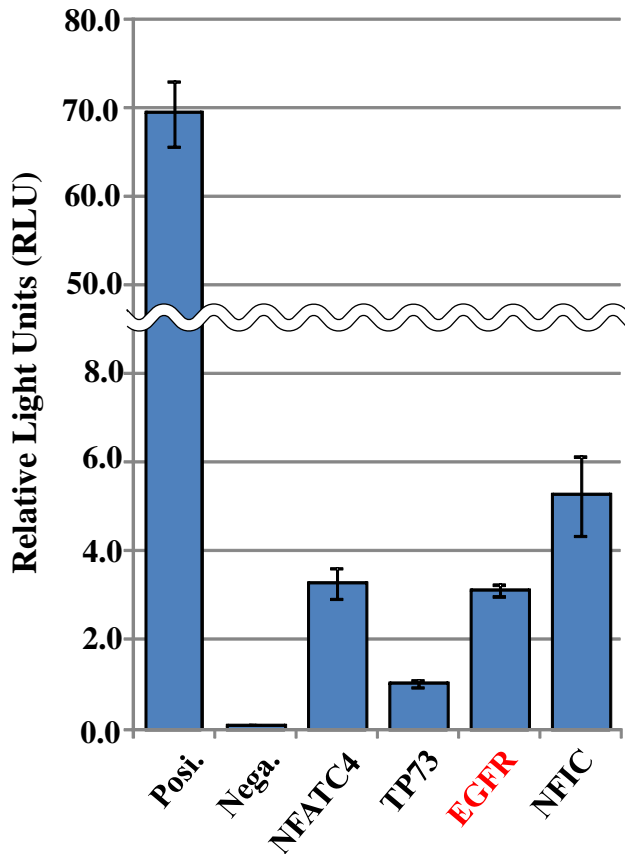
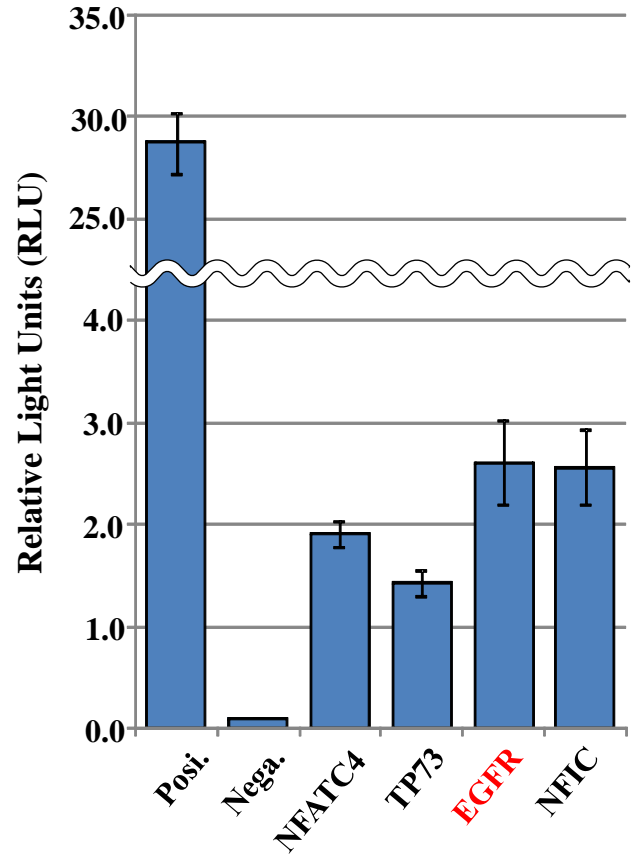


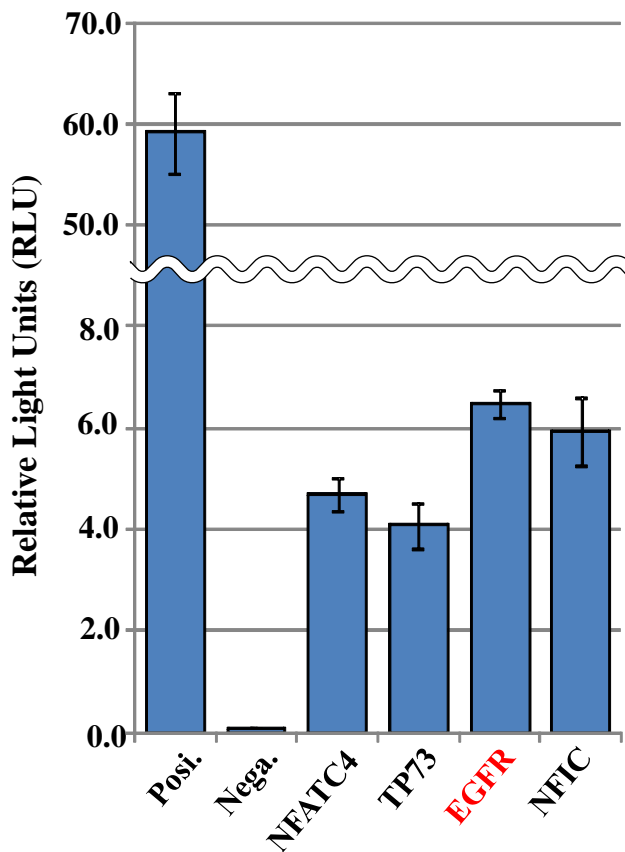
### HeLa cells



### 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)

[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.06.23

1st Nucleotide Sequence

File Name : Reference Seq. GNU  
Sequence Size : 5582

2nd Nucleotide Sequence

File Name : RDB7398F.fasta  
Sequence Size : 674

Unit Size to Compare = 1  
Pick up Location = 1

[99.541% / 654 bp] INT/OPT. Score : < 2601/ 2601 >

```
1'          GG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATA
          ** *****
1'' GTGCCAGAAC ATTTCTCTGG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATA

43' GCAAAGGGCA GGTCTGTAGC TTCACTTACT TCAGGATTGT GATTTTTGAC AGAGCCGAGA
          *****
61'' GCAAAGGGCA GGTCTGTAGC TTCACTTACT TCAGGATTGT GATTTTTGAC AGAGCCGAGA

103' GATCAGGGTT GTTGAACCAG GCCTGAAGGT CCTAGTGAAT CTCGTGAAGA GAGGAGGGGT
          *****
121'' GATCAGGGTT GTTGAACCAG GCCTGAAGGT CCTAGTGAAT CTCGTGAAGA GAGGAGGGGT

163' CTGGCTGTAA CATGGACCTA GAGGACATTT TTAGTGCAGG AGAAGGAACA GTGGGGATGG
          *****
181'' CTGGCTGTAA CATGGACCTA GAGGACATTT TTAGTGCAGG AGAAGGAACA GTGGGGATGG

223' GGTGGACTTG CCAAAGGAAT ATAGCTCAAG TTCCTGCAGC CCAAAAAAGC TCAGTTTCTT
          *****
241'' GGTGGACTTG CCAAAGGAAT ATAGCTCAAG TTCCTGCAGC CCAAAAAAGC TCAGTTTCTT
```



```

283' TTGCCAAAG CTTCCGCGAG TTTCCCTGGC ATTTCTCCTG CGGGAGCTAC AGGGGCAGTG
*****
301" TTGCCAAAG CTTCCGCGAG TTTCCCTGGC ATTTCTCCTG CGGGAGCTAC AGGGGCAGTG

343' GGACACTTAG CCTCTCTAAA AGCACCTCCA CGGCTGTTG TGTCAAGCCT TTATTCCAAG
*****
361" GGACACTTAG CCTCTCTAAA AGCACCTCCA CGGCTGTTG TGTCAAGCCT TTATTCCAAG

403' AGCTTCACTT TTGCGAAGTA ATGTGCTTCA CACATTGGCT TCAAAGTACC CATGGCTGGT
*****
421" AGCTTCACTT TTGCGAAGTA ATGTGCTTCA CACATTGGCT TCAAAGTACC CATGGCTGGT

463' TGCAATAAAC ATTAAGGAGG CCTGTCTCTG CACCCGGAGT TGGGTGCCCT CATTTCAGAT
*****
481" TGCAATAAAC ATTAAGGAGG CCTGTCTCTG CACCCGGAGT TGGGTGCCCT CATTTCAGAT

523' GATTTGAGG GTGCTTGACA AGATCTGAAG GACCCTCGGA CTTTAGAGCA CCACCTCGGA
*****
541" GATTTGAGG GTGCTTGACA AGATCTGAAG GACCCTCGGA CTTTAGAGCA CCACCTCGGA

583' CGCCTGGCAC CCCTGCCGCG CGGGCACGGC GACCTCCTCA GCTGCCAGGC CAGCCTCTGA
*****
601" CGCCTGGCAC CCCTGCCGCG CGGGCACGGC GAACTCCTCA GCTGCCANGC CAGCCTCTGA

643' TCCCCGAGAG GGTCCCGTAG TGCTGCAGGG GAGGTGGGGA CCCGAATAAA GGAGCAGTTT
*****
661" TCCCCGCGAG GGGG

```

1st Nucleotide Sequence

File Name : Reference Seq. GNU  
Sequence Size : 5582

2nd Nucleotide Sequence

File Name : RDB7398R.fasta (Complementary)  
Sequence Size : 724



Unit Size to Compare = 1  
Pick up Location = 1

[98.474% / 721 bp] INT/OPT. Score : < 2648/ 2758 >

721' CCGACGCTGG CTCTAAGGCT CGGCCAGTCT GTCTAAA-GC TGGT-ACAAG -TTTGC-TTT  
\*\*\*\* \*\*\*\*\* \*\* \*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*  
1" CAGGTCT GTCTAAAGGC TGGTAACAAG TTTTGCTTTT

777' GTAAAAC-AA AAGAAGGGAA AGGGGGAAGG GGA-CCCTGG CACAGATTG GCTCGACCTG  
\*\*\*\*\* \*\* \*\*\*\*\* \* \*\*\*\*\* \*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*  
38" GTAAAACAAA AAGAAGGGGA AGGGGGAAGG GGACCCCTGG CACAGATTG GCTCGACCTG

835' GACATAGGCT GGGCCTGCAA GTCCGCGGG ACCGGGTCCA GAGGGGCAGT GCTGGAACG  
\*\*\*\*\* \*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*  
98" AACATAGGCT GGGCTTCAA GTCCGCGGG ACCGGGTCCA GAGGGGCAGT GCTGGAACG

895' CCCCTCTCGG AAATTAATC CTCAGGGCAC CCGCTCCCCT CCCATGCGCC GCCCACTCC  
\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*  
158" CCCCTCTCGG AAATTAATC CTCAGGGCAC CCGCTCCCCT CCCATGCGCC GCCCACTCC

955' CGCCGGAGAC TAGGTCCGC GGGGGCCACC GCTGTCCACC GCCTCCGGCG GCCGCTGGCC  
\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*  
218" CGCCGGAGAC TAGGTCCGC GGGGGCCACC GCTGTCCACC GCCTCCGGCG GCCGCTGGCC

1015' TTGGGTCCCC GCTGCTGGT CTCCTCCCTC CTCCTCGCAT TCTCCTCCTC CTCTGCTCT  
\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*  
278" TTGGGTCCCC GCTGCTGGT CTCCTCCCTC CTCCTCGCAT TCTCCTCCTC CTCTGCTCT

1075' CCCGATCCCT CCTCCGCCG CTGGTCCCTC CTCCTCCCGC CCTGCCTCCC CGCGCCTCGG  
\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*  
338" CCCGATCCCT CCTCCGCCG CTGGTCCCTC CTCCTCCCGC CCTGCCTCCC CGCGCCTCGG

1135' CCCGCGGAG CTAGAGTCC GGGCAGCCCC CGGCGCAGCG CGGCCGAGC AGCCTCCGCC  
\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*  
398" CCCGCGGAG CTAGAGTCC GGGCAGCCCC CGGCGCAGCG CGGCCGAGC AGCCTCCGCC



1195' CCCCACCG TGTGAGCGCC CGACGCGGCC GAGGCGGCC GAGTCCGAG CTAGCCCGG  
 \*\*\*\*\*  
 458" CCCCACCG TGTGAGCGCC CGCCGCGGCC GAGGCGGCC GAGTCCGAG CTAGCCCGG  
  
 1255' CGGCCCGCC CGCCAGACC GGACGACAGG CCACCTCGTC GCGTCCGCC CGAGTCCCG  
 \*\*\*\*\*  
 518" CGGCCCGCC CGCCAGACC GGACGACAGG CCACCTCGTC GCGTCCGCC CGAGTCCCG  
  
 1315' CCTCGCGCC AACGCCAAA CCACGCGCA CGGCCCTG ACTCCGTCCA GTATTGATCG  
 \*\*\*\*\*  
 578" CCTCGCGCC AACGCCAAA CCACGCGCA CGGCCCTG ACTCCGTCCA GTATTGATCG  
  
 1375' GGAGAGCATC AAGATCTGGC CTCGGCGGCC AAGCTTGCA ATCCGTACT GTTGGTAAAG  
 \*\*\*\*\*  
 638" GGAGAGCATC AAGATCTGGC CTCGGCGGCC AAGCTTGCA ATCCGTACT GTTGGTAAAG  
  
 1435' CCACCATGGA AGATGCCAAA AACATTAAGA AGGGCCAGC GCCATTCTAC CCACTCGAAG  
 \*\*\*\*\*  
 698" CCACCATGGA AGATGCCAAA AACATTA