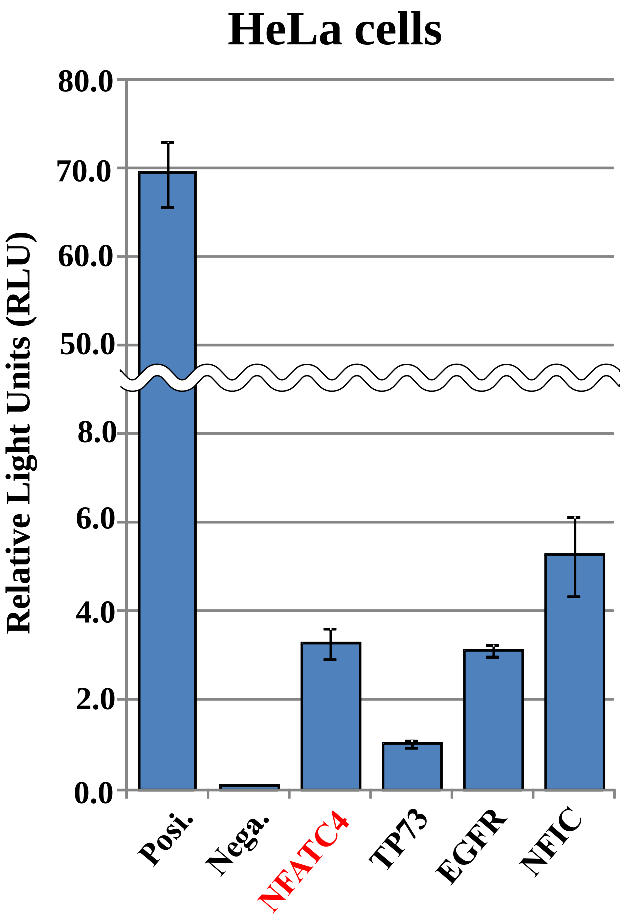
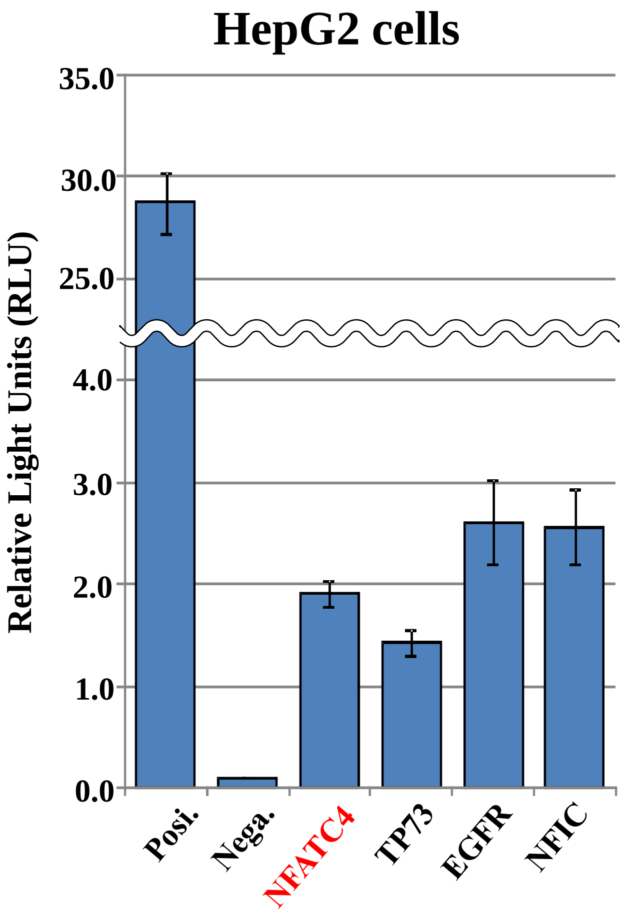
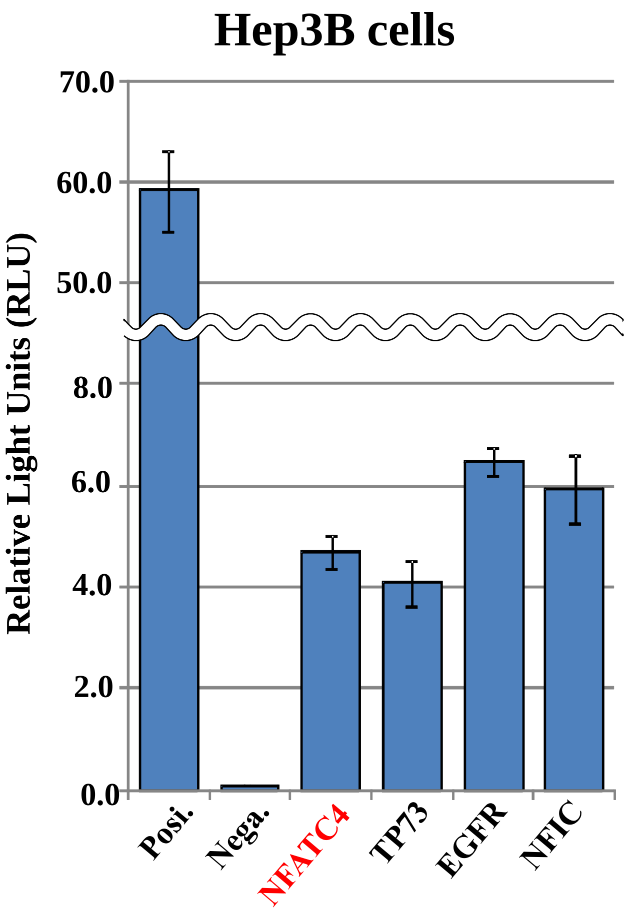
The Promoter Activities of Reporter Constructs


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 : 2010.03.02

1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5557

2nd Nucleotide Sequence
  File Name        : RDB7376F.fasta
  Sequence Size    : 558

  Unit Size to Compare = 1
  Pick up Location     = 1



[97.222% / 504 bp]     INT/OPT.Score : <   1752/  1856 >

    1’                      G GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT
                            * ********** ********** ********** **********
    1″ GGTGCCAGAA CATTTCTCTG GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT

   42’ CCCGTAGAGC CTGTTTCTCA TTAGAGTAAC GGGCGCGGTC CCCGCCCGGC TTCTGAGTGT
       ********** ********** ********** ********** ********** **********
   61″ CCCGTAGAGC CTGTTTCTCA TTAGAGTAAC GGGCGCGGTC CCCGCCCGGC TTCTGAGTGT

  102’ TTGTAAACGT CTGACCTGGG GCCGTCGCTT AACCGTTTAG TTGCTGGGAT GGGGCGGCGT
       ********** ********** ********** ********** ********** **********
  121″ TTGTAAACGT CTGACCTGGG GCCGTCGCTT AACCGTTTAG TTGCTGGGAT GGGGCGGCGT

  162’ TGGGGGTGCG GCCCTGAACC GGAGGGATTT AGAGACTGGA GACGCGGCCT CTAAGAGAGG
       ********** ********** ********** ********** ********** **********
  181″ TGGGGGTGCG GCCCTGAACC GGAGGGATTT AGAGACTGGA GACGCGGCCT CTAAGAGAGG

  222’ TTGAAACTGT GTGTGTGTGG GAGAAAATGA TAACCACCCT CCCATCTCTC CTACCCGCCA
       ********** ********** ********** ********** ********** **********
  241″ TTGAAACTGT GTGTGTGTGG GAGAAAATGA TAACCACCCT CCCATCTCTC CTACCCGCCA
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282’ GCCTCGCCAG TATCTCCCAC CGAGTCACGA ATCTCCCATC TAACTCCCTC TCACACAACC
     ********** ********** ********** ********** ********** **********
301″ GCCTCGCCAG TATCTCCCAC CGAGTCACGA ATCTCCCATC TAACTCCCTC TCACACAACC

342’ CAGGCCTCTC CAAGCCTGAC TTTCCCGGAA ACTCCAGTCC AGGTCTTCCT TCCTCCTCCA
     ********** ********** ********** ********** ********** **********
361″ CAGGCCTCTC CAAGCCTGAC TTTCCCGGAA ACTCCAGTCC AGGTCTTCCT TCCTCCTCCA

402’ GCCCAGGTGA CAGGTGTCCA GCCTGTT-GG GGGC-GGGGG GGCCAAGGAG GGGG-AAGAG
     ********** ********** ******* ** **** ***** ********** **** *****
421″ GCCCAGGTGA CAGGTGTCCA GCCTGTTGGG GGGCGGGGGG GGCCAAGGAG GGGGAAAGAG

459’ GA--GGGGAA CCCACA--GG GTCC--GGAG G-TTTCAGGC CCCTAGTAAA CCTGGCAAGG
     **  *** ** ******  ** ****  * ** * *******   **
481″ GAGGGGGAAA CCCACAGGGG GTCCGGGAAG GTTTTCAGGG GCCCCCTTAG TTAAAACCTT

512’ ATTTTTAGAA GAGCCGGAGT GGGATGCTAT CGGGTCAGAG ATTCATTCCA GACTACAGTT

541″ GGCCAAAGGG AATTTTTT
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1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5557

2nd Nucleotide Sequence
  File Name         : RDB7376R.fasta (Complementary)
  Sequence Size     : 740

  Unit Size to Compare = 1
  Pick up Location     = 1


[95.787% / 712 bp]     INT/OPT.Score : <   1028/  2562 >
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```
 661’ ATCTACGCCC ATCAAGGGCT GTGGGCCTAG GGACAGTTCT CAAAGCCTCT TTGGCTCGGA

   1″                                       CTGG CTCCCCCAAG AGGGGCAATT

 721’ CTGCTCCCAG AGGCATCCAG GCTGGCTAAG CGTTCTTCAT CTTTGGGGGT CC-TGGA-GG
                 *** *  ** **  * *      *  *** *  *  **** * ** **** **
  25″ CCAAGGGCCT GGGCTTAAAG GC--GGTTCT TTTCATTCTT TTGGGGGGTT CCTTGGAGGG

 779’ AAT-GGCTGA -TGGAGGCGC TG-ATTCGGC AGCGCAAAGA CTTCCAGAAG G-CCCGGGCA
      *** ******  ********* ** *** *** ********** ********** * ********
  83″ AATGGGCTGA TTGGAGGCGC TGAATTGGGC AGCGCAAAGA CTTCCAGAAG GCCCCGGGCA

 835’ GAGTAGCCCC AGGCAAGGGA GGCGGAAGAA TAGCCTTTTC CTCTTCCGAG CAACTCGGTG
      ********** ********** ********** ********** ********** **********
 143″ GAGTAGCCCC AGGCAAGGGA GGCGGAAGAA TAGCCTTTTC CTCTTCCGAG CAACTCGGTG

 895’ CCACTCTGCC CCCAGGACCC TCCTGGCCTC AGGCTTGGAG GGAAAGGGGA GGAGAAGTGG
      ********** ********** ********** ********** *********    ********
 203″ CCACTCTGCC CCCAGGACCC TCCTGGCCTC AGGCTTGGAG GGAAAGGGG- --AGAAGTGG

 955’ TTCTGCCTTG CTAGGTGCTA TCTACACAGT CTTCAGAATT TAAAAAAGGG TCTTCCGTGG
      ********** ********** ********** ********** ********** **********
 260″ TTCTGCCTTG CTAGGTGCTA TCTACACAGT CTTCAGAATT TAAAAAAGGG TCTTCCGTGG

1015’ GCTCTCTACC CTGGGGGCCC AGGATGTGGC CCCTTTAAGG CTCTCGGACC CAGAACCTTG
      ********** ********** ********** ********** ********** **********
 320″ GCTCTCTACC CTGGGGGCCC AGGATGTGGC CCCTTTAAGG CTCTCGGACC CAGAACCTTG

1075’ AACTGAGACT AGGGGAGGTG GGGGCTGGGC TCTCTGCGGG AAATGATTGT CACAACGGCG
      ********** ********** ********** ********** ********** **********
 380″ AACTGAGACT AGGGGAGGTG GGGGCTGGGC TCTCTGCGGG AAATGATTGT CACAACGGCG

1135’ GACCAATAGG CAACATTAGT ATCACTCTTG AAGGACCGTT TTCCAATTCA GTTTTTTTTT
      ********** ********** ********** ********** ********** * ********
 440″ GACCAATAGG CAACATTAGT ATCACTCTTG AAGGACCGTT TTCCAATTCA G-TTTTTTTT

1195’ TTTTGAGGGG GAGGGACTGA AGAGAGGACA GAGGGAGGGA GGGTGGGGGA GGACGAGGGG
      ********** ********** ********** ********** ********** **********
 499″ TTTTGAGGGG GAGGGACTGA AGAGAGGACA GAGGGAGGGA GGGTGGGGGA GGACGAGGGG
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1255' CGCGTGGTTT TCCCATCTCA TCCCTGGAGG AGGGGCTGGA GCATCCCCGG CAGCCAATCA
      ********** ********** ********** ********** ********** **********
 559″ CGCGTGGTTT TCCCATCTCA TCCCTGGAGG AGGGGCTGGA GCATCCCCGG CAGCCAATCA

1315' GGGACAGGCT GGGGGGGGGA CCGCTTTGAA GAAGTTTGGG GGATCAAGAT CTGGCCTCGG
      **********  ********* ********** ********** ********** **********
 619″ GGGACAGGCT -GGGGGGGGA CCGCTTTGAA GAAGTTTGGG GGATCAAGAT CTGGCCTCGG

1375' CGGCCAAGCT TGGCAATCCG GTACTGTTGG TAAAGCCACC ATGGAAGATG CCAAAAACAT
      ********** ********** ********** ********** ********** **********
 678″ CGGCCAAGCT TGGCAATCCG GTACTGTTGG TAAAGCCACC ATGGAAGATG CCAAAAACAT

1435' TAAGAAGGGC CCAGCGCCAT TCTACCCACT CGAAGACGGG ACCGCCGGCG AGCAGCTGCA
      ***
 738″ TAA
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