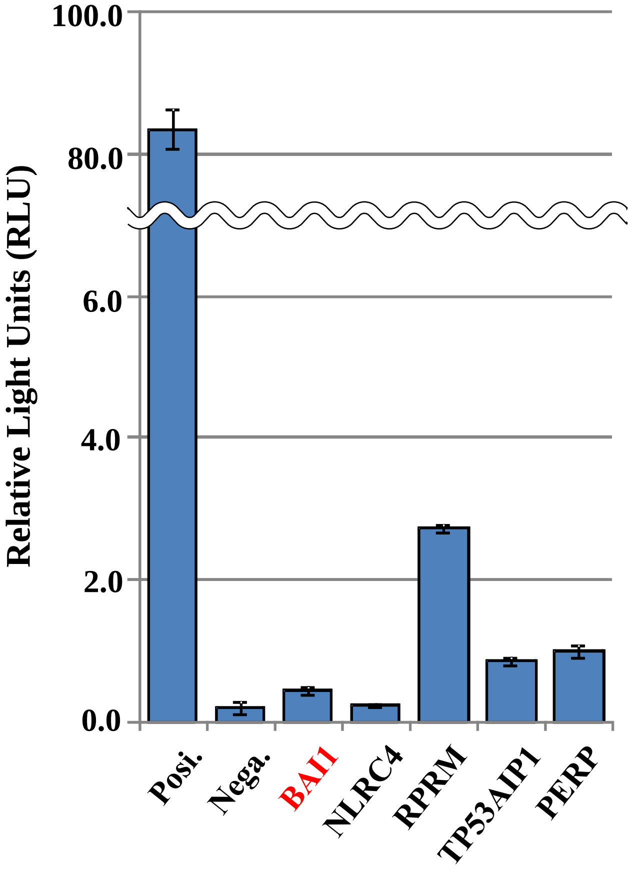
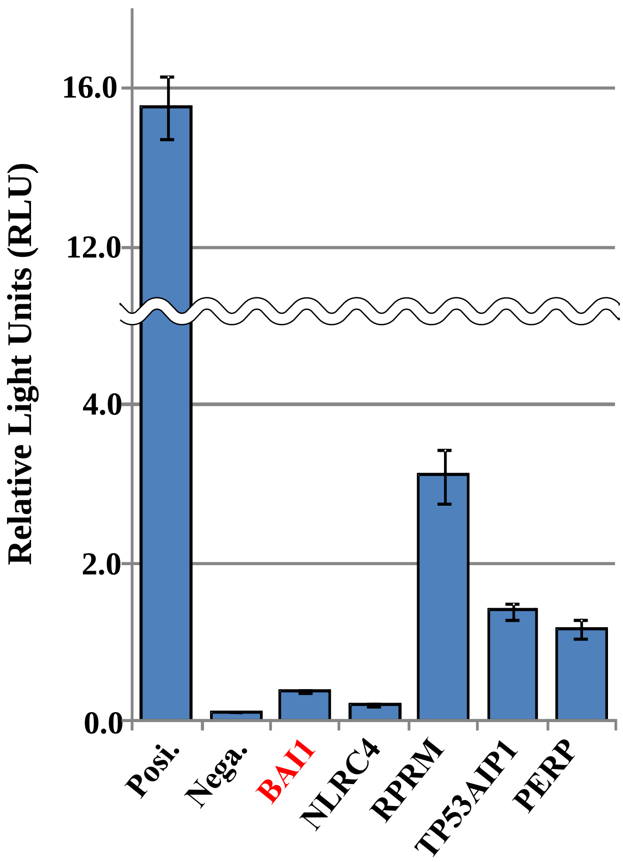
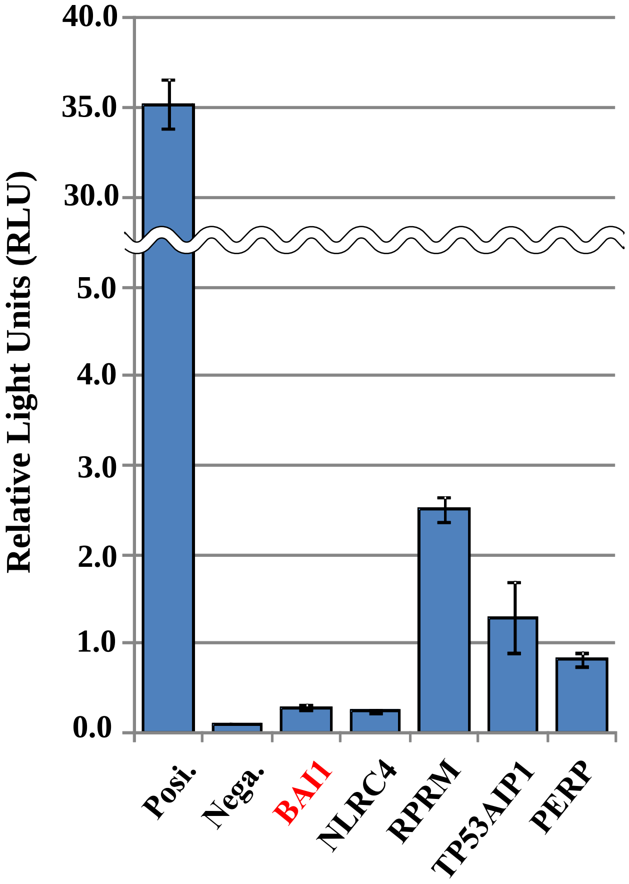
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

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

BAI1: pGL4-phBAI1 (RDB# 7401)
NLRC4: pGL4-phNLRC4 (RDB# 7406)
RPRM: pGL4-phRPRM (RDB# 7409)
TP53AIP1: pGL4-phTP53AIP1 (RDB#7410)
PERP: pGL4-phPERP (RDB#7411)

2010, 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   : 5610

2nd Nucleotide Sequence
  File Name       : RDB7401F.fasta
  Sequence Size   : 654

  Unit Size to Compare = 1
  Pick up Location     = 1



[96.850% / 635 bp]     INT/OPT.Score : <   1212/  2363 >

      1'                     GG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATC
                             ** ********** ********** ********** **********
      1" GTGCCAGAAC ATGTCTCTGG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATC

     43' ATTTGTGCGG TCAGCAGAGC GGAGGCAT-C CCCACCAGGA GGCCGGGTGG CCTGGGGGAG
         ********** ********** ******** * ********** ********** **********
     61" ATTTGTGCGG TCAGCAGAGC GGAGGCATGC CCCACCAGGA GGCCGGGTGG CCTGGGGGAG

    102' GGGGACTGGC TACAGCTCCC CTCCCTCCTG CACAGGCTCA AC-TGCTGGG TGGGATGGAC
         ***** **** * **** **  *** ****** * ******** ** ******* **********
    121" GGGGAGTGGC TGCAGCGCCG CTCGCTCCTG CGCAGGCTCA ACGTGCTGGG TGGGATGGAC

    161' GGCCTGGCCA GAGGCCTTGG GGGTGGTGAG GAGACTGAGG TCTGTAGGCA GAAGGAACTT
         ********** ********** ********** ********** ********** **********
    181" GGCCTGGCCA GAGGCCTTGG GGGTGGTGAG GAGACTGAGG TCTGTAGGCA GAAGGAACTT

    221' GCCAAGGTCC ACAGCGAGGT GGATGCCCGC TGGGCCCAGG GCAGCCCCGG ATCCAGGGCC
         ********** ********** ********** ********** ********** **********
    241" GCCAAGGTCC ACAGCGAGGT GGATGCCCGC TGGGCCCAGG GCAGCCCCGG ATCCAGGGCC
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281’ TTCACTGTAC CTCTGCTCAC CCGTGGCGCT GTGAGTGGGC AGTCACTCAA CCTGGGCCCT
     ********** ********** ********** ********** ********** **********
301″ TTCACTGTAC CTCTGCTCAC CCGTGGCGCT GTGAGTGGGC AGTCACTCAA CCTGGGCCCT

341’ CTCCTGGAGC TGGGAGGTGT CTCCTGGTGG CACAAATTTA GGGTCAGCCT GGGGCTCACG
     ********** ********** ********** ********** ********** **********
361″ CTCCTGGAGC TGGGAGGTGT CTCCTGGTGG CACAAATTTA GGGTCAGCCT GGGGCTCACG

401’ TATGGGTTCT CCGACCCACT CACTGTGACG GGTAAATTAT GGATT-CTCT CTGTGTCTCA
     ********** ********** ********** ********** ***** **** **********
421″ TATGGGTTCT CCGACCCACT CACTGTGACG GGTAAATTAT GGATTCCTCT CTGTGTCTCA

460’ GTTTTCCCAT CATG-AATGA TAGGAA-GTA ATGCTAGCCT TGCAGAGGAA GGGC-AGAGG
     ********** **** ***** ****** *** ********** ********** **** *****
481″ GTTTTCCCAT CATGAAATGA TAGGAAGGTA ATGCTAGCCT TGCAGAGGAA GGGCAAGAGG

517’ TGAGGTGGCT CCTGGTGGCT CCATCCCCCC TCCATCCCTC CCCAGGCCCT GTGCCTGTAG
     ********** ********** ** ******* ***.****** ********** **********
541″ TGAGGTGGCT CCTGGTGGCT CCCTCCCCCC TCCNTCCCTC CCCAGGCCCT GTGCCTGTAG

577’ CTTTAGGGCA CGAGGGCACA CGTGGGAGGG CCGAAAGAGA GCTTCCTGGC AGGAGCACCA
     ********** ******* ** *********  ** ***** *  *** ***** ***
601″ CTTTAGGGCA CGAGGGCCCA CGTGGGAGGT CCCAAAGAAA CCTTTCTGGC AGGG
```

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1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5610

2nd Nucleotide Sequence
  File Name        : RDB7401R.fasta (Complementary)
  Sequence Size    : 699

  Unit Size to Compare = 1
  Pick up Location     = 1
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```
[98.569% / 699 bp]     INT/OPT.Score : <   2280/  2689 >

  781' GCCAGACGGG AGGCTGGGGA ATGGCCCGAG TAACCTTTCT CCTGTGCTCC GGGCCCACTT
                                * ********** ********** ********** **********
    1″                          A ATGGCCCGAG TAACCTTTCT CCTGTGCTCC GGGCCCACTT

  841' CCC-TTCCCA C-GGGGTTTG CAGAATCTTC CT-GGGAAGG AGGAAGGTTA GAGAGGAGGG
       *** ****** * **** *** ********** .* **** ** *** ****** **********
   42″ CCCTTTCCCA CGGGGGGTTG CAGAATCTTC NTGGGGAGGG AGGGAGGTTA GAGAGGAGGG

  898' ACCAAGGTCA GCAGGAAAGA CAGAGCCTGA GAGAGCTACA CCCTCCACTC ACAGAGGGGC
       ********** ********** ********** ********** ********** **********
  102″ ACCAAGGTCA GCAGGAAAGA CAGAGCCTGA GAGAGCTACA CCCTCCACTC ACAGAGGGGC

  958' AGCCACGCAG AGCGTGGTGA GCGAGTGGGC AGGCAGGCCA GGGCCCCCGG GAGCCACGCC
       ********** ********** ********** ********** ********** **********
  162″ AGCCACGCAG AGCGTGGTGA GCGAGTGGGC AGGCAGGCCA GGGCCCCCGG GAGCCACGCC

 1018' AGGCTGCGTG GGCAAAGGGG TACCACCAAA AGCCCCAGGT GGACTGCCAG CCCCTCCCTG
       ********** ********** ********** ********** ********** **********
  222″ AGGCTGCGTG GGCAAAGGGG TACCACCAAA AGCCCCAGGT GGACTGCCAG CCCCTCCCTG

 1078' CTCAGGCTTG GGTGGAGGCG GAGGTACTTT GTTCCCCAAG CTGGGCCGCT GCCCCTGCAG
       ********** ********** ********** ********** ********** **********
  282″ CTCAGGCTTG GGTGGAGGCG GAGGTACTTT GTTCCCCAAG CTGGGCCGCT GCCCCTGCAG

 1138' GTGGTCACAT TGGTGAGTGG CAGACAGACA GGTGGACGGA GCAGGTGCCT GGGAGGGTGC
       ********** ********** ********** ********** ********** **********
  342″ GTGGTCACAT TGGTGAGTGG CAGACAGACA GGTGGACGGA GCAGGTGCCT GGGAGGGTGC

 1198' CAGGGCCTGT GTCTGCGGCC CAAAGTCCTC CTGCCCTCGT TGGTAGCAGG CTAAGCTGCC
       ********** ********** ********** ********** ********** **********
  402″ CAGGGCCTGT GTCTGCGGCC CAAAGTCCTC CTGCCCTCGT TGGTAGCAGG CTAAGCTGCC

 1258' TCCTCTGAGA GAGCCCACCC CCATGCCCAG AGCCCACGTC TCCCCAAGTG CTCACTCTGA
       ********** ********** ********** ********** ********** **********
  462″ TCCTCTGAGA GAGCCCACCC CCATGCCCAG AGCCCACGTC TCCCCAAGTG CTCACTCTGA
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1318’ CCCTCTGCTC TTTCTCTTCC AGCTGCTGCT GGTGGCCACA GGCTGGCACC AGGGCCCTGG
      ********** ********** ********** ********** ********** **********
 522″ CCCTCTGCTC TTTCTCTTCC AGCTGCTGCT GGTGGCCACA GGCTGGCACC AGGGCCCTGG

1378’ ACTTTAGAAG CCGTTGCTGC CCTCTCTGTC ACATCAAGAT CTGGCCTCGG CGGCCAAGCT
      ********** ********** ********** ********** ********** **********
 582″ ACTTTAGAAG CCGTTGCTGC CCTCTCTGTC ACATCAAGAT CTGGCCTCGG CGGCCAAGCT

1438’ TGGC-AATCC GGTACTGTTG GTAAAGCCAC CATGGAAGAT GCCAAA-AAC ATTAAGAAGG
      **** ***** ********** ********** ******* ** ****** *** ********
 642″ TGGCAAATCC GGTACTGTTG GTAAAGCCAC CATGGAACAT GCCAAACAAC ATTAAGAA
```