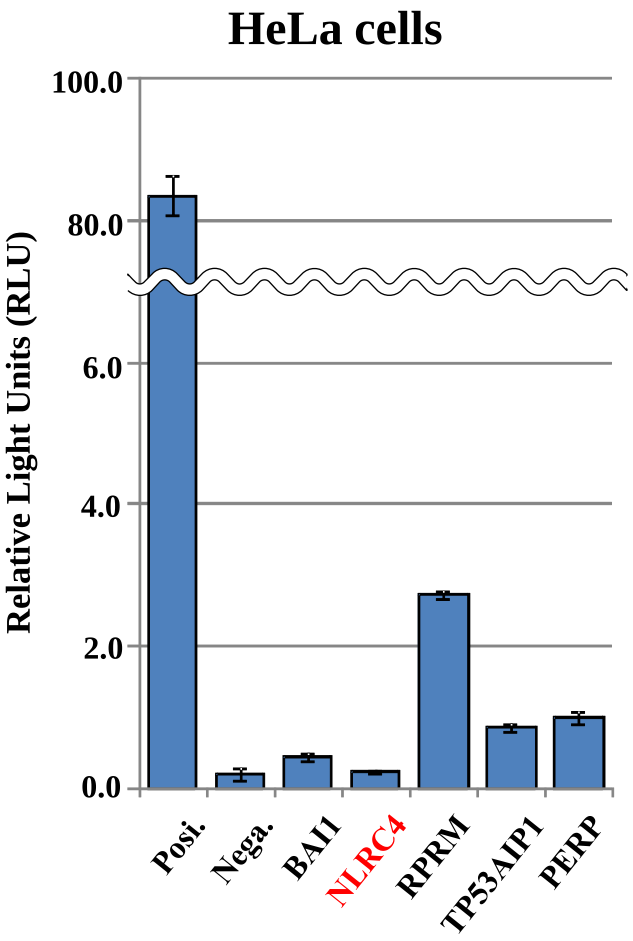
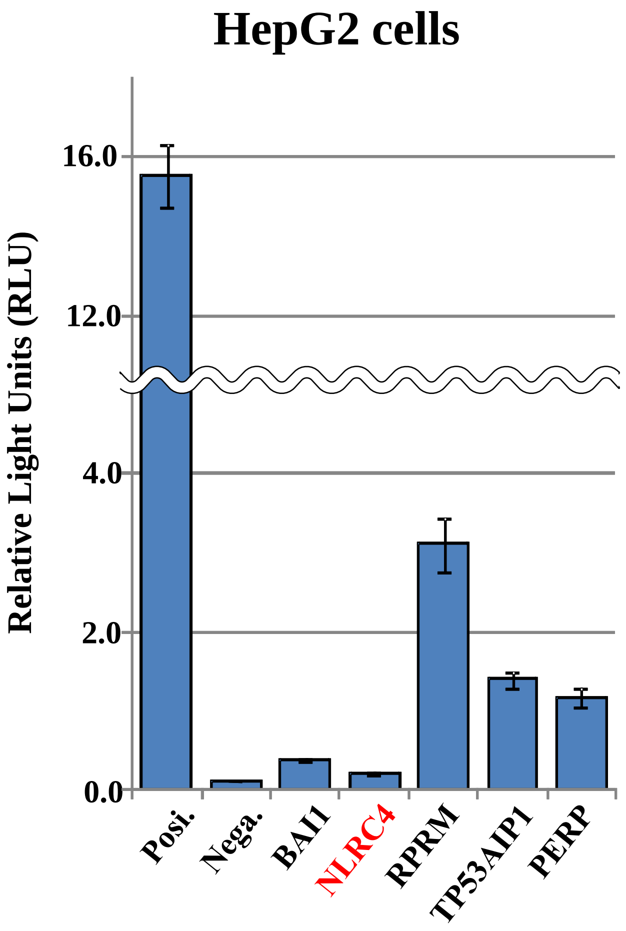
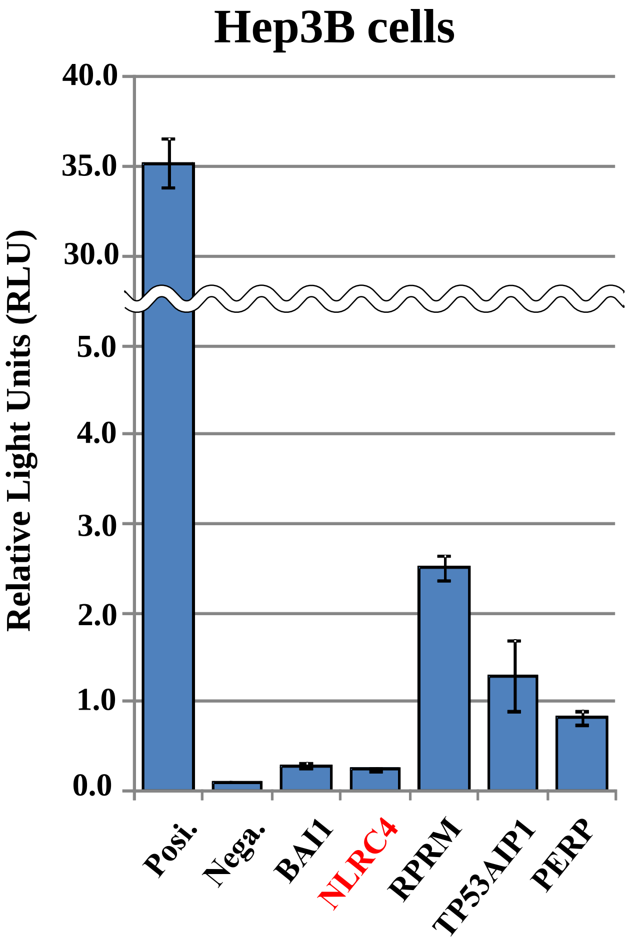
The Promoter Activities of Reporter Constructs



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 : 2009.06.30

1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5560

2nd Nucleotide Sequence
  File Name        : RDB7406F.fasta
  Sequence Size    : 657

  Unit Size to Compare = 1
  Pick up Location     = 1



[99.845% / 644 bp]     INT/OPT.Score : <   2408/  2560 >

      1'             GGCCTAACT GGCCGGTACC TGAGCTCGCT AGCCTCGAGG AT-TGGGAGC
                     ********* ********** ********** ********** ** *******
      1″ AACATGTCTC TGGCCTAACT GGCCGGTACC TGAGCTCGCT AGCCTCGAGG ATGTGGGAGC

     49' TTTAGGGGAG AATCCATTTA TGCCTCTTCC AGCTGCAGGT GGCTGCTGGC ATCTTTTGGC
         ********** ********** ********** ********** ********** **********
     61″ TTTAGGGGAG AATCCATTTA TGCCTCTTCC AGCTGCAGGT GGCTGCTGGC ATCTTTTGGC

    109' TCGTAGCCGT ATTACTCGAA TCTCTGCATT CATGGTCTTA CTGACTTCTC CTGTCAGTTT
         ********** ********** ********** ********** ********** **********
    121″ TCGTAGCCGT ATTACTCGAA TCTCTGCATT CATGGTCTTA CTGACTTCTC CTGTCAGTTT

    169' CAAATCTCCC TCTGGCTCTC TGTAATAAGG GACCATTATT AAGGGCCCAC CTGGATCATC
         ********** ********** ********** ********** ********** **********
    181″ CAAATCTCCC TCTGGCTCTC TGTAATAAGG GACCATTATT AAGGGCCCAC CTGGATCATC

    229' CAGAATTCTC TCCCCATCTT CAGAGCCTTA AATGGAACAT ATCTGGAAAG ACACAATATT
         ********** ********** ********** ********** ********** **********
    241″ CAGAATTCTC TCCCCATCTT CAGAGCCTTA AATGGAACAT ATCTGGAAAG ACACAATATT
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289' TACAGTTCCC AGGGATTAGG ATTTGGGATA TTTGGGTAGC CACTATTCAG CCTACTACAA
     ********** ********** ********** ********** ********** **********
301″ TACAGTTCCC AGGGATTAGG ATTTGGGATA TTTGGGTAGC CACTATTCAG CCTACTACAA

349' CCATATTTCT ACATTTTCCC TTTTTATTCT ATATTACATC ATTTATTAGT ACAAAAGTAA
     ********** ********** ********** ********** ********** **********
361″ CCATATTTCT ACATTTTCCC TTTTTATTCT ATATTACATC ATTTATTAGT ACAAAAGTAA

409' TAGGTGTTTG CTATGAAGAA TTAGAATATA CAGGTTGGGC ATGGTGGCTC CCGCCTGTAA
     ********** ********** ********** ********** ********** **********
421″ TAGGTGTTTG CTATGAAGAA TTAGAATATA CAGGTTGGGC ATGGTGGCTC CCGCCTGTAA

469' TCCCATTACT TTAGGAGGAC AACACAGGTG GATCACTGGA GACCAAGAGC TCAAGACCAG
     ********** ********** ********** ********** ********** **********
481″ TCCCATTACT TTAGGAGGAC AACACAGGTG GATCACTGGA GACCAAGAGC TCAAGACCAG

529' CTTGGCCAAC ATAGCAAAAC CCTGTCTCTA CTAAAAATAC AAAAAATTAG CCATGGTGGT
     ********** ********** ********** ********** ********** **********
541″ CTTGGCCAAC ATAGCAAAAC CCTGTCTCTA CTAAAAATAC AAAAAATTAG CCATGGTGGT

589' GGCCCACACC TGAAATCCCA GCTACTTGAG AGGCTGAGGC ACAAGAATTG CTTGAGCCTG
     ********** ********** ********** ********** ********** *****
601″ GGCCCACACC TGAAATCCCA GCTACTTGAG AGGCTGAGGC ACAAGAATTG CTTGAAA
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1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5560

2nd Nucleotide Sequence
  File Name        : RDB7406R.fasta (Complementary)
  Sequence Size    : 735

  Unit Size to Compare = 1
  Pick up Location     = 1
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[99.592% / 735 bp]     INT/OPT.Score : <   2707/  2915 >

  661' TGCAGTGAGC CAAGATTGAG CCACTGCACT CCACTCCAGC CTGGGCAACA GAACGAGACT
                                                       * *** **********
    1″                                                      CCACA GAACGAGACT

  721' CTGTCTCAAA TAAATAAATA AATAAATAAA TAAACAAATA AAATAAAAAA TAAATAA-GT
       ********** ********** ********** ********** ********** **.**** **
   16″ CTGTCTCAAA TAAATAAATA AATAAATAAA TAAACAAATA AAATAAAAAA TANATAAGGT

  780' TGATAAATAA AATTAGAATA TACAGATAAG CCAAAGACAG AAATTTAAAA TTGCTTATAA
       ********** ********** ********** ********** ********** **********
   76″ TGATAAATAA AATTAGAATA TACAGATAAG CCAAAGACAG AAATTTAAAA TTGCTTATAA

  840' TTGTATTCCC CAGCAATAAG CATCATTACT ATTTTGGTGG CTGTCTTTGC AGTTTTTTCT
       ********** ********** ********** ********** ********** **********
  136″ TTGTATTCCC CAGCAATAAG CATCATTACT ATTTTGGTGG CTGTCTTTGC AGTTTTTTCT

  900' CTTGAACATA TGTTTATATA TAGGTTTCAT TACAATTTAA AAATCTAGCT GATAGTGTAG
       ********** ********** ********** ********** ********** **********
  196″ CTTGAACATA TGTTTATATA TAGGTTTCAT TACAATTTAA AAATCTAGCT GATAGTGTAG

  960' CCCTCAATCT CACTTCAGAG AAACCCACCT CACAAGTTGG GAAACACTGA CACTGATGCC
       ********** ********** ********** ********** ********** **********
  256″ CCCTCAATCT CACTTCAGAG AAACCCACCT CACAAGTTGG GAAACACTGA CACTGATGCC

 1020' CCCTTAGAAA ACCCAGGATG TAGACATTTA TTTGCCGGGA AACTTTGGTA TCCCTCTATG
       ********** ********** ********** ********** ********** **********
  316″ CCCTTAGAAA ACCCAGGATG TAGACATTTA TTTGCCGGGA AACTTTGGTA TCCCTCTATG

 1080' GCAGATAGGC TACTGTCAGA ATGCTCTTTT TGAAATAAGA AGTTATGTAA CACAAAGACA
       ********** ********** ********** ********** ********** **********
  376″ GCAGATAGGC TACTGTCAGA ATGCTCTTTT TGAAATAAGA AGTTATGTAA CACAAAGACA

 1140' TGTTCCTGGT AGTTTATGCA AAGACAGAGG AAAGAGTATG CAAGAATGTC ATCCTCAAGG
       ********** ********** ********** ********** ********** **********
  436″ TGTTCCTGGT AGTTTATGCA AAGACAGAGG AAAGAGTATG CAAGAATGTC ATCCTCAAGG
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1200' GAAGTGCAGA GAGATTTCTT CAGTCCTCAG CTGAGTATAA GCTGGCCTCC TGGAGTCTGT
      ********** ********** ********** ********** ********** **********
 496″ GAAGTGCAGA GAGATTTCTT CAGTCCTCAG CTGAGTATAA GCTGGCCTCC TGGAGTCTGT

1260' GAACACAAAC GTCCAATGTG AGTGTGCCTG TGCAAGCCCC TGGCTGTTTA TACTCCGGAG
      ********** ********** ********** ********** ********** **********
 556″ GAACACAAAC GTCCAATGTG AGTGTGCCTG TGCAAGCCCC TGGCTGTTTA TACTCCGGAG

1320' GGTGTCCCCG TGCGTCATCG GTGGAGTGGA CCAAAACTGG ATCAAGATCT GGCCTCGGCG
      ********** ********** ********** ********** ********** **********
 616″ GGTGTCCCCG TGCGTCATCG GTGGAGTGGA CCAAAACTGG ATCAAGATCT GGCCTCGGCG

1380' GCCAAGCTTG GCAATCCGGT ACTGTTGGTA AAGCCACCAT GGAAGATGCC AAAAACATTA
      ********** ********** ********** ********** ********** **********
 676″ GCCAAGCTTG GCAATCCGGT ACTGTTGGTA AAGCCACCAT GGAAGATGCC AAAAACATTA
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