA AAGCTTCCTG GAGGAGGCGC AAGTGAACCG
       ********** ********** ********** ********** ********** **********
  237" TGGCCCCGAG GTAGAGGAAG ATTTAAGTAA AAGCTTCCTG GAGGAGGCGC AAGTGAACCG

  896' CAGGAGCTTT CCCGGACGCC CGAGAAAGGG AGAAACCCCG AAGGAATTCC TCCTCTCTCG
       ********** ********** ********** ********** ********** **********
  297" CAGGAGCTTT CCCGGACGCC CGAGAAAGGG AGAAACCCCG AAGGAATTCC TCCTCTCTCG

  956' GGGCTGGGTC TCCGCATCCA CGCCGGGTTT GGTTTCCCAG GCTATCCCAC GTGTTCGGGC
       ********** ********** ********** ********** ********** **********
  357" GGGCTGGGTC TCCGCATCCA CGCCGGGTTT GGTTTCCCAG GCTATCCCAC GTGTTCGGGC

 1016' GTCCGTGTCA ATCAGGTTTT CCCCGGCTGG GTCCGGGTTT AAAGGCTGCT GCTGCGCAGG
       ********** ********** ********** ********** ********** **********
  417" GTCCGTGTCA ATCAGGTTTT CCCCGGCTGG GTCCGGGTTT AAAGGCTGCT GCTGCGCAGG
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1076' GCGCTCCCAT GGTGCCGCGC GGCGGGCGGG TTTGGATTTT AAATCCCCGC GGCCAATCAG
      ********** ********** ********** ********** ********** **********
 477″ GCGCTCCCAT GGTGCCGCGC GGCGGGCGGG TTTGGATTTT AAATCCCCGC GGCCAATCAG

1136' TGGCGCGCAG GCTTTTGTAA CGTTCCCAGC GCCGCGTTTG AATTCGGGGA GGAGCGGAGC
      ********** ********** ********** ********** ********** **********
 537″ TGGCGCGCAG GCTTTTGTAA CGTTCCCAGC GCCGCGTTTG AATTCGGGGA GGAGCGGAGC

1196' GGTGCGGAGG CTCTGCTCGG ATCGAGGTCT GCAGCGCAGC TTCGGGAGCA TGAGTGCTGC
      ********** ********** ********** ********** ********** **********
 597″ GGTGCGGAGG CTCTGCTCGG ATCGAGGTCT GCAGCGCAGC TTCGGGAGCA TGAGTGCTGC

1256' AGTGACTATC AAGATCTGGC CTCGGCGGCC AAGCTTGGCA ATCCGGTACT GTTGGTAAAG
      ********** ********** ********** ********** ********** **********
 657″ AGTGACTATC AAGATCTGGC CTCGGCGGCC AAGCTTGGCA ATCCGGTACT GTTGGTAAAG

1316' CCACCATGGA AGATGCCAAA AACATTAAGA AGGGCCCAGC GCCATTCTAC CCACTCGAAG
      ********** ********** ********** *
 717″ CCACCATGGA AGATGCCAAA AACATTAAGA AC
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