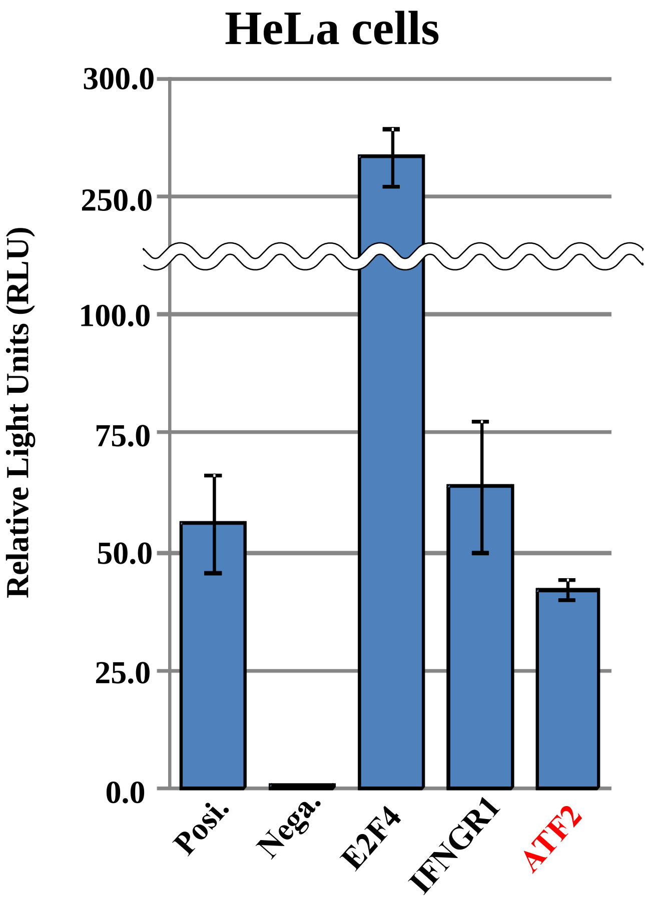
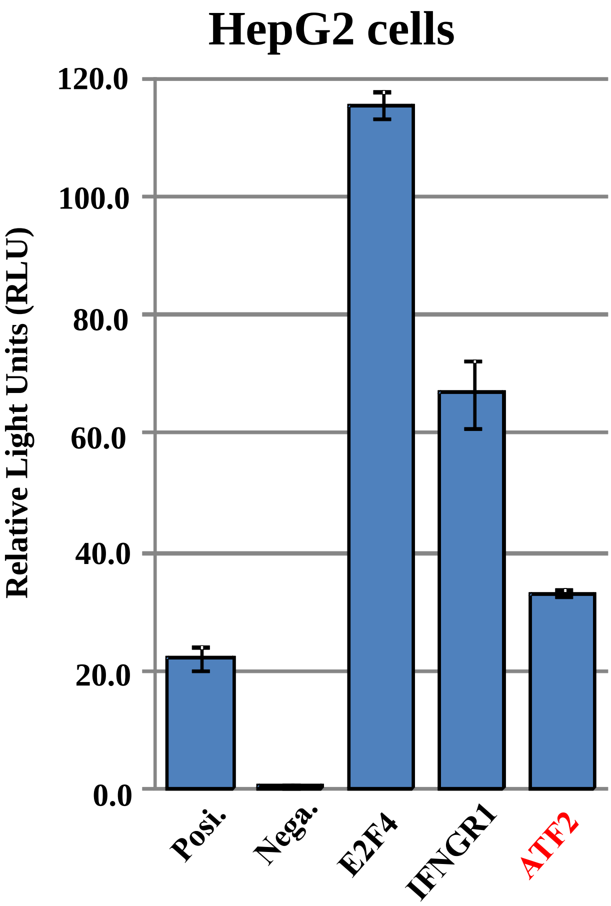
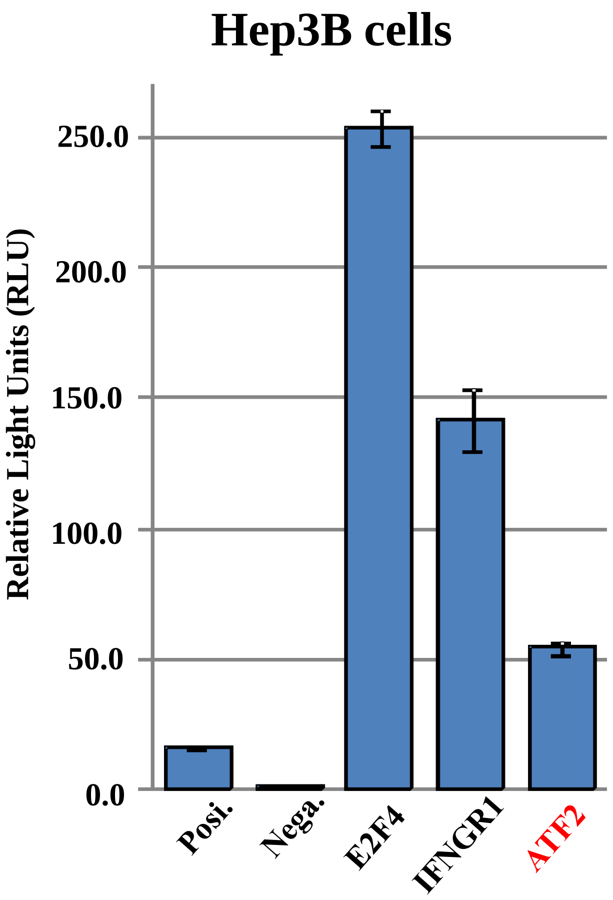
The Promoter Activities of Reporter Constructs







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

E2F4: pGL4-phE2F4 (RDB# 7714)
IFNGR1: pGL4-phIFNGR1(RDB# 7708)
ATF2: pGL4-phATF2 (RDB# 7712)

2010, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.03.09

1st Nucleotide Sequence
  File Name        : Reference Seq (insert)
  Sequence Size    : 1470

2nd Nucleotide Sequence
  File Name        : RDB7712F.fasta
  Sequence Size    : 688

Unit Size to Compare : 6

Percent Similarity   : 99.4
Percent Identity     : 99.4


     1' AAACCAAAGC TACTGCCCAA TTGAATCAAC ACTGGAAAAA ATTTCAAATG GAAAAACAAT
        ********** ********** ********** ********** ********** **********
    60" AAACCAAAGC TACTGCCCAA TTGAATCAAC ACTGGAAAAA ATTTCAAATG GAAAAACAAT

    61' TTTTTTAAAA AAATCTATTC TAATTGACCC AAACTTCTTT TGAAATGTCG TAACATTTGC
        ***** **** ********** ********** ********** ********** **********
   120" TTTTTAAAAA AAATCTATTC TAATTGACCC AAACTTCTTT TGAAATGTCG TAACATTTGC

   121' AGTTCTTTTT CTCACATTAG TTGTTTTGGG AGATGGAGAG AGAAGCATCT ATTTAATCAA
        ********** ********** ********** ********** ********** **********
   180" AGTTCTTTTT CTCACATTAG TTGTTTTGGG AGATGGAGAG AGAAGCATCT ATTTAATCAA

   181' TGCGTTCTAG ACCTAACAAT TGTGATGTCA ATCAAACATT TTGTCCACCA TTTCCATCAT
        ********** ********** ********** ********** ********** **********
   240" TGCGTTCTAG ACCTAACAAT TGTGATGTCA ATCAAACATT TTGTCCACCA TTTCCATCAT

   241' GAGTAATCTG AACTGTGAGG TTTTGCTGAC ATAATTAGTG TTACACTACA ATGGCACTAC
        ********** ********** ********** ********** ********** **********
   300" GAGTAATCTG AACTGTGAGG TTTTGCTGAC ATAATTAGTG TTACACTACA ATGGCACTAC
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301' TACATTACTG TTACTATATG GGGACGGTAC TTTCATTTTA AGTAGGAAAG TGTTAATAAT
     ********** ********** ***** **** ********** ********** **********
360″ TACATTACTG TTACTATATG GGGACAGTAC TTTCATTTTA AGTAGGAAAG TGTTAATAAT

361' TTGGCTTAAT GTTTCTTAAC TAAAATTAGT TTTAAAAGAG GACTGAGTTG GCTTATACAC
     ********** ********** ********** ********** ********** **********
420″ TTGGCTTAAT GTTTCTTAAC TAAAATTAGT TTTAAAAGAG GACTGAGTTG GCTTATACAC

421' ATGTATGCGG TCCAGAGACC TACCTGTTAA AATGTCAATG CCATTACAAT TTCACTTTTA
     ********** ********** ********** ********** ********** **********
480″ ATGTATGCGG TCCAGAGACC TACCTGTTAA AATGTCAATG CCATTACAAT TTCACTTTTA

481' TGCCAGATAT CATTCTTGAA CTTCAGGCTC ATTAACTCTC ATACTATCCC CCAAAACCTT
     ********** ********** ********** ********** ********** **********
540″ TGCCAGATAT CATTCTTGAA CTTCAGGCTC ATTAACTCTC ATACTATCCC CCAAAACCTT

541' TCAACAATTT TGAGAGTGTA TTTTATGTTA ATATATAAAC TAGTTCATAA TTTTGTTCCA
     ********** ********** ********** ********** ********** **********
600″ TCAACAATTT TGAGAGTGTA TTTTATGTTA ATATATAAAC TAGTTCATAA TTTTGTTCCA

601' GACTAGAAAT CAGTATTTAA TAAATGGAA
     ********** ********** ******  *
660″ GACTAGAAAT CAGTATTTAA TAAATGAGA
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1st Nucleotide Sequence
  File Name         : Reference Seq (insert)
  Sequence Size     : 1470

2nd Nucleotide Sequence
  File Name         : RDB7712R.fasta (Complementary)
  Sequence Size     : 706

Unit Size to Compare : 6
```

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Percent Similarity   : 98.8
Percent Identity     : 98.7

  853' CCCGGGGAGC CAAGGGGTGG GCTGAGGAAC GCAGCCTACT TTTACCCACC TCCCTACCTA
       ********** **   ** ** ** **** *  **** ***** ********** ***. * ***
  706″ CCCGGGGAGC CA---GGGGG GC-GAGG-AG GCAG-CTACT TTTACCCACC TCCN-AACTA

  913' GTGCTGGGAA GTGACGGAAA CGGAGACACC CGGCTCCT-G GGGCTGGGCT CGGAGGACCC
       * ***** ** * *** **** ********** ******** * ********** **********
  653″ G-GCTGGAAA GGGAC-GAAA CGGAGACACC CGGCTCCTGG GGGCTGGGCT CGGAGGACCC

  972' ATCCTGCTTT CCCTCTAGCA GCCTTTCCGG AGCTCACCAC CTTTCCTCCC CTCACACCGC
       ********** ********** ********** ****   *** ********** **********
  595″ ATCCTGCTTT CCCTCTAGCA GCCTTTCCGG AGCT---CAC CTTTCCTCCC CTCACACCGC

 1032' CAAAGCCCTG CCTAGCCCTT CACCGCCGCC TGCACCCGCG CCCTCCTCCA GCCGACAGCC
       ********** ********** ********** ********** ********** **********
  538″ CAAAGCCCTG CCTAGCCCTT CACCGCCGCC TGCACCCGCG CCCTCCTCCA GCCGACAGCC

 1092' AATCACAGTC TTCCACAGCT CCGGGTTTAC AGAAGTAACG CTCCTTGGGC CCTCTGGTCC
       ********** ********** ********** ********** ********** **********
  478″ AATCACAGTC TTCCACAGCT CCGGGTTTAC AGAAGTAACG CTCCTTGGGC CCTCTGGTCC

 1152' CGCCCCCTCC AGAACTGCTT CCCGCCCTTC GGGCTCCTTG TCCAATCATG AGCGCCCGAG
       ********** ********** ********** ********** ********** **********
  418″ CGCCCCCTCC AGAACTGCTT CCCGCCCTTC GGGCTCCTTG TCCAATCATG AGCGCCCGAG

 1212' TGCTCTTTGA TGCCCGTCCC CTCTACCCGC CCTGCCGAAG ACCCGCCTTC TTCTCCTTAA
       ********** ********** ********** ****** *** ********** **********
  358″ TGCTCTTTGA TGCCCGTCCC CTCTACCCGC CCTGCCAAAG ACCCGCCTTC TTCTCCTTAA

 1272' GCCTGACGGA ATCACCTGAC TCGGAGGCGC TCCCTCAGAA GGAAGGCAAG AAGGGGCGTG
       ********** ********** ********** ********** ********** **********
  298″ GCCTGACGGA ATCACCTGAC TCGGAGGCGC TCCCTCAGAA GGAAGGCAAG AAGGGGCGTG

 1332' TGGGTGAAGG GGAGGGGCGC CAGAAGGAAG GTGGGGATGC CGGGAGCGGG GCGAGCGGGC
       ********** ********** ********** ********** ********** **********
  238″ TGGGTGAAGG GGAGGGGCGC CAGAAGGAAG GTGGGGATGC CGGGAGCGGG GCGAGCGGGC
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1392’ GGGGGTTGTC AGTCCGATCT CGCGAGAGAG -GACGGAAGC CTGTGGGAGC CCGTGGCCTT
      ********** ********** **********  ******* * ********** **********
 178″ GGGGGTTGTC AGTCCGATCT CGCGAGAGAG TGACGGAACC CTGTGGGAGC CCGTGGCCTT

1451’ TAAAGTGCCG TTCAGCCTTT
      ********** **********
 118″ TAAAGTGCCG TTCAGCCTTT
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