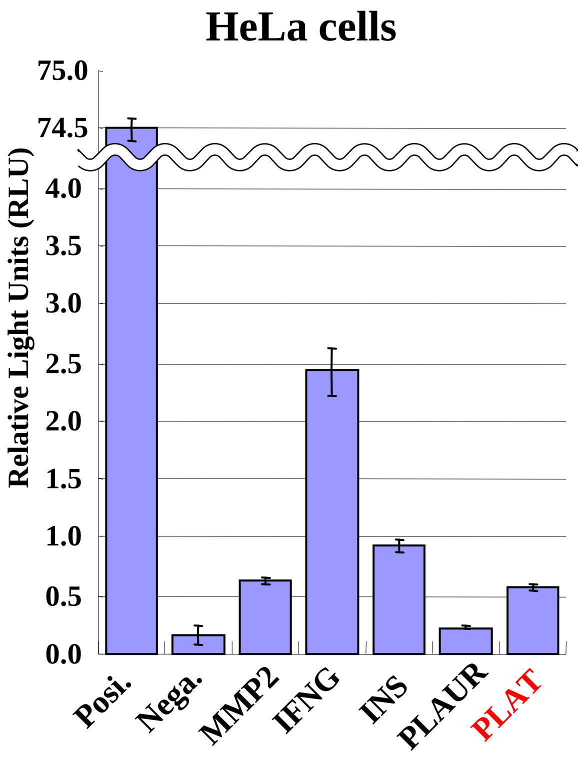
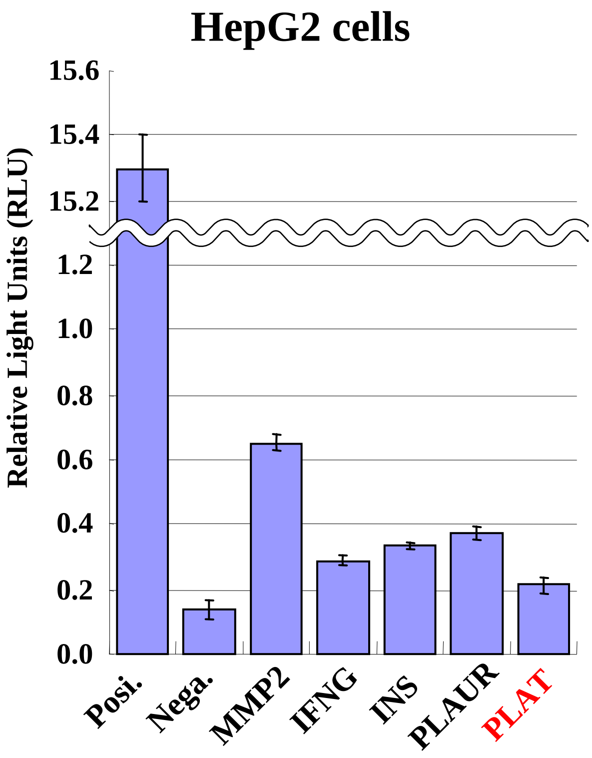
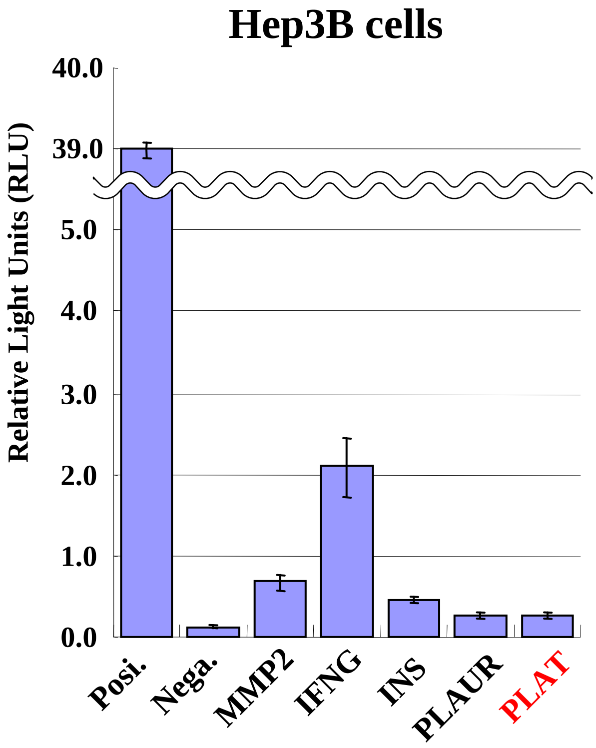
The Promoter Activities of Reporter Constructs


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 : 2009.06.23

1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5289

2nd Nucleotide Sequence
  File Name        : RDB7295F.fasta
  Sequence Size    : 580

  Unit Size to Compare = 1
  Pick up Location     = 1



[97.715% / 569 bp]     INT/OPT.Score : <    272/  2098 >

      1'                   GG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATC
                           ** ********** ********** ********** **********
      1″ GTGCCAGAAC ATTTCTCTGG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATC

     43' TTCCCTCCCT GCGTTCTTTC TTTCACNCTC TCTCTCATTT TTACAAGGTC TGGTCTCAGC
         ********** ********** ****** *** ********** ********** **********
     61″ TTCCCTCCCT GCGTTCTTTC TTTCAC-CTC TCTCTCATTT TTACAAGGTC TGGTCTCAGC

    103' CAGACATGAA CCAATGANTG ATAGATGCTC CTGCTGAGCC CTGTGATGTG CCAGGGCCCT
         ********** ******* ** ********** ********** ********** **********
    120″ CAGACATGAA CCAATGA-TG ATAGATGCTC CTGCTGAGCC CTGTGATGTG CCAGGGCCCT

    163' GACATGCGNT GGCTTCTCTC TGATCCTCAC GTGACCTGCA GATGCAAAAG CCAGAGCTCN
         ******** * ********** ********** ********** ********** *********
    179″ GACATGCG-T GGCTTCTCTC TGATCCTCAC GTGACCTGCA GATGCAAAAG CCAGAGCTC-

    223' AGCATAGTTG AAAATCTTGA TTGAGGTCAT ATCCCAGTTA CTGGCACAGC NCGGATTTAA
         ********** ********** ********** ********** **********  *********
    237″ AGCATAGTTG AAAATCTTGA TTGAGGTCAT ATCCCAGTTA CTGGCACAGC -CGGATTTAA
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283’ ACCTAAGACT TTCCCCTACA CGACAGGGCT TTTATTTCTC ANGTCATCTG AAAAGGTGTC
     ********** ********** ********** ********** * ******** **********
296″ ACCTAAGACT TTCCCCTACA CGACAGGGCT TTTATTTCTC A-GTCATCTG AAAAGGTGTC

343’ AGCAAGGGAA ATGGCTTGTC TATTTCCAGG GGNCATTTTA CAAGCAAATA CTGAAAGGCT
     ********** ********** ********** ** ******* ********** **********
355″ AGCAAGGGAA ATGGCTTGTC TATTTCCAGG GG-CATTTTA CAAGCAAATA CTGAAAGGCT

403’ TCGGTGGGCT TAAGGGCTGA TGGNCTTTGA TCGAATTTCA GGCATGTTGG CCCCAAGGCC
     ********** ********** *** ****** ********** ********** **********
414″ TCGGTGGGCT TAAGGGCTGA TGG-CTTTGA TCGAATTTCA GGCATGTTGG CCCCAAGGCC

463’ CTGTGTATAT TCCCNTGGGC CCACTCAAGG GGATGCTGGA GCCGGAAAGT CCCCGGAGGC
     ********** **** ***** ********** ********** *** ******  ****** **
473″ CTGTGTATAT TCCC-TGGGC CCACTCAAGG GGATGCTGGA GCCCGAAAGT TCCCGGAAGC

523’ CACCTNACTG CAGCCCTGCA CTTTACAAAG AAGAGAAAGA TTCTCCCTAA AATTACNAGA
     ***** **** ********** ********** ********** *******
532″ CACCT-ACTG CAGCCCTGCA CTTTACAAAG AAGAGAAAGA TTCTCCCCC
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1st Nucleotide Sequence
  File Name         : Reference Seq.GNU
  Sequence Size     : 5289

2nd Nucleotide Sequence
  File Name         : RDB7295R.fasta (Complementary)
  Sequence Size     : 600

  Unit Size to Compare = 1
  Pick up Location     = 1


[98.030% / 609 bp]     INT/OPT.Score : <    545/  2254 >
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 541' CACTTTACAA AGAAGAGAAA GATTCTCCCT AAAATTACNA GAACA-GGGC CAAAGATGCC
                                ****  ******** * ***** **** **********
   1″                          CCCCT AAAATTAC-A GAACAGGGGC CAAAGATGCC

 600' TACCGGAGCA AACCCCCATG GGGGCACCTC NCTACCGCAG GTGAGCCCAA GGCTGGTCCT
      ********** ********** **********  ********* ********** **********
  35″ TACCGGAGCA AACCCCCATG GGGGCACCTC -CTACCGCAG GTGAGCCCAA GGCTGGTCCT

 660' GCCTTCTCAG TGGCTACCCC CNCTGAGCTC CCGCCACCAC ACAAAGTGTT CCAATCCTTG
      ** ******* ********** * ******** ********** ********** **********
  94″ GCTTTCTCAG TGGCTACCCC C-CTGAGCTC CCGCCACCAC ACAAAGTGTT CCAATCCTTG

 720' TGCATCCTCC AGNTCCTTTT AACCTCTCAT GTCCTGAGAG GCCAGAGCTA CAGCCACAGA
      ********** ** ******* ********** ********** ********** **********
 153″ TGCATCCTCC AG-TCCTTTT AACCTCTCAT GTCCTGAGAG GCCAGAGCTA CAGCCACAGA

 780' TTCNCAGAAG ACACCCCACT CCCAGCCCCA ACCTGCTGCC TTTAGAATTA TAAANCACTT
      *** ****** ********** ********** ********** ********** **** *****
 212″ TTC-CAGAAG ACACCCCACT CCCAGCCCCA ACCTGCTGCC TTTAGAATTA TAAA-CACTT

 840' CTTGTCATCA CAGGGTCCTG AAAGTCCCTT TTAAGCCTGG GACACNTAGG ACTCTAAAGG
      ********** ********** ********** ********** ***** **** **********
 270″ CTTGTCATCA CAGGGTCCTG AAAGTCCCTT TTAAGCCTGG GACAC-TAGG ACTCTAAAGG

 900' AAGATGATTC TTAAGGTCCC ATCCCACTTC CAAATTNCCT GCGATTCAAT GACATCACGG
      ********** ********** ********** ****** *** ********** **********
 329″ AAGATGATTC TTAAGGTCCC ATCCCACTTC CAAATT-CCT GCGATTCAAT GACATCACGG

 960' CTGTGAATAA TCAGCCTGGC CCGAAGCNCA GGATGGGCTG TGCTGCTTCC ACCGTGAACT
      ********** ********** ******* ** ********** ********** **********
 388″ CTGTGAATAA TCAGCCTGGC CCGAAGC-CA GGATGGGCTG TGCTGCTTCC ACCGTGAACT

1020' TCCTCCCCCT GCTTTATANA AAACAGGCCT GCCTCAGCTC CCTCATGGCC CTGTCCACTG
      ********** ******** * ********** ********** ********** **********
 447″ TCCTCCCCCT GCTTTATA-A AAACAGGCCT GCCTCAGCTC CCTCATGGCC CTGTCCACTG

1080' AGCATCCTCA TCAAGATCTG GCCTCGGCGG CCAAGCTTGG CAATCCGGTA CTGTTGGTAA
      ********** ********** ********** ********** ********** **********
 506″ AGCATCCTCA TCAAGATCTG GCCTCGGCGG CCAAGCTTGG CAATCCGGTA CTGTTGGTAA
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1140' AGCCACCATG GAAGATGCCA AAAACATTAA GAAGGGCCCA GCGCCATTCT ACCCACTCGA
      ********** ********** ********** *****
 566" AGCCACCATG GAAGATGCCA AAAACATTAA GAAGG
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