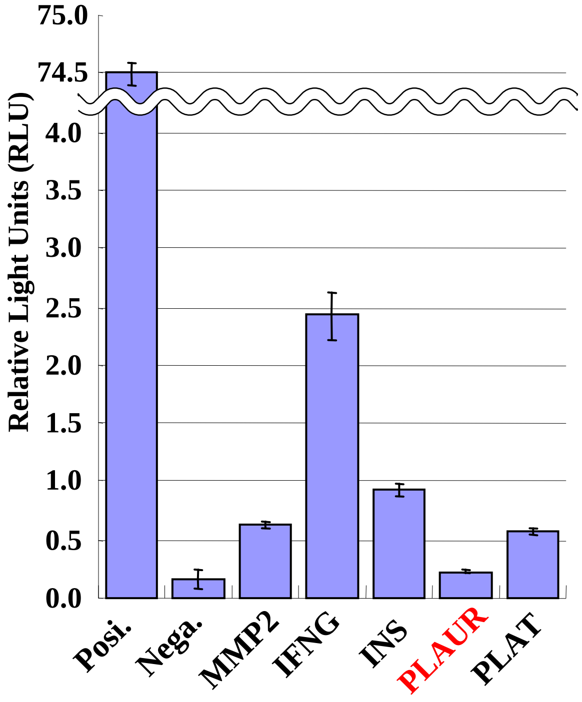
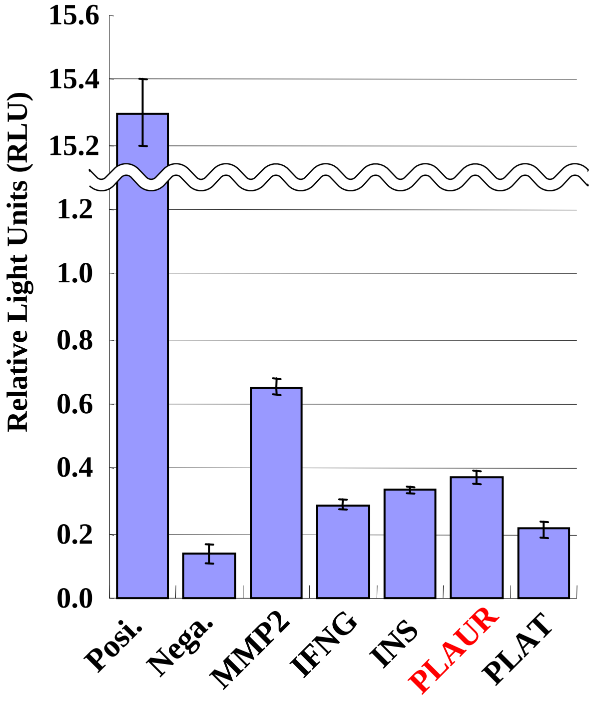
The Promoter Activities of Reporter Constructs

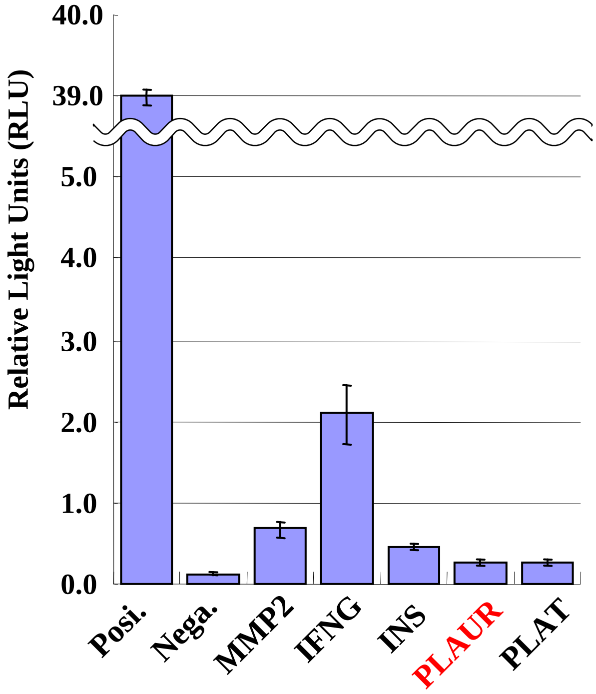
HeLa cells



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 : 2010.01.25

1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5486

2nd Nucleotide Sequence
  File Name         : RDB7312F.fasta
  Sequence Size     : 562

  Unit Size to Compare = 1
  Pick up Location     = 1



[89.655% / 551 bp]     INT/OPT.Score : <    409/  1705 >

     1'                  GGCC TAACTGGCCG GTACCTGAGC TCGCTAGCCT CGAGGATTTG
                            *  ***  .* *   .* ** *  ******  *   *   **
     1" CTTTATAGGG CAAGCCGTAC AAACAANCGG CANCTTGCGA TCGCTAAACA AGCCCATCAC

    45' AG----ACAG GGTCTCGCTC T-GTTGCCCA GGTNTGGAGT GCAGTGGTG- CAATCATAG-
        **    * *   *  ****** * **** ***  ** ****    ********  **  *****
    61" AGTACGAGAA CGGTTCGCTC TCGTTGACCA TGT-TGGATG ACAGTGGTGA CATACATAGA

    98' CTCACTGCAG CTTCCAGTTC CCAGGTNTCA AGCGGTCCTC CCACCTTAGC CTCCCAACTA
        * *** **** ********** ****** *** ********** ********** **********
   120" CACAC-GCAG CTTCCAGTTC CCAGGT-TCA AGCGGTCCTC CCACCTTAGC CTCCCAACTA

   158' CCTAGGACTA CAAGTACNGG GCCACTGCAC CCAGCTAATT TTATTTTATT TTTAATTTCT
        ********** ******* ** ********** ********** ********** **********
   178" CCTAGGACTA CAAGTAC-GG GCCACTGCAC CCAGCTAATT TTATTTTATT TTTAATTTCT

   218' TTTGGAAANG ATGAGGGCTC TTTATGTTTC CCAAGCTGAT CTTGAACTCC TGGCCCCAAN
        ******** * ********** ********** ********** ********** *********
   237" TTTGGAAA-G ATGAGGGCTC TTTATGTTTC CCAAGCTGAT CTTGAACTCC TGGCCCCAA-
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278’ GTGATCCTCC TGCCTTGGCT TCCCAAAGCA TTGGTGTTAC AGGCATGAGC NCACCTCATC
     ********** ********** ********** ********** **********  *********
295″ GTGATCCTCC TGCCTTGGCT TCCCAAAGCA TTGGTGTTAC AGGCATGAGC -CACCTCATC

338’ TGACCTCTTC TAAAATATTA TAAAATAAAT ACAGACATCA ANAATGAAAA CAAAAGAAAA
     ********** ********** ********** ********** * ******** **********
354″ TGACCTCTTC TAAAATATTA TAAAATAAAT ACAGACATCA A-AATGAAAA CAAAAGAAAA

398’ AGAAAAAACA AAACAAAAAT CCCCAAAACA ACNAACAACA AAAAATGCAG ACATCAATAA
     ********** ********** ********** ** ******* ********** **********
413″ AGAAAAAACA AAACAAAAAT CCCCAAAACA AC-AACAACA AAAAATGCAG ACATCAATAA

458’ CATTCACCAC TAAAT-ACTC TAGTNAAGCA TCTGCAAAAA CAAACAAACA AAC-AAAAAC
     ********** ***** **** **** ***** ********** ********** *** ******
472″ CATTCACCAC TAAATAACTC TAGT-AAGCA TCTGCAAAAA CAAACAAACA AACAAAAAAC

516’ CAGAATCCCA CCTAAGNCAT ACAGCCATTG TCGTAACAGT GATATCTACT TTTTTGGCTG
     ********** **  * .*** **********
531″ CAGAATCCCA CCCTAAGCAT ACAGCCATTG GG
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1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5486

2nd Nucleotide Sequence
  File Name        : RDB7312R.fasta (Complementary)
  Sequence Size    : 686

  Unit Size to Compare = 1
  Pick up Location     = 1


[90.103% / 677 bp]     INT/OPT.Score : <    243/  2058 >
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 661’ CGGCTCACTG CAACCCAACC TCCGNCCTC- CCGGGTTCAA GCGATTCTCC TGCCTCAGCC
                      ***  *  ** . * *  ******** * **** *** * ** ***** *
   1″                 CCACTC ACCACTCGCT CCGGGTTC-A GCGA-TCT-C TG-CTCAG-C

 720’ TCCTAAGTAA CACACANCAC GCCACTACGC CCGGCTAATT TTTGTATTTT TAGTAGAGAC
      **** *** * ****** *** *********  ******** * ****** *** **********
  42″ TCCT-AGT-A CACACA-CAC GCCACTACG- CCGGCTAA-T TTTGTA-TTT TAGTAGAGAC

 780’ GGGGTTTNCA CCATTAAGTG TTTTAATGTA GGTGCAATGC CTGGAATAGC TGCTGGCCNA
       ****** ** ********** ********** ********** ********** ******** *
  96″ -GGGTTT-CA CCATTAAGTG TTTTAATGTA GGTGCAATGC CTGGAATAGC TGCTGGCC-A

 840’ AAATGGAGGG CTCAACACAT TCCTTTAACA TTTACCAAGG ACCTACTTCN GTGCTGGGCA
      ********** ********** ********** ********** *********  **********
 153″ AAATGGAGGG CTCAACACAT TCCTTTAACA TTTACCAAGG ACCTACTTC- GTGCTGGGCA

 900’ CTGGTCCAGG AGCTGGGGGC ACAGCGGGAA GCAAAGCAAG NGGTTAAGTG TTTTAAGTGT
      ********** ********** ********** **********  ********* **********
 212″ CTGGTCCAGG AGCTGGGGGC ACAGCGGGAA GCAAAGCAAG -GGTTAAGTG TTTTAAGTGT

 960’ TTAAGAGATG CATATTTCAG GATGCATCTC TNAGATAAGG ACATTTTCCA AAATACCAGT
      ********** ********** ********** * ******** ********** **********
 271″ TTAAGAGATG CATATTTCAG GATGCATCTC T-AGATAAGG ACATTTTCCA AAATACCAGT

1020’ ATCCCTCCTG ACAAAACTAA CANAAAATCC TGTTAGCCAA ATAATCAGCC ACATTCATAT
      ********** ********** ** ******* ********** ********** **********
 330″ ATCCCTCCTG ACAAAACTAA CA-AAAATCC TGTTAGCCAA ATAATCAGCC ACATTCATAT

1080’ TTACCGTCAA AGTNTTTTAT CCTCATTTTA CAGCAGTGGA GAGCGATTGC CCCGGGTCCC
      ********** *** ****** ********** ********** ********** **********
 389″ TTACCGTCAA AGT-TTTTAT CCTCATTTTA CAGCAGTGGA GAGCGATTGC CCCGGGTCCC

1140’ ACGTNTAGGA AGAGAGAGAA CTGGGATTTG CACCCAGGCA ATCTGGGGAC AGAGCNTGTG
      **** ***** ********** ********** ********** ********** ***** ****
 448″ ACGT-TAGGA AGAGAGAGAA CTGGGATTTG CACCCAGGCA ATCTGGGGAC AGAGC-TGTG

1200’ ATCACAACTC CATGAGTCAG GGCCGAGCCA GCCCCTTCAC CACCAGNCCG GCCGCGCCCC
      ********** ********** ********** ********** ****** *** **    ****
 506″ ATCACAACTC CATGAGTCAG GGCCGAGCCA GCCCCTTCAC CACCAG-CCG GCGCGTCCCC
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```
1260' GGGAAGGGAA GTTTGTGGCG GAGGAGATCA AGATC-TGGC CTCGGCGGCC AAGCTTGGCA
      ********** ***    * * *********  ***** **.* ** ****.**      ** **
 565″ GGGAAGGGAA GTTGTGAGAG GAGGAGATC- AGATCGTGNC CTGGGCGNCC GTCTGTGTCA

1319' ATC-CGGTAC TGTTGGTAAA GCCACCATGG AAGATGCCAA AAACATTAAG AAGGGCCCAG
      *** **   .  **  **    *   * *  * *
 624″ ATCGCGCCTN AGTGTGTGTT GTTCCAAACG ATTGAGTTTC CATAGGTCTG GGGTTTCCCG

1378' CGCCATTCTA CCCACTCGAA GACGGGACCG CCGGCGAGCA GCTGCACAAA GCCATGAAGC

 684″ ACT
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