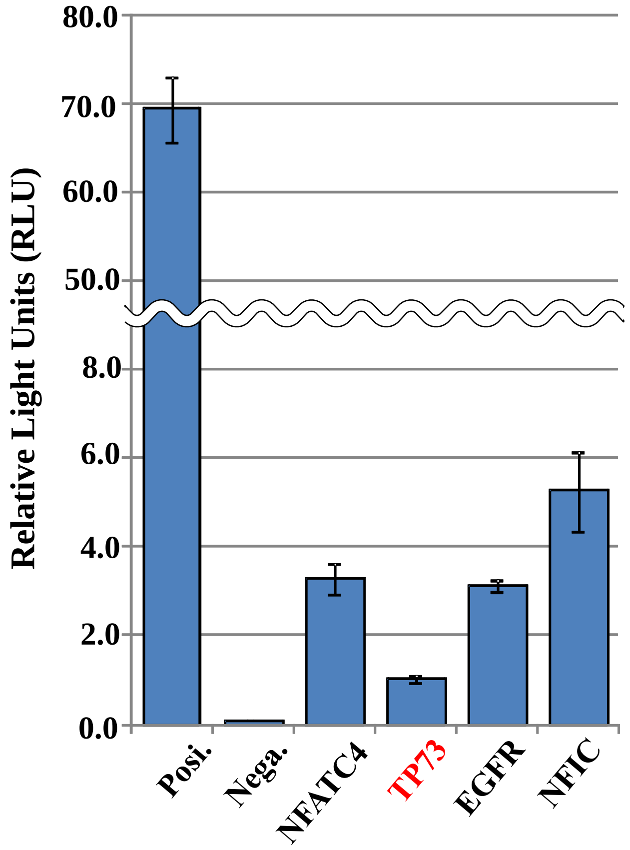
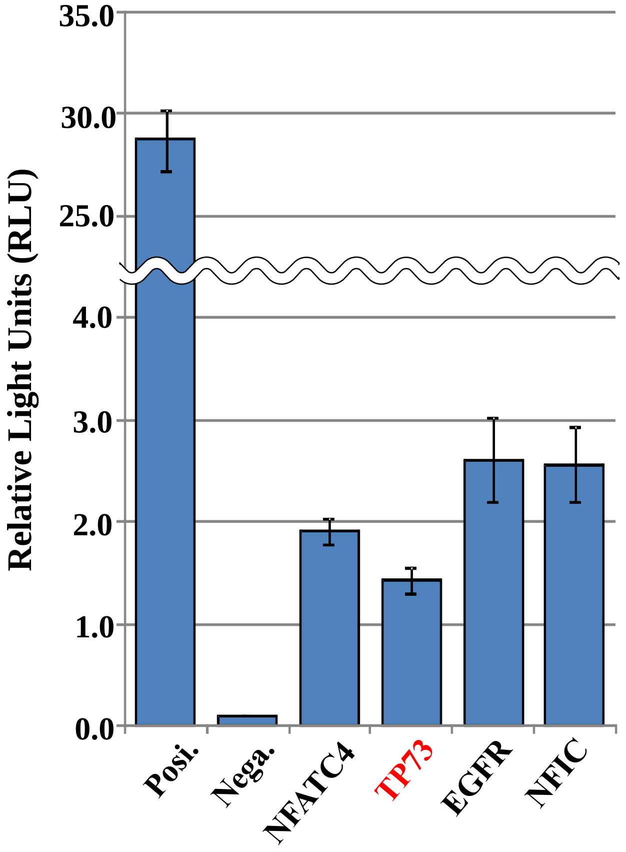
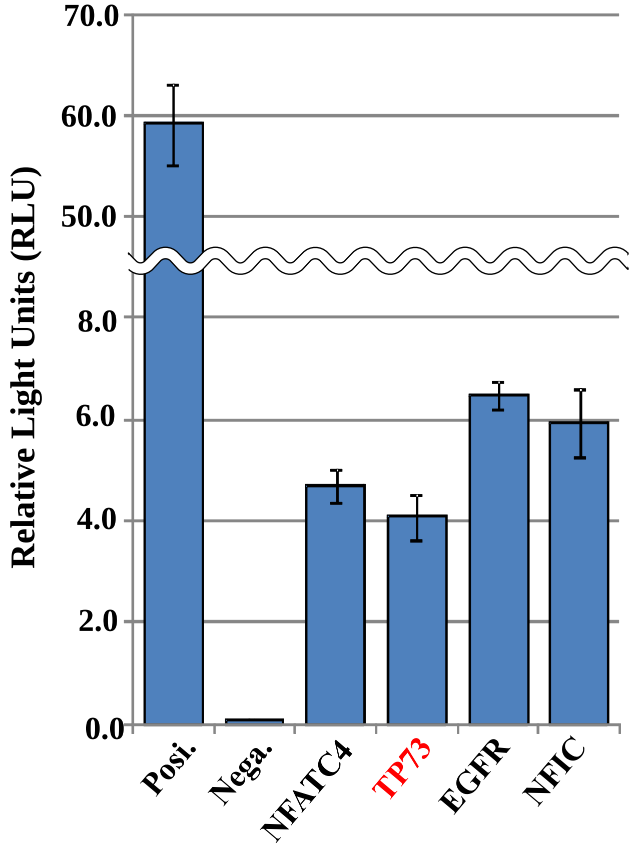
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

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

NFATC4: pGL4-phNFATC4 (RDB# 7376)
TP73: pGL4-phTP73 (RDB# 7381)
EGFR: pGL4-phEGFR (RDB# 7398)
NFIC: pGL4-phNFIC1 (RDB#7399)

2010, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.06.04

1st Nucleotide Sequence
  File Name       : Reference Seq.gnu
  Sequence Size   : 5574

2nd Nucleotide Sequence
  File Name       : RDB7381F.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 TGCCATGAAG ATGTGCGAGT
                                                    ********* **********
   76″                                              GCCATGAAG ATGTGCGAGT

   61’ CAGCCGGACC CTCCCCGTCA GGCGCGGACC CGCTGCGGCC AGAGAACCCA GTCTGCGCCA
       ********** ********** ********** ********** ********** **********
   95″ CAGCCGGACC CTCCCCGTCA GGCGCGGACC CGCTGCGGCC AGAGAACCCA GTCTGCGCCA

  121’ GCCCGGCTCG CTCGCGAAGC CACGGGCTTC ACTGACGCGA CTTTCCAAGA CGTGGGGGTC
       ********** ********** ********** ********** ********** **********
  155″ GCCCGGCTCG CTCGCGAAGC CACGGGCTTC ACTGACGCGA CTTTCCAAGA CGTGGGGGTC

  181’ ACCATGGGCA GAGGACATCG GTTCGGAGCC AGATCACGGG CCCCATAAGC ATCAGACCAT
       ********** ********** ********** ********** ********** **********
  215″ ACCATGGGCA GAGGACATCG GTTCGGAGCC AGATCACGGG CCCCATAAGC ATCAGACCAT

  241’ AAGCAGCGCC GCCACTGAGA GCCGCTCGGA ACTCGCCCAG CATGTCGGGT CCCCTAGCCA
       ********** ********** ********** ********** ********** **********
  275″ AAGCAGCGCC GCCACTGAGA GCCGCTCGGA ACTCGCCCAG CATGTCGGGT CCCCTAGCCA
```

```
    301' GGGCCTGGTG TACGTGGTCG AGGGCCCTGG AAGCCCCGAT GGCCTAGGAG GAGCAGGCGG
         ********** ********** ********** ********** ********** **********
    335″ GGGCCTGGTG TACGTGGTCG AGGGCCCTGG AAGCCCCGAT GGCCTAGGAG GAGCAGGCGG

    361' GCGGGGCGGC GGGTGTCGCT GGCCGGTAGA GAGCTTCGGC CTGACCTAGC GCAGGTCTGG
         ********** ********** ********** ********** ********** **********
    395″ GCGGGGCGGC GGGTGTCGCT GGCCGGTAGA GAGCTTCGGC CTGACCTAGC GCAGGTCTGG

    421' TGCGCGCAGA GAACAACTCC AAGCGCACCG ACGCCCGCGA GCTCCTTCCA AACACCGAAC
         ********** ********** *
    455″ TGCGCGCAGA GAACAACTCC A
```

```
1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5574

2nd Nucleotide Sequence
  File Name        : RDB7381R.fasta (Complementary)
  Sequence Size    : 400

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

```
[98.750% / 400 bp]     INT/OPT.Score : <   1048/  1548 >

    961' AAGATCGCGG TCGGGTCTGG CCCGCGGGAG GGGCCCTGGC GCCGGACC-T GCTTCGGCCC
                          **** ********** ********** ******** * **********
     99″                  CTGG CCCGCGGGAG GGGCCCTGGC GCCGGACCTT GCTTCGGCCC

   1020' TGCGTGGGCG GCCTCGCCGG GCTCTGCAGG AGCGACGCGC GCCAAAAGGC GGCGGGAAGG
         ********** ********** ********** ********** ********** **********
    143″ TGCGTGGGCG GCCTCGCCGG GCTCTGCAGG AGCGACGCGC GCCAAAAGGC GGCGGGAAGG
```

```
1080' AGGCGGGGCA GAGCGCGCCC GGGACCCCG- -ACTTGGACG CGGCCAGCTG GAGAGGCGGA
      ********** ********** *********   *  ****** ********** **********
 203" AGGCGGGGCA GAGCGCGCCC GGGACCCCGA AATATGGACG CGGCCAGCTG GAGAGGCGGA

1138' GCGCCGGGAG GAGACCTTGG CCCCGCCGCG ACTCGGTGGC CCGCGCTGCC TTCCCGCGCG
      ********** ********** ********** ********** ********** **********
 263" GCGCCGGGAG GAGACCTTGG CCCCGCCGCG ACTCGGTGGC CCGCGCTGCC TTCCCGCGCG

1198' CCGGGCTAAA AAGGCGCTAA CGCCCGCGGC CGCCTACTCC CCGCGGCGCC TCCCCTCCCC
      ********** ********** ********** ********** ********** **********
 323" CCGGGCTAAA AAGGCGCTAA CGCCCGCGGC CGCCTACTCC CCGCGGCGCC TCCCCTCCCC

1258' GCGCCCATAT AACCCGCCTA GGGGCCGGGC AGCCCGCCCT GCCTCCCCGC CCGCGCACCC
      ********** ********** ********** ********** ********** **********
 383" GCGCCCATAT AACCCGCCTA GGGGCCGGGC AGCCCGCCCT GCCTCCCCGC CCGCGCACCC

1318' GCCCGGAGGC TCGCGCGCCC GCGAAGGGGA CGCAGCGAAA CCGGGGCCCG CGCCAGATCA
      ********** ********** ********** ********** ********** ******
 443" GCCCGGAGGC TCGCGCGCCC GCGAAGGGGA CGCAGCGAAA CCGGGGCCCG CGCCAG
```