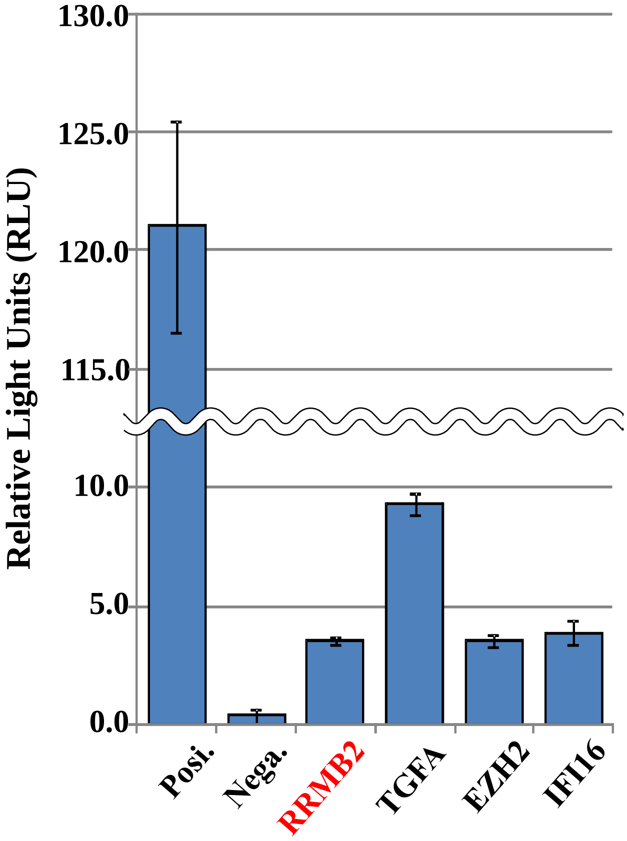
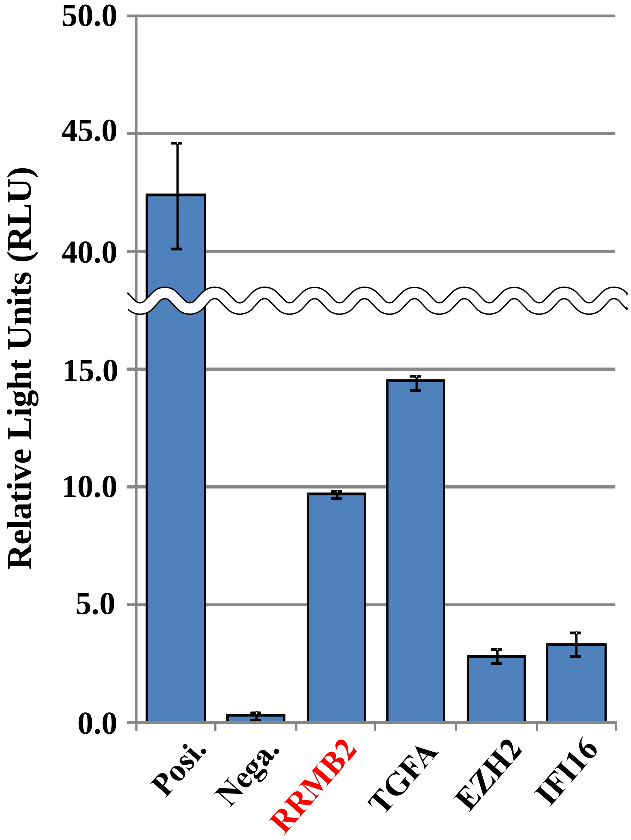
The Promoter Activities of Reporter Constructs

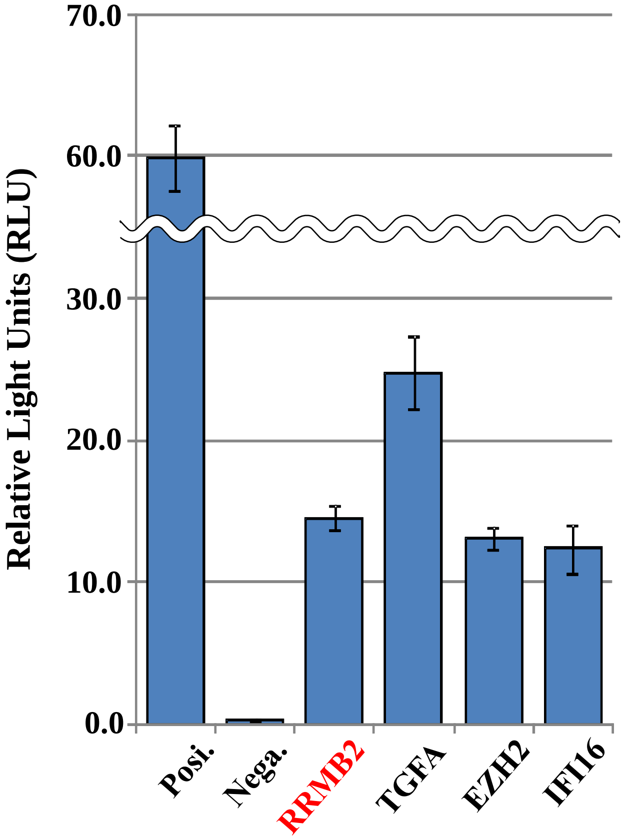
HeLa cells



HepG2 cells



Hep3B cells



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

RRMB2: pGL4-phRRMB2 (RDB# 7346)
TGFA: pGL4-phTGFA (RDB# 7348)
EZH2: pGL4-phEZH2 (RDB# 7370)
IFI16: pGL4-phIFI16 (RDB#7372)

2009, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.03.02

1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5565

2nd Nucleotide Sequence
  File Name        : RDB7346F.fasta
  Sequence Size    : 583

  Unit Size to Compare = 1
  Pick up Location     = 1



[98.932% / 562 bp]     INT/OPT.Score : <   1756/  2190 >

      1'                          GGCCTAA CTGGCCGGTA CCTGAGCTCG CTAGCCTCGA
                                  ******* ********** ********** **********
      1″ TGCAGGTGCC AGAACATTAC TCTGGCCTAA CTGGCCGGTA CCTGAGCTCG CTAGCCTCGA

     38' GGATTGATGC CCGACACACA ATTATTGTTT GATGACTTTA ATTGAATCTG ATTATTTGCC
         ********** ********** ********** ********** ********** **********
     61″ GGATTGATGC CCGACACACA ATTATTGTTT GATGACTTTA ATTGAATCTG ATTATTTGCC

     98' ACGTGGCCTA TAGTAAATTG AGACTCAGTT GCCTAGCAGA ATGTATGTGG CTATTATTTA
         ********** ********** ********** ********** ********** **********
    121″ ACGTGGCCTA TAGTAAATTG AGACTCAGTT GCCTAGCAGA ATGTATGTGG CTATTATTTA

    158' AAGTTCACAG ATGAAAAAAA TTTCACTCAG CATTTGACCC CTAGTAGTTG CTTTAAGAAA
         ********** ********** ********** ********** ********** **********
    181″ AAGTTCACAG ATGAAAAAAA TTTCACTCAG CATTTGACCC CTAGTAGTTG CTTTAAGAAA

    218' GACTGTCTAC CCCTACGCTA TGGCAGGTTT GAGAAAGGGC TTTCAGCATT TTCAACGCTT
         ********** ********** ********** ********** ********** **********
    241″ GACTGTCTAC CCCTACGCTA TGGCAGGTTT GAGAAAGGGC TTTCAGCATT TTCAACGCTT
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278’ AAAGTGAGAT CTTGATCCTA TTTACCATCC TTCAGCCAGC CACAAAACAG GTGCATGCTG
     ********** ********** ********** ********** ********** **********
301″ AAAGTGAGAT CTTGATCCTA TTTACCATCC TTCAGCCAGC CACAAAACAG GTGCATGCTG

338’ TTCAGGTCAT GGCAAGATCC CGTCAATCTT TCAGCTTCAA ACTACTTAAA CAAATCTCTC
     ********** ********** ********** ********** ********** **********
361″ TTCAGGTCAT GGCAAGATCC CGTCAATCTT TCAGCTTCAA ACTACTTAAA CAAATCTCTC

398’ TTCCATTTTA TTTTTGTTAG ACCAAACTA- TTTTTTTCAA AATATATTTT TTTCAAAATA
     **********  ********* *********  ********** ********** **********
421″ TTCCATTTTA ATTTTGTTAG ACCAAACTAT TTTTTTTCAA AATATATTTT TTTCAAAATA

457’ TTTGCCTGAC TTTAGTAACG TGTCCCTCTC CCCCTCACTC ACCCGCATTC ACACACACAC
     ********** ********** ********** ********** *********   *********
481″ TTTGCCTGAC TTTAGTAACG TGTCCCTCTC CCCCTCACTC ACCCGCATT- -CACACACAC

517’ ACACACACTT TCCCCCAGAC ACTTCCCCTT TTCGGTTGTT TACGCACGAA ACCAGCCAGC
     **********  ********* ********** **********  ****
539″ ACACACACTT CCCCCCAGAC ACTTCCCCTT TTCGGTTGTT AACGC
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1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5565

2nd Nucleotide Sequence
  File Name        : RDB7346R.fasta (Complementary)
  Sequence Size    : 582

  Unit Size to Compare = 1
  Pick up Location     = 1


[98.282% / 582 bp]     INT/OPT.Score : <   2132/  2219 >
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                                         * *. ** ***  ** ** *** ******
   1″                                    CCCNGGG AGTGGGGCCG AGCGGGAGGA

 898’ GGC-GGGGCC -GATGAGGTG A-GGTGGGGC CAGCTGGAGT AGGCTAAGCA GTCCAGAGCA
      *** ******  ********* * ******** ********** ********** **********
  28″ GGCGGGGGCC GGATGAGGTG AGGGTGGGGC CAGCTGGAGT AGGCTAAGCA GTCCAGAGCA

 955’ GGGGGCGTCC CTCAGTGGAA AGCCGGGCGA CTGGGCGGTG CAACAGAGTA AGGCGGGGCC
      ********** ********** ********** ********** ********** **********
  88″ GGGGGCGTCC CTCAGTGGAA AGCCGGGCGA CTGGGCGGTG CAACAGAGTA AGGCGGGGCC

1015’ AGCGGAAGCA GGGAGATTTC CTTAGGCCGC AGGCGGGGAA ATGGGGCTGG CCGGGGTAGG
      ********** ********** ********** ********** ********** **********
 148″ AGCGGAAGCA GGGAGATTTC CTTAGGCCGC AGGCGGGGAA ATGGGGCTGG CCGGGGTAGG

1075’ CGGAGCCCCG AGGCAGGGGA GGCGTGGCTG GCAGAGGTAG GCGGTGCCCC AAGGCAGGCG
      ********** ********** ********** ********** ********** **********
 208″ CGGAGCCCCG AGGCAGGGGA GGCGTGGCTG GCAGAGGTAG GCGGTGCCCC AAGGCAGGCG

1135’ GGGCTTGCCG AGACAGGGAT AATCCCTTAG GCCACAGGCT GGGAGGCAGG GCAGGCCGAG
      ********** ********** ********** ********** ********** **********
 268″ GGGCTTGCCG AGACAGGGAT AATCCCTTAG GCCACAGGCT GGGAGGCAGG GCAGGCCGAG

1195’ GCGGGGAGGA TCCCTTAGGC CGCAGTAGGG GAGGCGGGTC GGCCGAGGCG GGGAGAAACC
      ********** ********** ********** ********** ********** **********
 328″ GCGGGGAGGA TCCCTTAGGC CGCAGTAGGG GAGGCGGGTC GGCCGAGGCG GGGAGAAACC

1255’ CTTAGGCCGC AGGCGGGGAG GCGGGGCTGG CCGAAGTTAG GCGGAGCCCC GAGGCGGGGG
      ********** ********** ********** ********** ********** **********
 388″ CTTAGGCCGC AGGCGGGGAG GCGGGGCTGG CCGAAGTTAG GCGGAGCCCC GAGGCGGGGG

1315’ AGGCGGGGCC GGGCCGGCGC AGGGAGAGTC ACTCAATGGA CAGGCGAGAA ATCAAGATCT
      ********** ********** ********** ********** ********** **********
 448″ AGGCGGGGCC GGGCCGGCGC AGGGAGAGTC ACTCAATGGA CAGGCGAGAA ATCAAGATCT

1375’ GGCCTCGGCG GCCAAGCTTG GCAATCCGGT ACTGTTGGTA AAGCCACCAT GGAAGATGCC
      ********** ********** ********** ********** ********** **********
 508″ GGCCTCGGCG GCCAAGCTTG GCAATCCGGT ACTGTTGGTA AAGCCACCAT GGAAGATGCC
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   1435’ AAAAACATTA AGAAGGGCCC AGCGCCATTC TACCCACTCG AAGACGGGAC CGCCGGCGAG
         ********** *****
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[Reference Sequence]

Name of clone : pGL4-phRRM2B

Feature:

<Nucleotide sequence of 5’ upstream gene region of the RRM2B : 42-1364>

The 5’ upstream sequence of the gene derives from a reference sequence of the human.

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