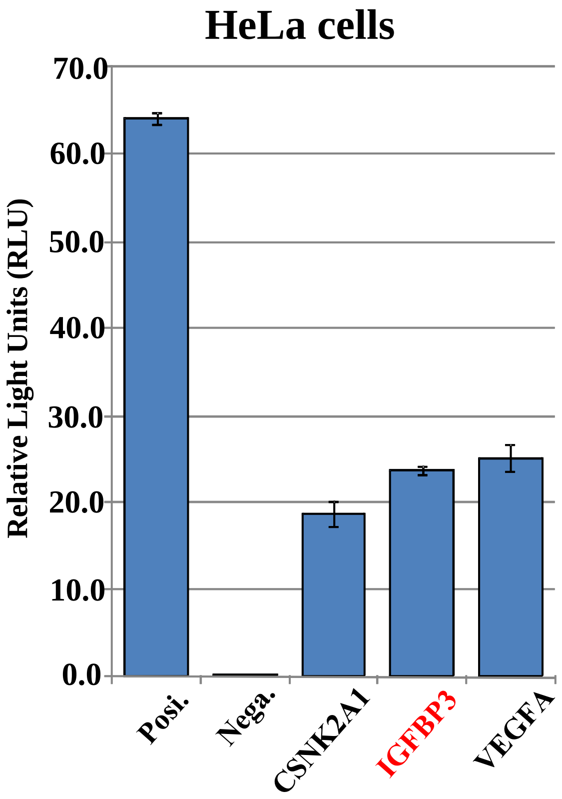
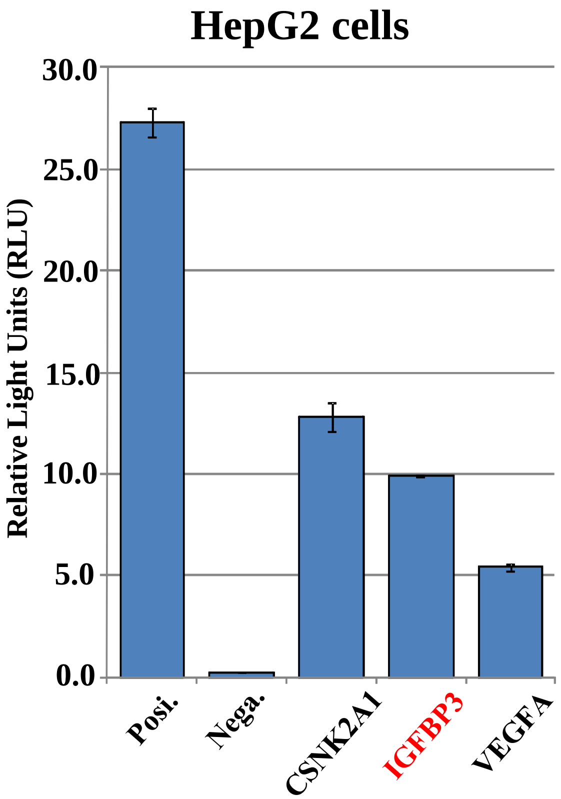
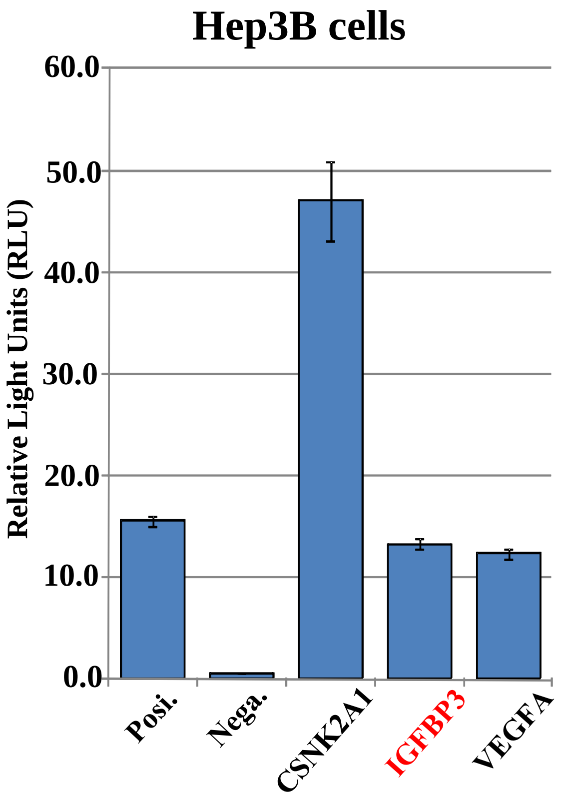
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

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

CSNK2A1: pGL4-phCSNK2A1 (RDB# 7483)
IGFBP3: pGL4-phIGFBP3 (RDB# 7568)
VEGFA: pGL4-phVEGFA (RDB# 7681)

20010, DNA Bank, RIKEN BioResource Center

```
[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.03.01

1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5444

2nd Nucleotide Sequence
  File Name         : RDB7568F.fasta
  Sequence Size     : 695

  Unit Size to Compare = 1
  Pick up Location     = 1



[96.515% / 660 bp]     INT/OPT.Score : <   1896/  2418 >

     1’                    GG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATT
                           ** ********** ********** ********** **********
     1″ GTGCCAGAAC ATTTCTCTGG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATT

    43’ CTTTGGAAAA GTGCCTTGAA AAATTTAATC CTCAATCCAA TCCTGGACCA CCAGCGTCCT
        ********** ********** ********** ********** ********** **********
    61″ CTTTGGAAAA GTGCCTTGAA AAATTTAATC CTCAATCCAA TCCTGGACCA CCAGCGTCCT

   103’ CTGTTGGTCA CCGAAGGGAG GGGGTGCGCA GACAAAACTG AAGAAACTCG AGTGCCAGAG
        ********** ********** ********** ********** ********** **********
   121″ CTGTTGGTCA CCGAAGGGAG GGGGTGCGCA GACAAAACTG AAGAAACTCG AGTGCCAGAG

   163’ AAGGCCGACA GGAGTTACAG CGACCTCAGC GCGCAATTGC GCCCCCGAAC TTTACTGAAA
        ********** ********** ********** ********** ********** **********
   181″ AAGGCCGACA GGAGTTACAG CGACCTCAGC GCGCAATTGC GCCCCCGAAC TTTACTGAAA

   223’ AGTGTTTAGA TTGCAGAGAT AAGCTAGAAT CCCAACGCAT CGAGAATACA GTAATACGAA
        ********** ********** ********** ********** ********** **********
   241″ AGTGTTTAGA TTGCAGAGAT AAGCTAGAAT CCCAACGCAT CGAGAATACA GTAATACGAA
```

```
283' GTCGCCTTCA AAAAATGACA ATGAAAATTG CCTATTAAAG GACTATTTGG TTAATTACGT
     ********** ********** ********** ********** ********** **********
301" GTCGCCTTCA AAAAATGACA ATGAAAATTG CCTATTAAAG GACTATTTGG TTAATTACGT

343' TTCAGCAGTG CCCAGTTTAT TGTCTTTATT ATTCTTTTGT CATGGGTGTA AACTCCATTT
     ********** ********** ********** ********** * ******** **********
361" TTCAGCAGTG CCCAGTTTAT TGTCTTTATT ATTCTTTTGT CGTGGGTGTA AACTCCATTT

403' GAAAACATAA TCAGGGAGAA TACCCAAGAC AAGAAGAACA GTTGTCATTT AAAATATTTG
     ********** ********** ********** ********** ********** **********
421" GAAAACATAA TCAGGGAGAA TACCCAAGAC AAGAAGAACA GTTGTCATTT AAAATATTTG

463' AAAAGCCCTG -CCTTAAGGA CGCATTCGCT TGCCGGTCCA CTCTTAATTG GAGACTTGCG
     **********  ********* ********** ********** ********** * *******
481" AAAAGCCCTG CCCTTAAGGA CGCATTCGCT TGCCGGTCCA CTCTTAATTG GGGACTTGCC

522' GTGTAGCAAC ACGTGAGAGT CTTCTTGCGT TGAGAAGTAA GCCTGGAAAG GGGCGAAGGC
     ********** ********** ********** ********** *********  **** ****
541" GTGTAGCAAC ACGTGAGAGT CTTCTTGCGT TGAGAAGTAA GCCTGGAAA- GGGCCAAGG-

582' CCCGGGCGCA TCTTCAGATG CGTATTTGTG GGCCCCTGGG GATATAAACA GCCCAGCGG-
     ********** ** ******* *********   * ******* ***** ***   **** ***
599" CCCGGGCGCA TC-TCAGATG CGTATTTGT- -GGCCCTGGG GATAT-AAC- -CCCACCGGT

641' GTGTAAATTA AACCCCGCAG TGCCTTGGCT CCCTGAGACC CAAATGTAAG TCAGAAATGT
     ** ****     * ** **
653" GTATAAACCG CATCCGGCTC TAACCCAATT AGTNAATTCA AAA
```

1st Nucleotide Sequence
  File Name   : Reference Seq.gnu
  Sequence Size   : 5444

2nd Nucleotide Sequence
  File Name   : RDB7568R.fasta (Complementary)
  Sequence Size   : 233

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



[100.000% / 231 bp]     INT/OPT.Score : <    924/    924 >

   1081' GCGCCGACCC GCCCCCCTCC CAACCCCCAC TCCTGGGCGC GCCGTTCCGG GGCGTGTCCT
                 ** ********** ********** ********** ********** **********
      1″         CC GCCCCCCTCC CAACCCCCAC TCCTGGGCGC GCCGTTCCGG GGCGTGTCCT

   1141' GGGCCACCCC GGCTTCTATA TAGCGGCCGG CGCGCCCGGG CCGCCCAGAT GCGAGCACTG
         ********** ********** ********** ********** ********** **********
     53″ GGGCCACCCC GGCTTCTATA TAGCGGCCGG CGCGCCCGGG CCGCCCAGAT GCGAGCACTG

   1201' CGGCTGGGCG CTGAGGATCA GCCGCTTCCT GCCTGGATTC CACATCAAGA TCTGGCCTCG
         ********** ********** ********** ********** ********** **********
    113″ CGGCTGGGCG CTGAGGATCA GCCGCTTCCT GCCTGGATTC CACATCAAGA TCTGGCCTCG

   1261' GCGGCCAAGC TTGGCAATCC GGTACTGTTG GTAAAGCCAC CATGGAAGAT GCCAAAAACA
         ********** ********** ********** ********** ********** *********
    173″ GCGGCCAAGC TTGGCAATCC GGTACTGTTG GTAAAGCCAC CATGGAAGAT GCCAAAAACC

   1321' TTAAGAAGGG CCCAGCGCCA TTCTACCCAC TCGAAGACGG GACCGCCGGC GAGCAGCTGC

    233″ A
```