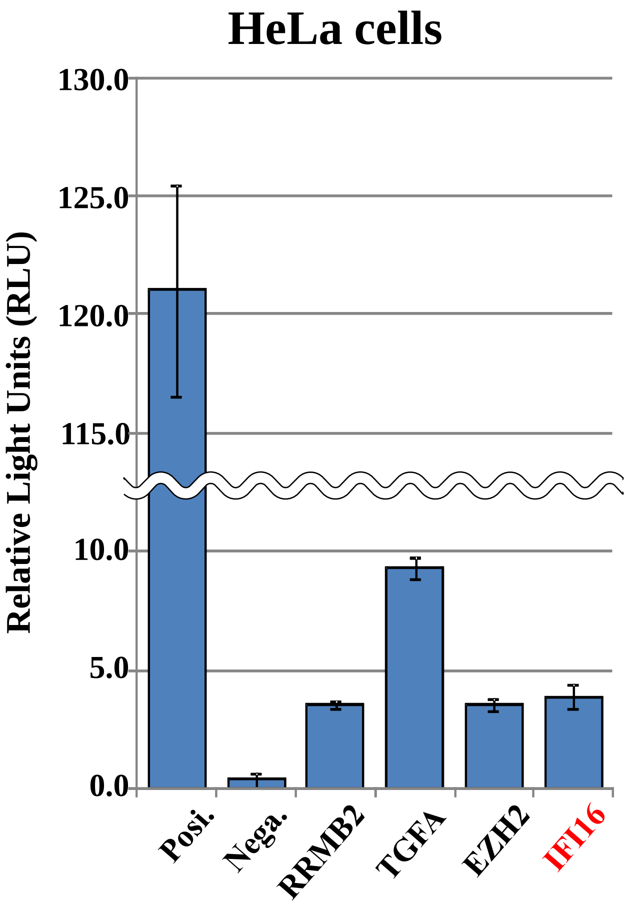
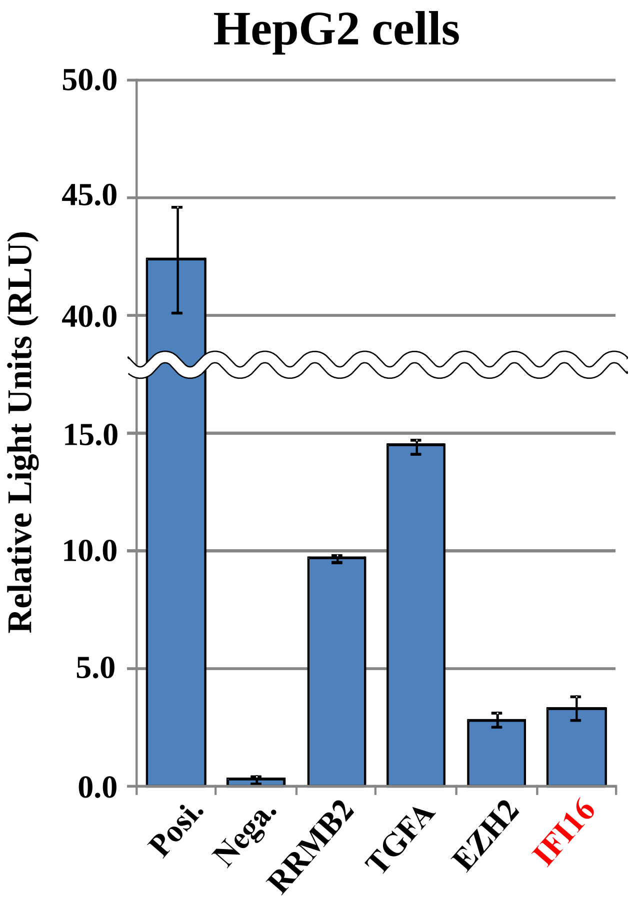
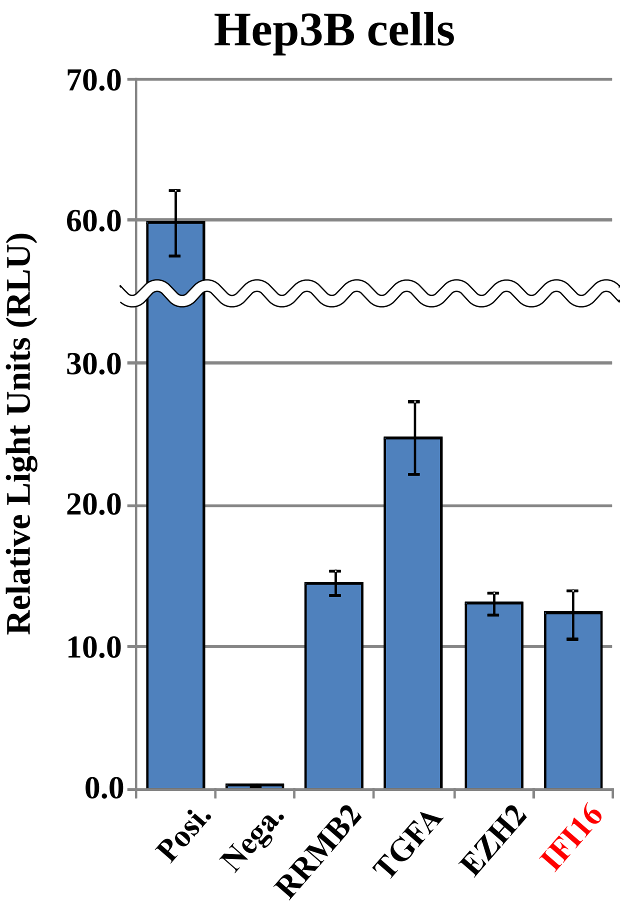
The Promoter Activities of Reporter Constructs


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

```
[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.03.02

1st Nucleotide Sequence
  File Name       : Reference Seq.gnu
  Sequence Size   : 5558

2nd Nucleotide Sequence
  File Name       : RDB7372F.fasta
  Sequence Size   : 642

  Unit Size to Compare = 1
  Pick up Location     = 1



[98.074% / 623 bp]     INT/OPT.Score : <   1756/  2360 >

     1’                     G GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGG-A
                            * ********** ********** ********** ******** *
     1″ GTGCCAGAAC ATTGTCTCTG GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAA

    41’ TGGTTCCCAG TGACTGCCTT AATATCCTTC TCTACCTACT GCCTTAAGGC CAACTCAATG
        ********** ********** ********** ********** ********** **********
    61″ TGGTTCCCAG TGACTGCCTT AATATCCTTC TCTACCTACT GCCTTAAGGC CAACTCAATG

   101’ TA-TCCACG- TAAAGAGTAC CCTAAAGCCA GTAAAAGATT ATCACGAACA CCCAGAGATG
        ** ******  ********** ********** ********** ********** **********
   121″ TATTCCACGT TAAAGAGTAC CCTAAAGCCA GTAAAAGATT ATCACGAACA CCCAGAGATG

   159’ TTTATGGCCA TCATTCCAGA TCCTCTTTGC TTTTTCTTGA CTTACTCCTT TTTTGATAAA
        ********** ********** ********** ********** ********** **********
   181″ TTTATGGCCA TCATTCCAGA TCCTCTTTGC TTTTTCTTGA CTTACTCCTT TTTTGATAAA

   219’ GTTATTCATA TGGTTTCAAA TCCAGAATTC AGCTATTCAC TTCATGGCCC TAGTTTGGAT
        ********** ********** ********** ********** ********** **********
   241″ GTTATTCATA TGGTTTCAAA TCCAGAATTC AGCTATTCAC TTCATGGCCC TAGTTTGGAT
```

```
279' TAAAACAATC AGCTTTCTTT TGCTCTGTAG ATGGCCTTGG ACAGTACATA TTAACAGTCT
     ********** ********** ********** ********** ********** **********
301″ TAAAACAATC AGCTTTCTTT TGCTCTGTAG ATGGCCTTGG ACAGTACATA TTAACAGTCT

339' ATGGGGCCCC TTTTCCACTC ATGACCACAT CCTGCTTGCA GATCTGCTGC TGGGTTAACA
     ********** ********** ********** ********** ********** **********
361″ ATGGGGCCCC TTTTCCACTC ATGACCACAT CCTGCTTGCA GATCTGCTGC TGGGTTAACA

399' CCACATCATC TGCTAGTTGA TGCCATTTAT TTGACATCCT GGGGTTACAG CACGCTAAAG
     ********** ********** ********** ********** ********** **********
421″ CCACATCATC TGCTAGTTGA TGCCATTTAT TTGACATCCT GGGGTTACAG CACGCTAAAG

459' GGCACCCACT GTCCTTAACA GAGAAAAATA CACTGCTGAG CAGAGGATTA AACAGACTCC
     ********** ********** ********** ********** ********** **********
481″ GGCACCCACT GTCCTTAACA GAGAAAAATA CACTGCTGAG CAGAGGATTA AACAGACTCC

519' TCACACTACC GGAAGTTCAG TGCATTTTC- CAGGATTTTC -AAGTCTTCG ATGCTGTCAT
     ********** ********** *********  **********  ********* **********
541″ TCACACTACC GGAAGTTCAG TGCATTTTCA CAGGATTTTC AAAGTCTTCG ATGCTGTCAT

577' GTTGAGAGTC CACTATCCAC -GTTTGTTTA TCCAGGAATA ATGCAGAAAA TCTGAGCATT
     ********** ****** ***  *** ***** **** * * *  *
601″ GTTGAGAGTC CACTATACAC GGTTAGTTTA TCCAAGGAAA TT
```

```
1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5558

2nd Nucleotide Sequence
  File Name         : RDB7372R.fasta (Complementary)
  Sequence Size     : 524

  Unit Size to Compare = 1
  Pick up Location     = 1
```

```
[97.901% / 524 bp]     INT/OPT.Score : <   1980/  1993 >

   901' TGCCACTGCC ACTCTGTGCA CAGGAAAGGA GGGGAGAAGA AGCCATGTTG CTTCTCTTAT
                     ***** ********** ********** ********** **********
     1″               GGGTGCA CAGGAAAGGA GGGGAGAAGA AGCCATGTTG CTTCTCTTAT

   961' ATTTGAGCAT CATTTAAGGG AATATAAGTC TCTAATGACT CACATGTAAG TCTGCTGGGT
        ********** ********** ********** ********** ********** **********
    48″ ATTTGAGCAT CATTTAAGGG AATATAAGTC TCTAATGACT CACATGTAAG TCTGCTGGGT

  1021' AAGAAAGTTC TAATGTTGGA ACTCCTTTCA GCTATCGAAT TTTGTAAGAA AAAAAACTTA
        ********** ********** ********** ********** ********** **********
   108″ AAGAAAGTTC TAATGTTGGA ACTCCTTTCA GCTATCGAAT TTTGTAAGAA AAAAAACTTA

  1081' TTTGTGTTTA TATACATTTA TGAGATACAA GTGTAATTTC GTTACATGGA TATATGCCAT
        ********** ********** ********** ********** ********** **********
   168″ TTTGTGTTTA TATACATTTA TGAGATACAA GTGTAATTTC GTTACATGGA TATATGCCAT

  1141' ATTGGTGAAG TCAGAGATTT CAGTGTGCAC ATCACCCGAA AAATGTTAAC TGTACCCATT
        ********** ********** ********** ********** ********** **********
   228″ ATTGGTGAAG TCAGAGATTT CAGTGTGCAC ATCACCCGAA AAATGTTAAC TGTACCCATT

  1201' AAAGTAATTT CTCATCCCCC ATTTCCCCTC ACCACATGCT CCAGCCCTTG CCAGGAAACT
        ********** ********** ********** ********** ********** **********
   288″ AAAGTAATTT CTCATCCCCC ATTTCCCCTC ACCACATGCT CCAGCCCTTG CCAGGAAACT

  1261' GTTCATTTTC TCTGACTAAC AGAAACGAAA GCTAAAAACA CTGGTGGGAG GAGTCTCCAC
        ********** ********** ********** ********** ********** **********
   348″ GTTCATTTTC TCTGACTAAC AGAAACGAAA GCTAAAAACA CTGGTGGGAG GAGTCTCCAC

  1321' ATTGTTTCCT ACTCCATTTT CTCTGGGGCA ATAGCAGATC AAGATCTGGC CTCGGCGGCC
        ********** ********** ********** ********** ********** **********
   408″ ATTGTTTCCT ACTCCATTTT CTCTGGGGCA ATAGCAGATC AAGATCTGGC CTCGGCGGCC

  1381' AAGCTT-GGC AATCCGGTAC TGTTGGTAAA GCCAC-CATG GAAGATGCCA AAAACATTAA
        ****** *** ***** **** *****  *** ***** ** * * *** **** ** ***. *
   468″ AAGCTTGGGC AATCC-GTAC TGTTGTGAAA GCCACTCAGG GTAGA-GCCA AATACANCA
```