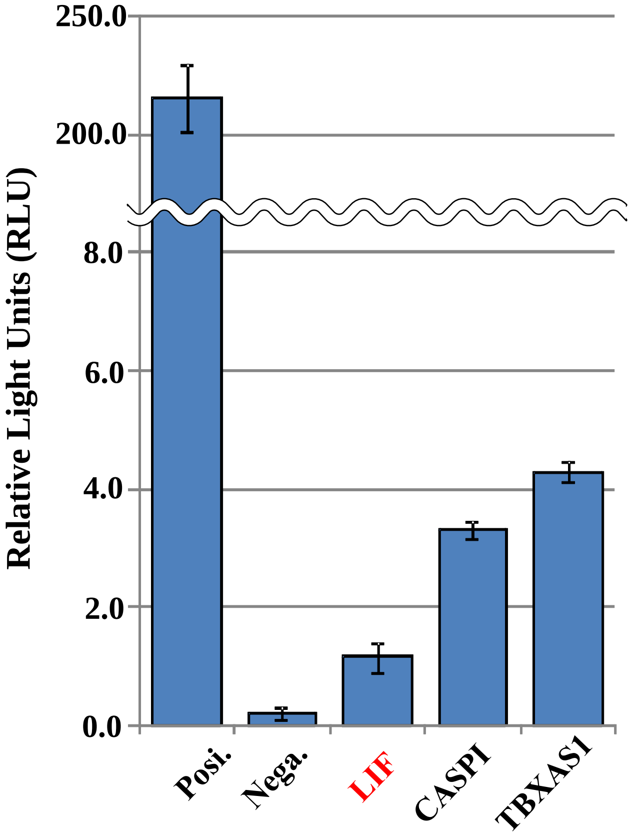
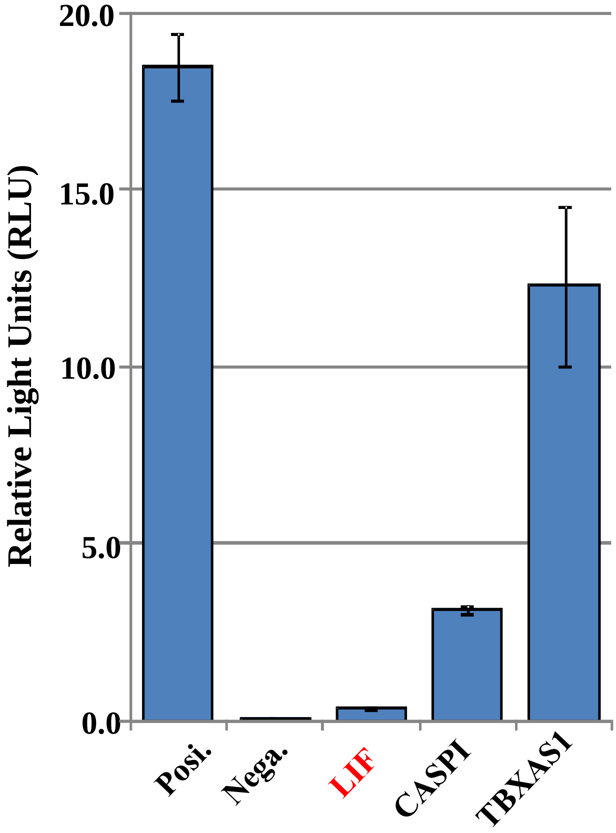
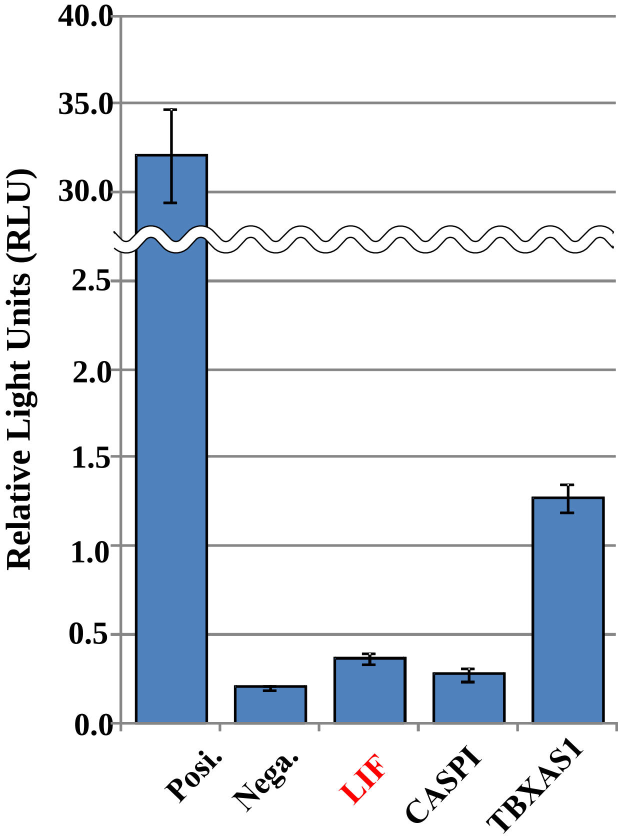
The Promoter Activities of Reporter Constructs



HeLa cells



HepG2 cells



Hep3B cells

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

LIF: pGL4-phLIF (RDB# 7417)
CASP1: pGL4-phCASP1 (RDB# 7338)
TBXAS1:pGL4-phTBXAS1 (RDB# 7347)

2010, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.06.26

1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5546

2nd Nucleotide Sequence
  File Name        : RDB7417F.fasta
  Sequence Size    : 400

  Unit Size to Compare = 1
  Pick up Location     = 1



[100.000% / 400 bp]     INT/OPT.Score : <   1600/  1600 >

      1' GGCCTAACTG GCCGGTACCT GAGCTCGCTA GCCTCGAGGA TCTGGCCTTG GAAAACCAAC
                                                      ********* **********
     61″                                              CTGGCCTTG GAAAACCAAC

     61' TCACACACCT TGATCTCAGG TCAGGGTCAG GCGGAAGGGC TGGGAAGGGG CCACAGGGGA
         ********** ********** ********** ********** ********** **********
     80″ TCACACACCT TGATCTCAGG TCAGGGTCAG GCGGAAGGGC TGGGAAGGGG CCACAGGGGA

    121' CTAAATCATC TCCTGGTACT GGGGGTCCCC TGGCAGCTTT AGGGACGGCA TGGCCCCAGA
         ********** ********** ********** ********** ********** **********
    140″ CTAAATCATC TCCTGGTACT GGGGGTCCCC TGGCAGCTTT AGGGACGGCA TGGCCCCAGA

    181' CGCGTGGCCA TGCTGTCTGG CCGGCATTCC CGCATCTCAT AGGGTGTATT TATTTTCACT
         ********** ********** ********** ********** ********** **********
    200″ CGCGTGGCCA TGCTGTCTGG CCGGCATTCC CGCATCTCAT AGGGTGTATT TATTTTCACT

    241' TTTCTGTTGC ATTTCTTGGA GGTGTCCCTG TGCTCATTTT GCCCGGCTCC CCACTGCTCC
         ********** ********** ********** ********** ********** **********
    260″ TTTCTGTTGC ATTTCTTGGA GGTGTCCCTG TGCTCATTTT GCCCGGCTCC CCACTGCTCC
```

```
   301’ TTTCTGCCCT TCCTCATTCA CAAATCGCCT GGCCTCAGAA GACGCCAGAA CATGTGACAC
        ********** ********** ********** ********** ********** **********
   320″ TTTCTGCCCT TCCTCATTCA CAAATCGCCT GGCCTCAGAA GACGCCAGAA CATGTGACAC

   361’ TGCCTTAGAG CCTCTAGAAG CACTTTTTGG GGACCTCCAT CATTCTCTGA GGCTGGGCTC
        ********** ********** ********** ********** ********** **********
   380″ TGCCTTAGAG CCTCTAGAAG CACTTTTTGG GGACCTCCAT CATTCTCTGA GGCTGGGCTC

   421’ AAAGGGGCTT CCAAGGCAGG TCTGGAAGGG ACCAGCCACT TCTCAGTTTC CCCAACCATC
        ********** ********** *
   440″ AAAGGGGCTT CCAAGGCAGG T
```

```
1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5546

2nd Nucleotide Sequence
  File Name        : RDB7417R.fasta (Complementary)
  Sequence Size    : 175

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

```
[96.552% / 174 bp]     INT/OPT.Score : <    654/   656 >

  1141’ ATCAATCAAA TTCTTAGAAG AGGGAAAAAG TCTGTTC-TC CCCACCCTCC CCCCTCACTC
                                          **..* *  ***  ***** **********
    85″                                  TTGNNCGTT CCCCACCTCC CCCCTCACTC

  1200’ GTCCCCCCCC TTCACTCTCA CTTTCTTCCA TTCATAATTT CCTATGATGC ACCTCAAACA
        ********** ********** ********** ********** ********** **********
   114″ GTCCCCCCCC TTCACTCTCA CTTTCTTCCA TTCATAATTT CCTATGATGC ACCTCAAACA
```

```
1260' ACTTCCTGGA CTGGGGATCC CGGCTAAATA TAGCTGTTTC TGTCTTACAA CACAGGCTCC
      ********** ********** ********** ********** ********** **********
 174″ ACTTCCTGGA CTGGGGATCC CGGCTAAATA TAGCTGTTTC TGTCTTACAA CACAGGCTCC

1320' AGTATATAAA TCAGGCAAAT TCCCCAATCA AGATCTGGCC TCGGCGGCCA AGCTTGGCAA
      ********** ********** ******
 234″ AGTATATAAA TCAGGCAAAT TCCCCA
```