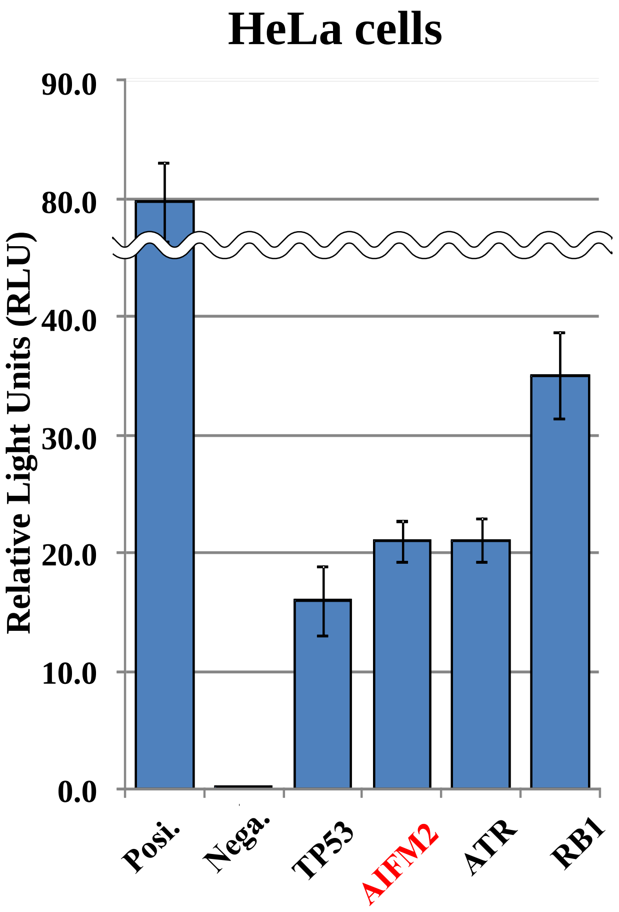
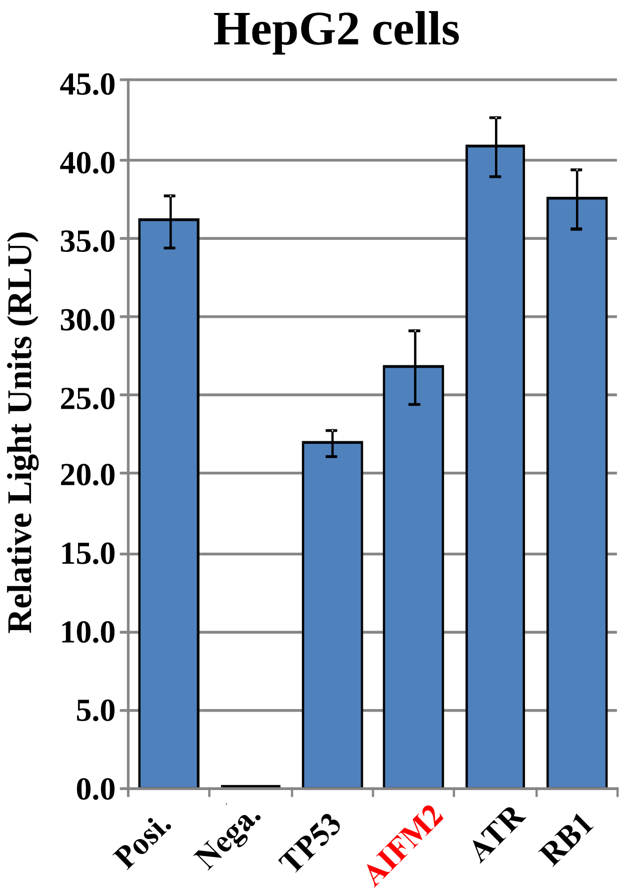
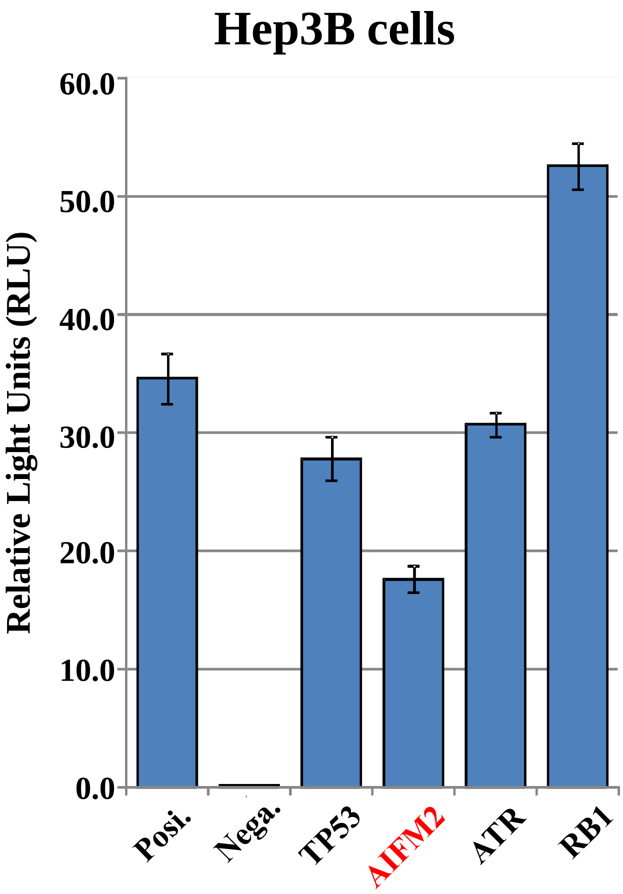
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

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

TP53: pGL4-phTP53 (RDB# 7330)
AIFM2: pGL4-phAIFM2 (RDB# 7332)
ATR: pGL4-phATR (RDB# 7334)
RB1: pGL4-phRB1 (RDB#7345)

2010, 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     : 5520

2nd Nucleotide Sequence
  File Name         : RDB7332F.fasta
  Sequence Size     : 529

  Unit Size to Compare = 1
  Pick up Location     = 1



[100.000% / 509 bp]     INT/OPT.Score : <   2036/  2036 >

      1’                       GGCCTAACTG GCCGGTACCT GAGCTCGCTA GCCTCGAGGA
                               ********** ********** ********** **********
      1″ AGGTGCCAGA ACATTTCTCT GGCCTAACTG GCCGGTACCT GAGCTCGCTA GCCTCGAGGA

     41’ TTGGCCCTTA TCCACAACTC TTAAAGTAGG TGCTAATATT TGCAGTAAGT AGATGGAGAT
         ********** ********** ********** ********** ********** **********
     61″ TTGGCCCTTA TCCACAACTC TTAAAGTAGG TGCTAATATT TGCAGTAAGT AGATGGAGAT

    101’ GGCTTATCTT TCGCTGAGTT AGCTTGGTCT GATTTGAGCT GGCAATACAC TGCCTTCCAG
         ********** ********** ********** ********** ********** **********
    121″ GGCTTATCTT TCGCTGAGTT AGCTTGGTCT GATTTGAGCT GGCAATACAC TGCCTTCCAG

    161’ GTCATTGTCC TGCCTGTGGG TCTTTGCACA TCCAGACCAC ACTTCCTTCC TCTTTACCTA
         ********** ********** ********** ********** ********** **********
    181″ GTCATTGTCC TGCCTGTGGG TCTTTGCACA TCCAGACCAC ACTTCCTTCC TCTTTACCTA

    221’ AATCTACCTC TTTCTCATCC TTGGAGAGAA GTATTTGCAC CCTTCCTTTG CCCTCAGTCT
         ********** ********** ********** ********** ********** **********
    241″ AATCTACCTC TTTCTCATCC TTGGAGAGAA GTATTTGCAC CCTTCCTTTG CCCTCAGTCT
```

```
   281' TTCTTTTTTA TTTTTTCATT TCATTTCATT TATTATTATT ATTATTATTA TTTTTTTTTT
        ********** ********** ********** ********** ********** **********
   301″ TTCTTTTTTA TTTTTTCATT TCATTTCATT TATTATTATT ATTATTATTA TTTTTTTTTT

   341' GAGACAGAAT CTCACAGTCA CCTAGGCTGG AGTGCAGTGG AATGATCATG GTTCACTGTA
        ********** ********** ********** ********** ********** **********
   361″ GAGACAGAAT CTCACAGTCA CCTAGGCTGG AGTGCAGTGG AATGATCATG GTTCACTGTA

   401' GCCTCAAACT CCTGGGCTCA AGCAATCCTC CCACCTCAGC TTCCCGAGAA GCTGGGACTA
        ********** ********** ********** ********** ********** **********
   421″ GCCTCAAACT CCTGGGCTCA AGCAATCCTC CCACCTCAGC TTCCCGAGAA GCTGGGACTA

   461' CAGGTGTGCA CCAACAAGCC CGGCTAATTT TTGTAGGTCT CGCTATGTTG CCCAGGCTGG
        ********** ********** ********** ********** *********
   481″ CAGGTGTGCA CCAACAAGCC CGGCTAATTT TTGTAGGTCT CGCTATGTT
```

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1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5520

2nd Nucleotide Sequence
  File Name        : RDB7332R.fasta (Complementary)
  Sequence Size    : 671

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

```
[97.941% / 680 bp]     INT/OPT.Score : <   1764/  2611 >

   721' CAGGAACCTT GTCAGTTTTC TCTCCAAGTT ATCCCTCCAA CGCCTAGCAC AGTGCCTGGC
          *.* **** ********** ***** ** * ********** ********** **********
     1″  GGNACCCTT GTCAGTTTTC TCTCCCAGAT ATCCCTCCAA CGCCTAGCAC AGTGCCTGGC
```

```
 781’ AAATGTAGGA GCTCAACAGG GTTTGCGGAA TTATTATGTG TATGTCTGAA GGAAGGATGT
      ********** ********** ********** ********** ********** **********
  60″ AAATGTAGGA GCTCAACAGG GTTTGCGGAA TTATTATGTG TATGTCTGAA GGAAGGATGT

 841’ TGGCAGTGCG CCCAACGTGT GAGGGGAACC CCACTCTCCA AGGTTCCAGT GGCTTTAAAG
      ********** ********** ********** ********** ********** **********
 120″ TGGCAGTGCG CCCAACGTGT GAGGGGAACC CCACTCTCCA AGGTTCCAGT GGCTTTAAAG

 901’ GTGTCCTCGA GAAAATCAGA GGAACAGGGG GATGCTTGTT TTCCTTCCTT CCTTCTCTCT
      ********** ********** ********** ********** ********** ****
 180″ GTGTCCTCGA GAAAATCAGA GGAACAGGGG GATGCTTGTT TTCCTTCCTT CCTT------

 961’ CTCTCTCTCT CTCTCTCTCT CTCTCTCTCT CTCTCTCTCT CTCTCTCTCT CTTTTTTGCT
          ****** ********** ********** ********** ********** **********
 234″ ----CTCTCT CTCTCTCTCT CTCTCTCTCT CTCTCTCTCT CTCTCTCTCT CTTTTTTGCT

1021’ TTAAAGTATG CTGAAAGGAC ACTTTAAACC AAGTCTGAAT GGCTCGGCAG GACTGGGGCG
      ********** ********** ********** ********** ********** **********
 290″ TTAAAGTATG CTGAAAGGAC ACTTTAAACC AAGTCTGAAT GGCTCGGCAG GACTGGGGCG

1081’ CGGGTGCTGG CAGGAGCCGG AGAGGCGACA TCTGGCCATG GGAGCATTTG TTTCAAAGTT
      ********** ********** ********** ********** ********** **********
 350″ CGGGTGCTGG CAGGAGCCGG AGAGGCGACA TCTGGCCATG GGAGCATTTG TTTCAAAGTT

1141’ CAAGGCCGTT CGCTCAGGGT CAAGGTTAGT CCGGCGGGCC GTTCGGAGAC CAGCCCCAGC
      ********** ********** ********** ********** ********** **********
 410″ CAAGGCCGTT CGCTCAGGGT CAAGGTTAGT CCGGCGGGCC GTTCGGAGAC CAGCCCCAGC

1201’ GTGCCAGGAC CGTTTCCGGG GCCTGGCCGG GGCGTTGCCG CGGGGTCGGG GACCAGCACG
      ********** ********** ********** ********** ********** **********
 470″ GTGCCAGGAC CGTTTCCGGG GCCTGGCCGG GGCGTTGCCG CGGGGTCGGG GACCAGCACG

1261’ AGTGCTGAGT CACGCCCCGC CCGGGAGCGC CTCGGGTCAG TAACTCGGGA AGACGACCAA
      ********** ********** ********** ********** ********** **********
 530″ AGTGCTGAGT CACGCCCCGC CCGGGAGCGC CTCGGGTCAG TAACTCGGGA AGACGACCAA

1321’ TCAAGATCTG GCCTCGGCGG CCAAGCTTGG CAATCCGGTA CTGTTGGTAA AGCCACCATG
      ********** ********** ********** ********** ********** **********
 590″ TCAAGATCTG GCCTCGGCGG CCAAGCTTGG CAATCCGGTA CTGTTGGTAA AGCCACCATG
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```
1381' GAAGATGCCA AAAACATTAA GAAGGGCCCA GCGCCATTCT ACCCACTCGA AGACGGGACC
      ********** ********** **
 650" GAAGATGCCA AAAACATTAA GA
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