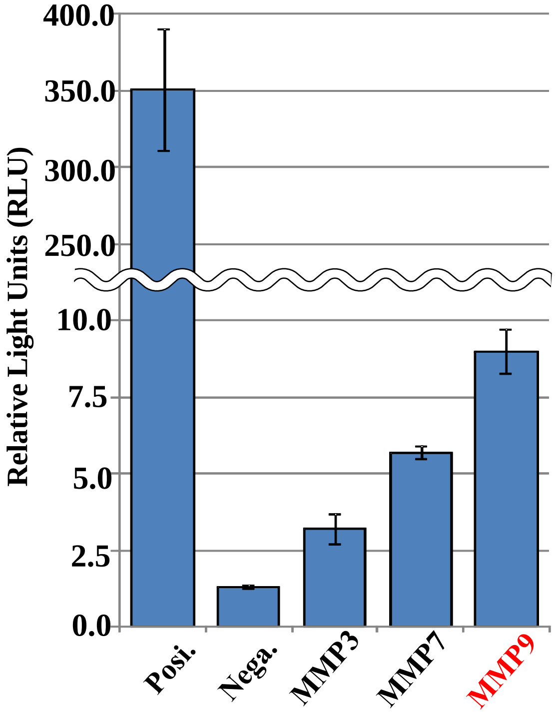
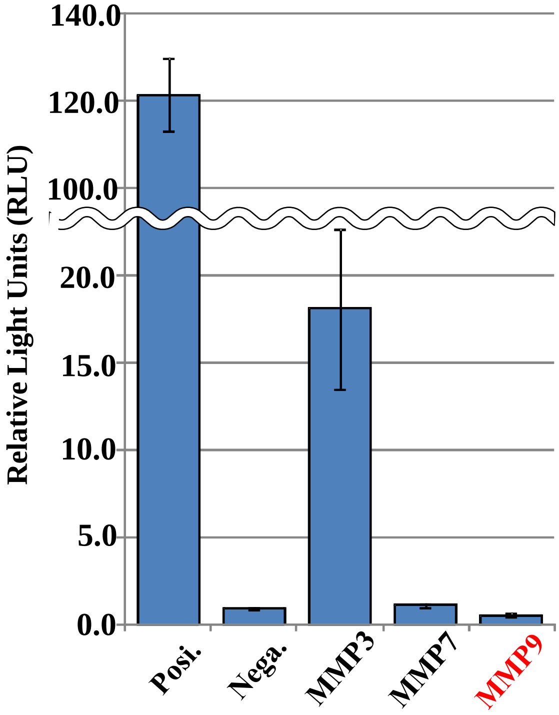
The Promoter Activities of Reporter Constructs

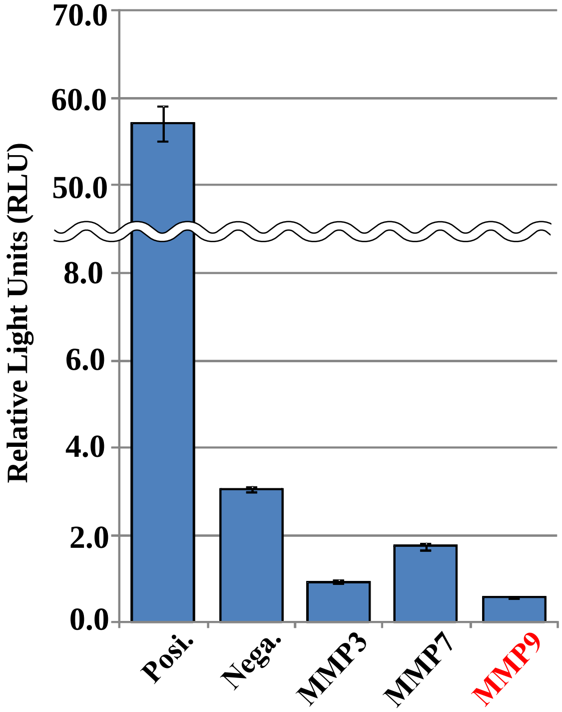
HeLa cells



HepG2 cells



Hep3B cells



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

MMP3: pGL4-phMMP3 (RDB# 7535)
MMP7: pGL4-phMMP7 (RDB# 7536)
MMP9: pGL4-phMMP9 (RDB# 7537)

2010, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.11.06
1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5612

2nd Nucleotide Sequence
  File Name         : RDB7537F.fasta
  Sequence Size     : 664
  Unit Size to Compare = 1
  Pick up Location     = 1
[96.037% / 656 bp]     INT/OPT.Score : <    364/  2322 >

     1'                    GG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATA
                           ** ********** ********** ********** **********
     1" GTGCCAGAAC ATTTCTCTGG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATA

    43' GGGCTGGAGA ACTGAAAGGG CTCCTATAGA NTTATTTTCC CCCATATCCT GCCCCAATTT
        ********** ********** **********  ********* ********** **********
    61" GGGCTGGAGA ACTGAAAGGG CTCCTATAGA -TTATTTTCC CCCATATCCT GCCCCAATTT

   103' GCAGTTGAAG AATCCTAAGC TNGACAAAGG GGAAGGCATT TACTCCAGGT TACACTGCAG
        ********** ********** * ******** ********** ********** **********
   120" GCAGTTGAAG AATCCTAAGC T-GACAAAGG GGAAGGCATT TACTCCAGGT TACACTGCAG

   163' CTTAGAGCCC AANTAACCTG GTTTGGTGAT TCCAAGTTAG AATCATGGTC TTTTGGCAGG
        ********** ** ******* ********** ********** ********** **********
   179" CTTAGAGCCC AA-TAACCTG GTTTGGTGAT TCCAAGTTAG AATCATGGTC TTTTGGCAGG

   223' GTCNTCGCTC TGTTGCCCAG GCTGGAGTGC AGTGACATAA TCATGGCTCA CTGTNATCCT
        *** ****** ********** ********** ********** ********** **** *****
   238" GTC-TCGCTC TGTTGCCCAG GCTGGAGTGC AGTGACATAA TCATGGCTCA CTGT-ATCCT

   283' TGACCTTCTT TCTGGGCTCA AGCAATCCTC CCACCTCGGC CTCCCNAAAG TGCTAAGATT
        ********** ********** ********** ********** ***** **** **********
   296" TGACCTTCTT TCTGGGCTCA AGCAATCCTC CCACCTCGGC CTCCC-AAAG TGCTAAGATT

   343' ACAGGAATGA GCCACCATAC CTGGCCCTGA ATCTTGNGGT CTTGGCCTTA GTAATTAAAA
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     ********** ********** ********** ****** *** ********** **********
355″ ACAGGAATGA GCCACCATAC CTGGCCCTGA ATCTTG-GGT CTTGGCCTTA GTAATTAAAA

403’ CCAATCACCA CCATCCGTTG CGGACTTNAC AACCTACAGT GTTCTAAACA TTTTATATGT
     ********** ********** ******* ** ********** ********** **********
414″ CCAATCACCA CCATCCGTTG CGGACTT-AC AACCTACAGT GTTCTAAACA TTTTATATGT

463’ TTGATCTCAT TTAATCCTNC ACAT--CAAT TTAGGGACAA AGAGCCCCCC A-CCCCCCG-
     ********** ******** * ****   *** ********** ********** . *******
473″ TTGATCTCAT TTAATCCT-C ACATCCAAAT TTAGGGACAA AGAGCCCCCC NCCCCCCCGT

519’ TTTTTTTTTT TACNAGCTGA GGAAACACTT CAAAGTGGTA AGACATTTGC CCGAGGTCCT
     ********** *  .****** **** ***** ********** ********** **********
532″ TTTTTTTTTT TTACAGCTGA GGAACCACTT CAAAGTGGTA AGACATTTGC CCGAGGTCCT

579’ GAAGNGAAGA GAGTAAAGCC ATGTCTGCTG -TTTTCTAGA GGCTGCTACT GTCCCCNTTT
     **** ***** **********  *** *****  ******* * ********** ****** **
592″ GAAG-GAAGA GAGTAAAGCC CTGTTTGCTG TTTTTCTAAA GGCTGCTACT GTCCCC-TTA

638’ ACTGCCCTGA AGATTCAGCC TGCGGAAGAC AGGGGGTTGC CCCAGTGNGA ATTCCCCAGC
     ********** ****
650″ ACTGCCCTGA AGATC
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1st Nucleotide Sequence
  File Name          : Reference Seq.gnu
  Sequence Size      : 5612
2nd Nucleotide Sequence
  File Name          : RDB7537R.fasta (Complementary)
  Sequence Size      : 814
  Unit Size to Compare = 1
  Pick up Location      = 1
[94.365% / 834 bp]     INT/OPT.Score : <    781/  2824 >

601’ GTCTGCTGTT TTCTAGAGGC TGCTACTGTC CCCNTTTACT GCCCTGAAGA TTCAGCCTGC
                                                                   **
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   1″                                                     CC CNGAAATCGC

 661' GGAAGACAGG GGGTTGCCCC AGTGNGAATT CCCCAGCCTT GCCTAGCAGA GCCCATTCCT
       *  ** * * *** ** *** *  *.***    ***** *** * ****** * * *******
  13″ CGCGGA-ACG GGGGTG-CCC A--GGGAA-- TCCCAG-CTT G-CTAGCA-A G-CCATTCC-

 721' TCCGCCCCCA GATGANAGCA GGGAGAGGAA GCTGAGTCAA AGAAGGCTGT CAGGGAGGGA
      ********** **.** **** ******** * ** ******* ********** ****  ****
  62″ TCCGCCCCCA GANGA-AGCA GGGAGAGGGA GC-GAGTCAA AGAAGGCTGT CAGGAGGGGA

 781' AAAAGANGGA CAGAGCCTGG AGTGTGGGGA GGGGTTTGGG GAGGATATCT GACCTGGNGA
      ****** *** ********** ********   ********** ********** *** *** **
 120″ AAAAGA-GGA CAGAGCCTGG AGTGTGGGAG GGGGTTTGGG GAGGATATCT GACATGG-GA

 841' GGGGGTGTTG CAAAAGGCCA AGGATGGGCC AGGGGGATCA TTAGTTTCNA GAAAGAAGTC
      ********** ********** ********** **********  ******* * **********
 178″ GGGGGTGTTG CAAAAGGCCA AGGATGGGCC AGGGGGATCA ATAGTTTC-A GAAAGAAGTC

 901' TCAGGGAGTC TTCCATCACT TTCCCTTGGC TGACCACTGN GAGGCTTTCA GACCAAGGGA
      ********** ********** ********** *********  ********** **********
 237″ TCAGGGAGTC TTCCATCACT TTCCCTTGGC TGACCACTG- GAGGCTTTCA GACCAAGGGA

 961' TGGGGGATCC CTCCAGCTTC ATCCCCCTCC NCTCCCTTTC ATACAGTTCC CACAAGCTCT
      ********** ********** **********  ********* ********** **********
 296″ TGGGGGATCC CTCCAGCTTC ATCCCCCTCC -CTCCCTTTC ATACAGTTCC CACAAGCTCT

1021' GCAGTTTGCA AAACCCTACC CNCTCCCCTG AGGGCCTGCG GTTTCCTGCG GGTCTGGGGT
      ********** ********** * ******** ***** **** ***** **** **********
 355″ GCAGTTTGCA AAACCCTACC C-CTCCCCTG AGGGCGTGCG GTTTCTTGCG GGTCTGGGGT

1081' CTTGCCTGAC TTNGGCAGTG GAGACTGCGG GCAGTGGAGA GAGGAGGAGG TGGTGTAAGC
      ********** ** ******* ********** ********** ********** **********
 414″ CTTGCCTGAC TT-GGCAGTG GAGACTGCGG GCAGTGGAGA GAGGAGGAGG TGGTGTAAGC

1141' CCTNTTCTCA TGCTGGTGCT GCCACACACA CACACACACA CACACACACA CACANCACAC
      *** ****** ********** ********** ********** ********** ***
 473″ CCT-TTCTCA TGCTGGTGCT GCCACACACA CACACACACA CACACACACA CAC-------

1201' ACACACACAC CCTGACCCCT GAGTCAGCAC TTGCCTGTCA AGGAGNGGGT GGGGTCACAG
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      ********** ********** ********** ********** ***** **** **********
 525″ ACACACACAC CCTGACCCCT GAGTCAGCAC TTGCCTGTCA AGGAG-GGGT GGGGTCACAG

1261’ GAGCGCCTCC TTAAAGCCCC CACAACAGCA GCTGCANGTC AGACACCTCT GCCCTCACCA
      ********** ********** ********** ****** *** ********** **********
 584″ GAGCGCCTCC TTAAAGCCCC CACAACAGCA GCTGCA-GTC AGACACCTCT GCCCTCACCA

1321’ TGAGCCTCTG GCAGCCCCTG GTCCTGGTGC TCCTGGTGCT GGGCTGCTGC TTTGCTGCCC
      ********** ********** ********** ********** ********** **********
 643″ TGAGCCTCTG GCAGCCCCTG GTCCTGGTGC TCCTGGTGCT GGGCTGCTGC TTTGCTGCCC

1381’ CCAGACAGCG CCAGTCCACC CTTGTGCTCT TATCAAGATC TGGCCTCGGC GGCCAAGCTT
      ********** ********** ********** ********** ********** **********
 703″ CCAGACAGCG CCAGTCCACC CTTGTGCTCT TATCAAGATC TGGCCTCGGC GGCCAAGCTT

1441’ GGCAATCCGG TACTGTTGGT AAAGCCACCA TGGAAGATGC CAAAAACATT AAGAAGGGCC
      ********** ********** ********** ********** ********** **
 763″ GGCAATCCGG TACTGTTGGT AAAGCCACCA TGGAAGATGC CAAAAACATT AA
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