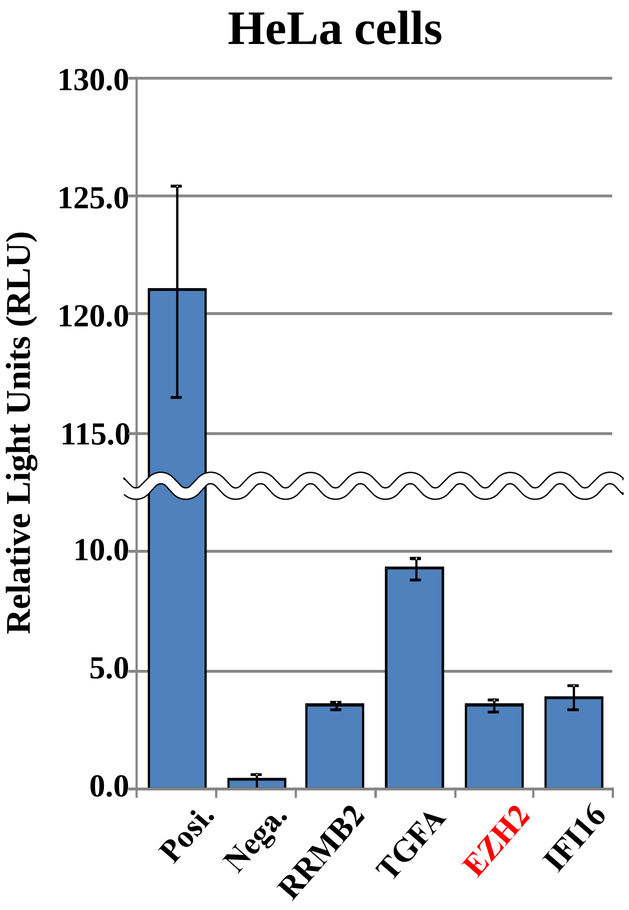
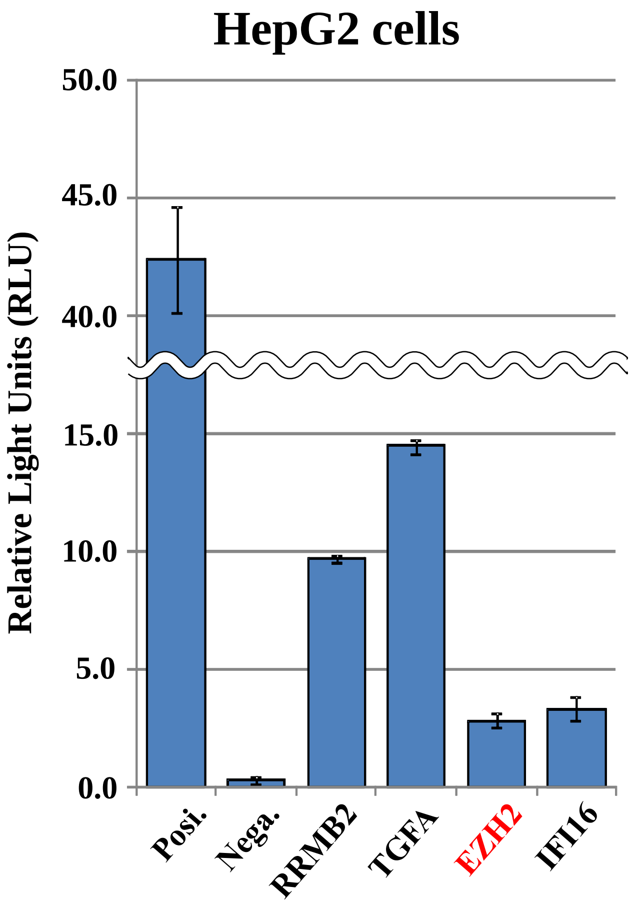
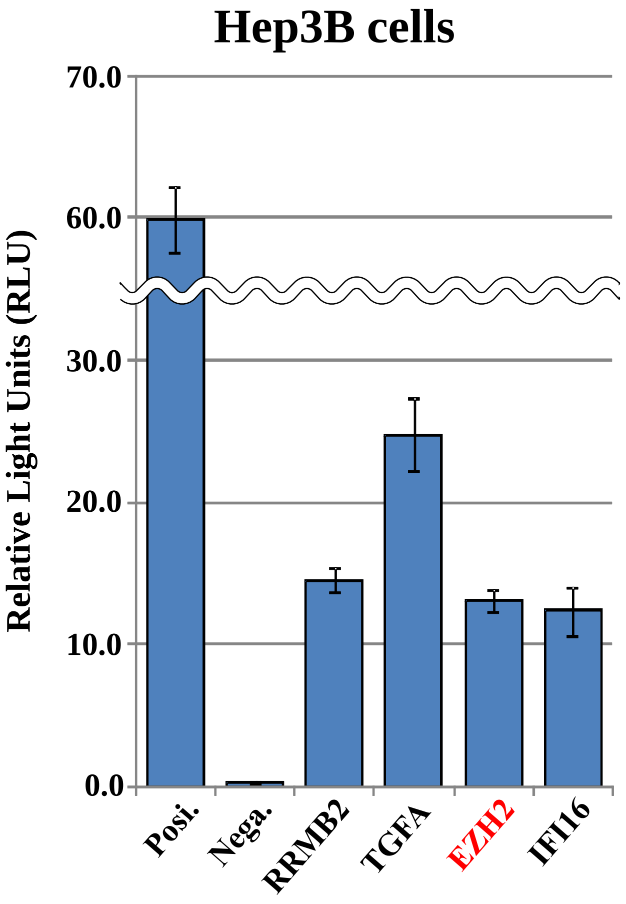
The Promoter Activities of Reporter Constructs







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    : 5447

2nd Nucleotide Sequence
  File Name        : RDB7370F.fasta
  Sequence Size    : 692

  Unit Size to Compare = 1
  Pick up Location     = 1



[99.106% / 671 bp]     INT/OPT.Score : <   2280/  2628 >

      1’                     G GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT
                             * ********** ********** ********** **********
      1″ GGTGCCAGAA CATTTCTCTG GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT

     42’ CGCCTTGCAA ATATCCTCAC ACTTTGCAGA GGCGGCAAGT GAACAGTGCT CATCTTGATA
         ********** ********** ********** ********** ********** **********
     61″ CGCCTTGCAA ATATCCTCAC ACTTTGCAGA GGCGGCAAGT GAACAGTGCT CATCTTGATA

    102’ AAGGATTTTT AACACTGACA CGTGCTTAGA ACTACGAACA GTGGAAGGGT CTGAAATGGC
         ********** ********** ********** ********** ********** **********
    121″ AAGGATTTTT AACACTGACA CGTGCTTAGA ACTACGAACA GTGGAAGGGT CTGAAATGGC

    162’ AGCAATGTCG CCCTTTCACA GGTTTCTAGG GCGATAAGCA CTGCAAGCTC GGCCAGCCAA
         ********** ********** ********** ********** ********** **********
    181″ AGCAATGTCG CCCTTTCACA GGTTTCTAGG GCGATAAGCA CTGCAAGCTC GGCCAGCCAA

    222’ AGTCCAGCGG TGGGGGAAAA AACGGCCAAG GCAGCAGCAG ACATAATCAA ACAGGGCCCG
         ********** ********** ********** ********** ********** **********
    241″ AGTCCAGCGG TGGGGGAAAA AACGGCCAAG GCAGCAGCAG ACATAATCAA ACAGGGCCCG
```

```
282' GGTCGGCGGC GGTGGCTCAC GCCTGTAATC CCAGCACTTT GGGAGGCCGA GGCGGGCGGA
     ********** ********** ********** ********** ********** **********
301″ GGTCGGCGGC GGTGGCTCAC GCCTGTAATC CCAGCACTTT GGGAGGCCGA GGCGGGCGGA

342' TCACCAGAAG TCGGGAGTTC GAGACCAGCC TGACCAAGAC CCGTCTCTAC TAAAAATAGA
     ********** ********** ********** ********** ********** **********
361″ TCACCAGAAG TCGGGAGTTC GAGACCAGCC TGACCAAGAC CCGTCTCTAC TAAAAATAGA

402' AAATTAGCCG GGCGTGGTGG CGCATGCCTG TAATCCAGCT ACTCGGGAGG CTGAGGCATG
     ********** ********** ********** ********** ********** **********
421″ AAATTAGCCG GGCGTGGTGG CGCATGCCTG TAATCCAGCT ACTCGGGAGG CTGAGGCATG

462' AGAATCGCTT GAACCCGGAA GGCGGAGGTT GCGGTGAGTC GAGATCGCGC CATTGCACTC
     ********** ********** ********** ********** ********** **********
481″ AGAATCGCTT GAACCCGGAA GGCGGAGGTT GCGGTGAGTC GAGATCGCGC CATTGCACTC

522' CAGCCTGGAC AACCAGAGCG AAACTCCGTC TCAGGAG-AA AAAAAAAAAA GTAGTAACGG
     ********** ********** ********** ******* ** ********** **********
541″ CAGCCTGGAC AACCAGAGCG AAACTCCGTC TCAGGAGAAA AAAAAAAAAA GTAGTAACGG

581' GTCCGGCGGC AGCGCGCGGG CCGGGCGAGC GTCTCCCGGC AAACGCGGCG CCACAGCTGA
     ** ******* **********  * ******* ********** ********** **********
601″ GTTCGGCGGC AGCGCGCGGG GCCGGCGAGC GTCTCCCGGC AAACGCGGCG CCACAGCTGA

641' GCCGACCTCC -GGGGCCCGC GCCCTCCCCT CCCCGGGCAC CACTAGGAGC GGCCAGCCCG
     ***** ****  ********* **********
661″ GCCGAACTCC GGGGGCCCGC GCCCTCCCCT TT
```

1st Nucleotide Sequence
  File Name　　　: Reference Seq.gnu
  Sequence Size　: 5447

2nd Nucleotide Sequence
  File Name　　　: RDB7370R.fasta (Complementary)
  Sequence Size　: 510

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



[98.232% / 509 bp]     INT/OPT.Score : <   1716/  1950 >

  781' GCTTCCAGCA CCCGCCCCGC CCCTCCCCCG CCCGGGAACT CTGCGGCGCC GGTTCCCGCC
                                               * *********  **********
    1"                                        AT CTGCGGCGCG GGTTCCCGCC

  841' AAGAGCCGCC GGCGCTTCGT CCCGCCCTTC GGCCGGTTCC CGCCACCTAT CCTCCCCGCC
       ****** **  ********** ** ******* ********** ********** **********
   23" AAGAGCGGCG GGCGCTTCGT CCGGCCCTTC GGCCGGTTCC CGCCACCTAT CCTCCCCGCC

  901' TCCCGTCCGC GGCGGGCTCC GGGCCCCCGC GATGTCTCCC GGTCCCCGCG TGCCTGCACA
       ********** ********** ********** ********** ********** **********
   83" TCCCGTCCGC GGCGGGCTCC GGGCCCCCGC GATGTCTCCC GGTCCCCGCG TGCCTGCACA

  961' CCGCCTTCCT GAGAGGCGCC GTGTGTTCAG CGAAAGAACA AAGAGACGGC GGCGGCGCTT
       ********** ********** ********** ********** ********** **********
  143" CCGCCTTCCT GAGAGGCGCC GTGTGTTCAG CGAAAGAACA AAGAGACGGC GGCGGCGCTT

 1021' CCACACGGCC AGTGGCGTCC CTTACAGCGA ACCCCGCCGC CGCCCGCGCG CGCACGCGCT
       ********** ********** ********** ********** ********** **********
  203" CCACACGGCC AGTGGCGTCC CTTACAGCGA ACCCCGCCGC CGCCCGCGCG CGCACGCGCT

 1081' GCCAGTGCCC GCCCGCCCAC GAGCCCTGAG CGCACTCTGC GTGGGGCTGG CTCGGCGCCT
       ********** ********** ********** ********** ********** **********
  263" GCCAGTGCCC GCCCGCCCAC GAGCCCTGAG CGCACTCTGC GTGGGGCTGG CTCGGCGCCT

 1141' CCGAGCCCGG CGGGCCCTGT GATTGGACGG GCGCCCGCCT CGCGTCCCGC CAATCGGGGC
       ********** ********** ********** ********** ********** **********
  323" CCGAGCCCGG CGGGCCCTGT GATTGGACGG GCGCCCGCCT CGCGTCCCGC CAATCGGGGC

 1201' GGCGCTTGAT TGGGCTGGGG GGGCCAAATA AAAGCGATGG CGATTGATCA AGA-TCTGGC
       ********** ********** ********** ********** ********** *** ******
  383" GGCGCTTGAT TGGGCTGGGG GGGCCAAATA AAAGCGATGG CGATTGATCA AGATTCTGGC
```

```
1260' CTCGGCGGCC AAGCTTGGCA ATCCGGTACT GTTGGTAAAG CCACCATGGA A--GATGCCA
      ********** ********** ********** ********** ********** *   ******
 443" CTCGGCGGCC AAGCTTGGCA ATCCGGTACT GTTGGTAAAG CCACCATGGA ACGAATGCCA

1318' AA-AACATTA AGAAGGGCCC AGCGCCATTC TACCCACTCG AAGACGGGAC CGCCGGCGAG
      ** *****
 503" AACAACAT
```