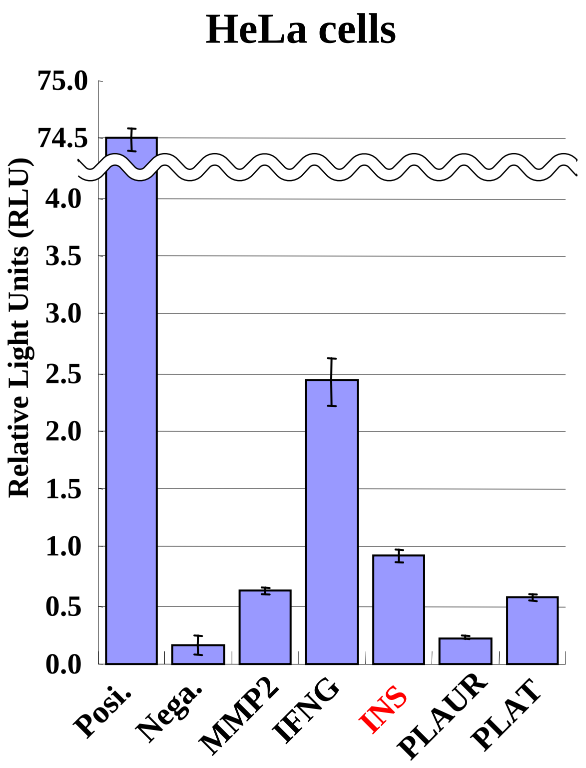
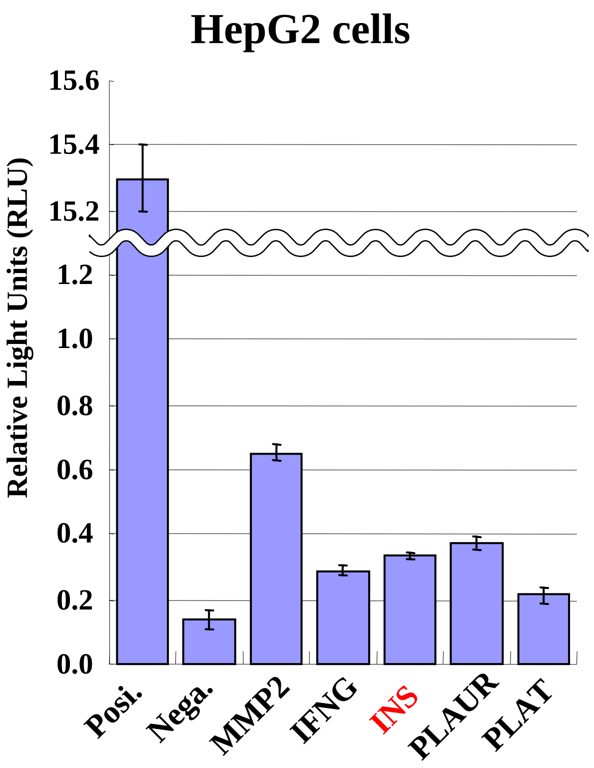
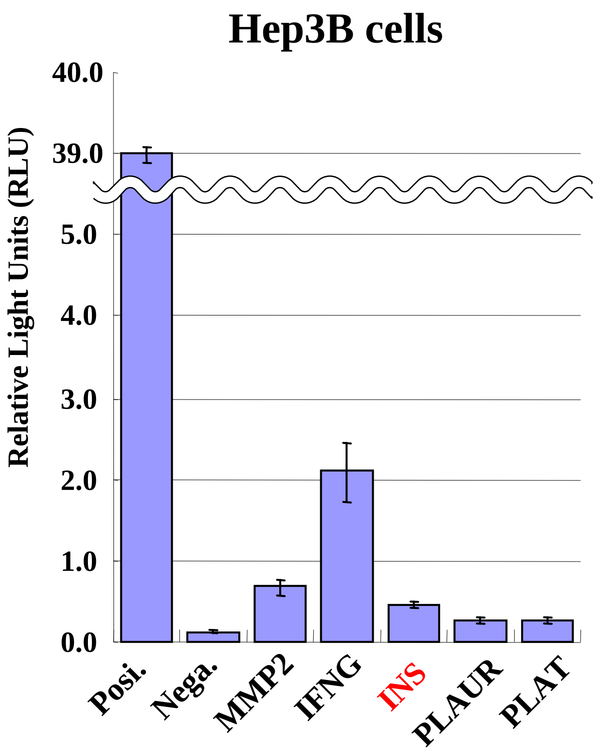
The Promoter Activities of Reporter Constructs



HeLa cells



HepG2 cells



Hep3B cells

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

MMP2: pGL4-phMMP2 (RDB#7314)
IFNG: pGL4-phIFNG(RDB#7297)
INS:pGL4-phINS (RDB#7387)
PLAUR:pGL4-phPLAUR (RDB#7312)
PLAT:pGL4-phPLAT (RDB#7295)

2009, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.06.12

1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5526

2nd Nucleotide Sequence
  File Name         : RDB7387F.fasta
  Sequence Size     : 345

  Unit Size to Compare = 1
  Pick up Location     = 1



[98.176% / 329 bp]     INT/OPT.Score : <    253/  1220 >

      1'                     G GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT
                             * ********** ********** ********** **********
      1″ NNNNNCAGAA CATTTCTCTG GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT

     42' ACCTCCAGGT GCCTGTTCTN GGGGAGCTGG GAGGGCCGGA GGGGTGTACC CCAGGGGCTC
         ********** *********  ********** ********** ********** **********
     61″ ACCTCCAGGT GCCTGTTCT- GGGGAGCTGG GAGGGCCGGA GGGGTGTACC CCAGGGGCTC

    102' AGCCCAGATG NACACTATGG GGGTGATGGT GTCATGGGAC CTGGCCAGGA GAGGGGAGAT
         **********  ********* ********** ********** ********** **********
    120″ AGCCCAGATG -ACACTATGG GGGTGATGGT GTCATGGGAC CTGGCCAGGA GAGGGGAGAT

    162' GNGGCTCCCA GAAGAGGAGT GGGGGCTGAG AGGGTGCCTG GGGGGCCAGG ACNGGAGCTG
         * ******** ********** ********** ********** ********** ** *******
    179″ G-GGCTCCCA GAAGAGGAGT GGGGGCTGAG AGGGTGCCTG GGGGGCCAGG AC-GGAGCTG

    222' GGCCAGTGCA CAGCTTCCCA CACCTGCCCA CCCCCAGAGT CCTNGCCGCC ACCCCCAGAT
         ********** ********** ********** ********** *** ****** **********
    237″ GGCCAGTGCA CAGCTTCCCA CACCTGCCCA CCCCCAGAGT CCT-GCCGCC ACCCCCAGAT
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    282' CACACGGAAG ATGAGGTCCG AGTGGCCTGC TGAGNGACTT GCTGCTTGTC CCCAGGTCCC
         ********** ********** ********** **** ***** ********
    296″ CACACGGAAG ATGAGGTCCG AGTGGCCTGC TGAG-GACTT GCTGCTTGGG G




1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5526

2nd Nucleotide Sequence
  File Name        : RDB7387R.fasta (Complementary)
  Sequence Size    : 472

  Unit Size to Compare = 1
  Pick up Location     = 1



[98.734% / 474 bp]     INT/OPT.Score : <   1174/  1833 >

    901' GACAGGGGTG TGGGGACAGG GGTCTGGNGG ACAGCAGCGC AAAGAGCCCC GCCCTGCAGC
                                              ****** ********** **********
      1″                                     CCAGCGC AAAGAGCCCC GCCCTGCAGC

    961' CTCCAGCTCT CCTGGTCTNA ATGTGGAAAG TGGCCCAGGT GAGGGCTTTG CTCTCCTGGA
         ********** ******** * ********** ********** ********** **********
     28″ CTCCAGCTCT CCTGGTCT-A ATGTGGAAAG TGGCCCAGGT GAGGGCTTTG CTCTCCTGGA

   1021' GACATTTGCN CCCCAGCTGT GAGCAGGGAC AGGTCTGGCC ACCGGGCCCC TGGTTAAGAC
         *********  ********** ********** ********** ********** **********
     87″ GACATTTGC- CCCCAGCTGT GAGCAGGGAC AGGTCTGGCC ACCGGGCCCC TGGTTAAGAC

   1081' TCTAATGACC CGCTGGTCCT GAGGAAGAGG TGCTGACGAC CAAGGAGATC TTCCCACAGA
         ********** ********** ********** ********** ********** **********
    146″ TCTAATGACC CGCTGGTCCT GAGGAAGAGG TGCTGACGAC CAAGGAGATC TTCCCACAGA
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1141’ CCCAGCACCA GGGAAATGGT CCGGAAATTG CAGCCTCAGC CCCCAGCCAT CTGCCGACCC
      ********** ********** ********** ********** ********** **********
 206″ CCCAGCACCA GGGAAATGGT CCGGAAATTG CAGCCTCAGC CCCCAGCCAT CTGCCGACCC

1201’ CCCCACCCCA GGCCCTAATG GGCCAGGCGG CAGGGGTTGA GAGGTAGGGG AGATGGGCTC
      ********** ********** ********** **********  ********* **********
 266″ CCCCACCCCA GGCCCTAATG GGCCAGGCGG CAGGGGTTGA CAGGTAGGGG AGATGGGCTC

1261’ TGAGACTATA AAGCCAGCGG GGGCCCAGCA GCCCTCAGCC CTCCAGGACA GGCTGCATCA
      ********** ********** ********** ********** ********** **********
 326″ TGAGACTATA AAGCCAGCGG GGGCCCAGCA GCCCTCAGCC CTCCAGGACA GGCTGCATCA

1321’ GAAGAATCAA GATCTGGCCT CGGCGGCCAA GCTTGGCAAT CCGGTACTGT TGGTAAAGCC
      **** ***** ********** ********** ********** ********** **********
 386″ GAAG-ATCAA GATCTGGCCT CGGCGGCCAA GCTTGGCAAT CCGGTACTGT TGGTAAAGCC

1381’ ACCATGGAAG ATGCCAAAAA CATTAAGAAG GGCCCAGCGC CATTCTACCC ACTCGAAGAC
      ********** ******** * ******.*
 445″ ACCATGGAAG ATGCCAAACA CATTAANA
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