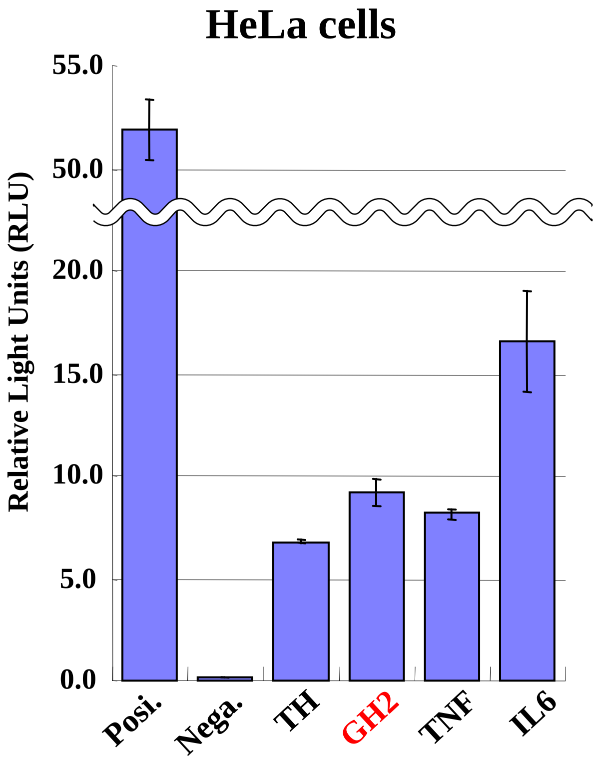
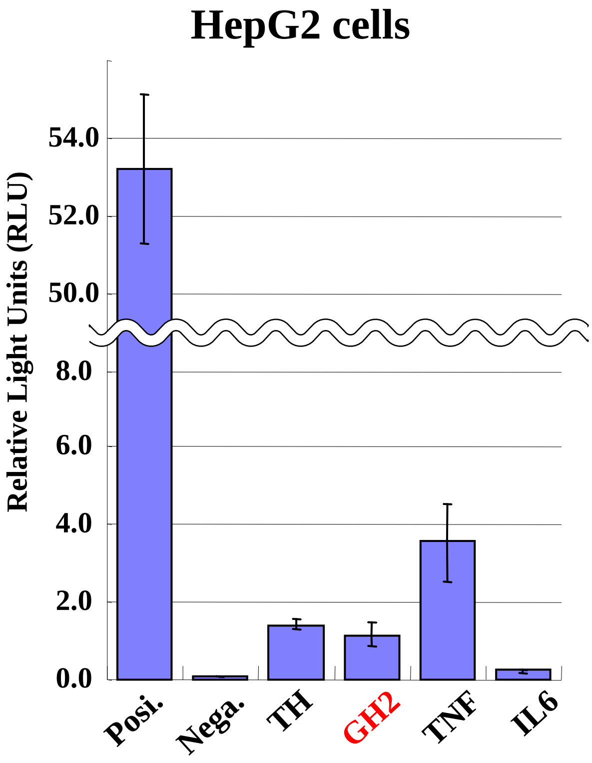
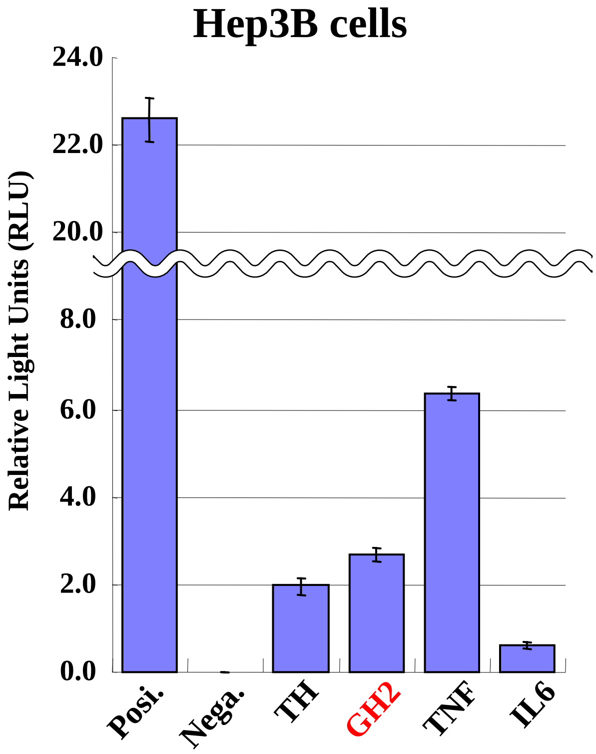
The Promoter Activities of Reporter Constructs







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

TH: pGL4-phTH (RDB#7301)
GH2: pGL4-phGH2(RDB#7309)
TNF:pGL4-phTNF (RDB#7310)
IL6: pGL4-phIL6 (RDB#7313)

2009, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.06.25

1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5432

2nd Nucleotide Sequence
  File Name        : RDB7309F.fasta
  Sequence Size    : 617

  Unit Size to Compare = 1
  Pick up Location     = 1



[97.360% / 606 bp]     INT/OPT.Score : <    321/  2224 >

    1'                     G GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT
                           * ********** ********** ********** **********
    1″ GGTGCCAGAA CATGTCTCTG GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT

   42' -TGAGGTGGA GTCTTGCTCT GTTGCCAAGG TTGGNAGTGC AGCAGCACGA TCTCCGCTCA
        ********* ********** **********  * *.***** ********** **********
   61″ GTGAGGTGGA GTCTTGCTCT GTTGCCAAGG GTTGGAGTGC AGCAGCACGA TCTCCGCTCA

  101' CTGCAAGCTC TGCCTCCCGG ATTCANCGCC ATTCTCCTGC CTCAGCCTCC CGAGTAGCTG
       ********** ********** ***** **** ********** ********** **********
  121″ CTGCAAGCTC TGCCTCCCGG ATTCA-CGCC ATTCTCCTGC CTCAGCCTCC CGAGTAGCTG

  161' GGAATACAGG CGCCCGNCCA CTACGCCCAG CTAACTTTTT TGCATTTTTA GTACAGAGTG
       ********** ****** *** ********** ********** ********** **********
  180″ GGAATACAGG CGCCCG-CCA CTACGCCCAG CTAACTTTTT TGCATTTTTA GTACAGAGTG

  221' GATTTCANCC TGGTTAGCCA AGATGGTCTT GATCTACTGA CCTCGTGATC CGCCCGCCNT
       ******* ** ********** ********** ********** ********** ******** *
  239″ GATTTCA-CC TGGTTAGCCA AGATGGTCTT GATCTACTGA CCTCGTGATC CGCCCGCC-T
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281' CGGCCTCCCA AAGTGCTGGG ATTACAGGCA TGAGCCACCG CGCCCAGCCN TGATAGAGCA
     ********** ********** ********** ********** *********  **********
297" CGGCCTCCCA AAGTGCTGGG ATTACAGGCA TGAGCCACCG CGCCCAGCC- TGATAGAGCA

341' TCTTTCGGCG TGATGTGTTC TGAGTTCCAA AGCTGAGGAA NGAGACTCAA ATCTTCAAGA
     ********** ********** ********** **********  ********* **********
356" TCTTTCGGCG TGATGTGTTC TGAGTTCCAA AGCTGAGGAA -GAGACTCAA ATCTTCAAGA

401' GCTCTTCTAA CTTTGAGATT CTCTGATGGT TNTCAGGGCT ATGGGAGGAA GAGCTTGTGG
     ********** ********** ********** * ******** ********** **********
415" GCTCTTCTAA CTTTGAGATT CTCTGATGGT T-TCAGGGCT ATGGGAGGAA GAGCTTGTGG

461' TCCGTGTCTG CTCCCGGGAT TTNCTGTTTC TTGGTTTGTG TCTCTGCTGC AAGTCCAAGG
     ********** ********** ** ******* ********** ********** ****.*****
474" TCCGTGTCTG CTCCCGGGAT TT-CTGTTTC TTGGTTTGTG TCTCTGCTGC AAGTNCAAGG

521' AGCTGGGGCA ATANCCTTGA GTCTGGGTTC TTCGTCCCCA GGGACCTGGG GGAGCCCCAG
     ********** *** ****** ********** ********** **** ***** **********
533" AGCTGGGGCA ATA-CCTTGA GTCTGGGTTC TTCGTCCCCA GGGAACTGGG GGAGCCCCAG

581' CAATNGCTCA GGGAAAGGGG AGAGCAAAGT GTGGGGTTGG TTCTCTCTAG TGGTCNAGTG
     **** ***** ********** *****
592" CAAT-GCTCA GGGAAAGGGG AGAGCCC
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1st Nucleotide Sequence
  File Name         : Reference Seq.GNU
  Sequence Size     : 5432

2nd Nucleotide Sequence
  File Name         : RDB7309R.fasta (Complementary)
  Sequence Size     : 598

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

```
[96.705% / 607 bp]     INT/OPT.Score : <    402/  2126 >

  661’ CTCAGGCTGA CCCAGGAGTC CTCAGCNAGA AGTGGAATTC AGGACTGAAT CGTGCTCACA
                                                             *********
    1″                                                      GGTGCTCACA

  721’ A-CCCCCACA ATCTATTGNG CTGTGCTTGG CCCCTTTTCC CAACACACAC ATTCTGTCTG
       * ******** ******** * ********** ********** ********** **********
   11″ ACCCCCCACA ATCTATTG-G CTGTGCTTGG CCCCTTTTCC CAACACACAC ATTCTGTCTG

  780’ GTGGGTGGAN GGTTAAACAT GCGGGGAGGA GGAAAGGGAT AGGATAGAGA ATGGGATGTG
       *********  ********** ********** ********** ********** **********
   70″ GTGGGTGGA- GGTTAAACAT GCGGGGAGGA GGAAAGGGAT AGGATAGAGA ATGGGATGTG

  840’ NGTCGGTAGG GGGTCTCAAG GACTGGCTAT CCTGACATCC TTCGCCGCGT GNCAGGTTGG
        ********* ********** ********** ********** ********** * ********
  129″ -GTCGGTAGG GGGTCTCAAG GACTGGCTAT CCTGACATCC TTCGCCGCGT G-CAGGTTGG

  900’ CCACCATGGC CTGCGGCCAG AGGGCACCCA CGTGACCCTT AANAGAGAGG ACAAGTTGGG
       ********** ********** ********** ********** ** ******* **********
  187″ CCACCATGGC CTGCGGCCAG AGGGCACCCA CGTGACCCTT AA-AGAGAGG ACAAGTTGGG

  960’ TGGTATCTCT GGCTGACACT CTGTGCACAA CCCNTCACAA CACTGGTGAC GGTGGGAAGG
       ********** ********** ********** *** ****** ********** **********
  246″ TGGTATCTCT GGCTGACACT CTGTGCACAA CCC-TCACAA CACTGGTGAC GGTGGGAAGG

 1020’ GAAAGATGAC AAGCCAGGGG GCATNGATCC CAGCATGTGT GGGAGGAGCT TCTAAATTAT
       ********** ********** **** ***** ********** ********** **********
  305″ GAAAGATGAC AAGCCAGGGG GCAT-GATCC CAGCATGTGT GGGAGGAGCT TCTAAATTAT

 1080’ CCATTAGCAC AAGCCNCGTC AGTGGCCCCA TGCATAAATG TACACAGAAA CAGGTGGGGT
       ********** ***** **** ********** ********** ********** **********
  364″ CCATTAGCAC AAGCC-CGTC AGTGGCCCCA TGCATAAATG TACACAGAAA CAGGTGGGGT

 1140’ CAACAGNTGG GAGAGAAGGG GCCAGGGTAT AAAAAGGGCC CACAAGAG-A CCAGCTCANA
       ****** *** ********** ********** ********** ******** * ******** *
  423″ CAACAG-TGG GAGAGAAGGG GCCAGGGTAT AAAAAGGGCC CACAAGAGAA CCAGCTCA-A
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1199' GGATCCCAAG GCCCA-ACT- CCCCGAACCA CTCAGATCAA GATCTGGCCT CGGCGGCCAA
      ********** ***** ***  ********** ********** ********** **********
 481″ GGATCCCAAG GCCCACACTC CCCCGAACCA CTCAGATCAA GATCTGGCCT CGGCGGCCAA

1257' GCTTGGCA-A TCCGGTACTG TTGGTAAAGC C--ACCATGG AA-GATGCCA AA-AACATTA
      ******** * ********** ********** *    ****** ** ******* ** *****
 541″ GCTTGGCACA TCCGGTACTG TTGGTAAAGC CAACCCATGG AACGATGCCA AACAACAT
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