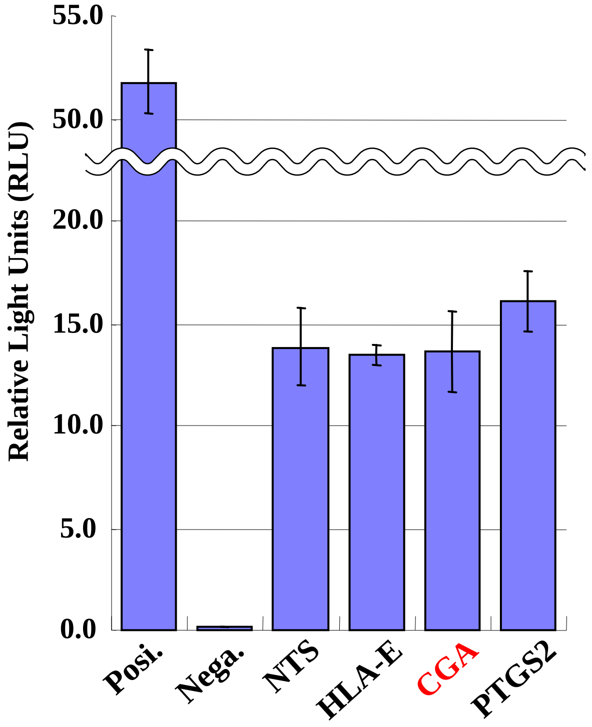
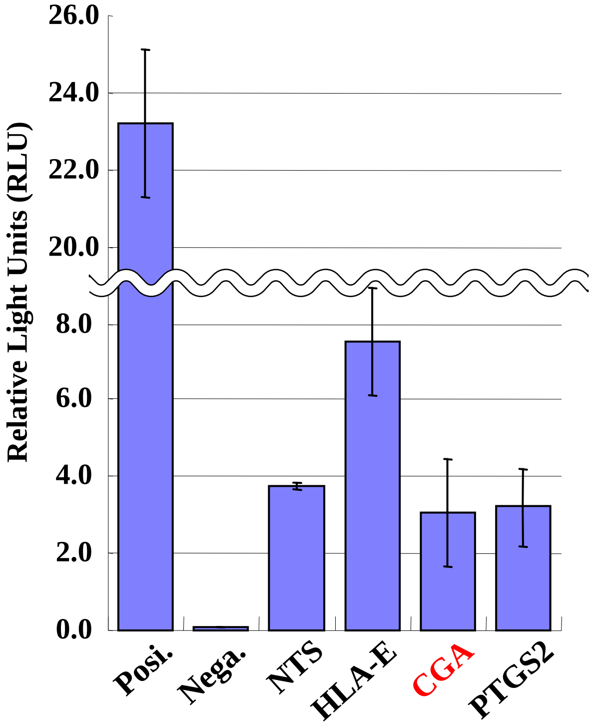
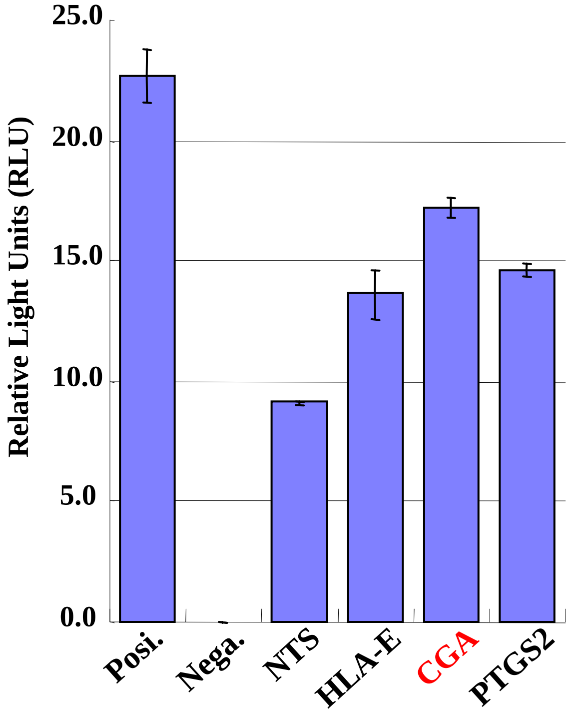
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

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

NTS: pGL4-phNTS (RDB#7308)
HLA-E: pGL4-phHLA-E(RDB#7388)
CGA:pGL4-phCGA (RDB#7456)
PTGS2: pGL4-phPTGS2 (RDB#7300)

2009, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.07.09

1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5539

2nd Nucleotide Sequence
  File Name         : RDB7456F.prj
  Sequence Size     : 400

  Unit Size to Compare = 1
  Pick up Location     = 1



[98.039% / 408 bp]     INT/OPT.Score : <    230/  1504 >

     1' GGCCTAACTG GCCGGTACCT GAGCTCGCTA GCCTCGAGGA TGCCAACATG GTGAAACTCC
                                                    ********* **********
     1"                                              GCCAACATG GTGAAACTCC

    61' TGTCTCTACN CAAAAATACA AAAATTAGCC AGGCATTATG GCGCACACCT GTAGTCCCAG
        *********  ********** ********** ********** ********** **********
    20" TGTCTCTAC- CAAAAATACA AAAATTAGCC AGGCATTATG GCGCACACCT GTAGTCCCAG

   121' NCTACTCGGA GGCTGAGGCA GGAGAAGTGC TTGAACCCGG GAGGTGTAGA CNTGCAGTGA
         ********* ********** ********** ********** ********** * ********
    79" -CTACTCGGA GGCTGAGGCA GGAGAAGTGC TTGAACCCGG GAGGTGTAGA C-TGCAGTGA

   181' GATTGTGCCA CTGCACTCCA GCTTGGGAGA CAGAGCGAGA TTNCCGTCTC CCCCACTCGT
        ********** ********** ********** ********** ** ******* **********
   137" GATTGTGCCA CTGCACTCCA GCTTGGGAGA CAGAGCGAGA TT-CCGTCTC CCCCACTCGT

   241' CCCCCAAAAA GGAGCATCAC TAAGAAAAGG TGANATGGTT GGGATGCATA CTGGAAGGAA
        ********** ********** ********** *** ****** ********** **********
   196" CCCCCAAAAA GGAGCATCAC TAAGAAAAGG TGA-ATGGTT GGGATGCATA CTGGAAGGAA
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    301' ACAACGGAAA TCTGAAAAGG TGTANAGAAC CTAAACAAAT TTGTTTATCA CAGAAAATAA
         ********** ********** **** ***** ********** ********** **********
    255″ ACAACGGAAA TCTGAAAAGG TGTA-AGAAC CTAAACAAAT TTGTTTATCA CAGAAAATAA

    361' ATCACAAAAC AACTTNTGCG TTCTTTGGCA AGTTTCTTTA TGTTAAACAA GAATTGCTTT
         ********** ***** **** ********** ********** ********** **********
    314″ ATCACAAAAC AACTT-TGCG TTCTTTGGCA AGTTTCTTTA TGTTAAACAA GAATTGCTTT

    421' TTGCATNCAC ATAGATCTTC TAAACTCTTT GTTGAAGAGG TCCTTGGTAG TCTGTATNCT
         ****** *** ********** *********
    373″ TTGCAT-CAC ATAGATCTTC TAAACTCTT




1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5539

2nd Nucleotide Sequence
  File Name         : RDB7456R.prj (Complementary)
  Sequence Size     : 400

  Unit Size to Compare = 1
  Pick up Location     = 1



[98.280% / 407 bp]     INT/OPT.Score : <    380/  1516 >

    901' ATGCTCTATA TCTATTTTCG GAAATCTATA GCTCTTNGTT TAGGTAAATA TCAGGTACTT
                                            ***** *** ********** **********
      1″                                    CTCTT-GTT TAGGTAAATA TCAGGTACTT

    961' AGCTAATTAA ATGTCTCTTG TTTATAGNGA AAGTGTCAGC TTTCAGGATG TTATGTGTAT
         ********** ********** ******* ** ********** ********** **********
     29″ AGCTAATTAA ATGTCTCTTG TTTATAG-GA AAGTGTCAGC TTTCAGGATG TTATGTGTAT
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1021’ GGCTCAATAA AATTACGTNA CAAAGTGACA GCGTACTCTC TTTTCATGGG CTGACCTTGT
      ********** ******** * ********** ********** ********** **********
  88″ GGCTCAATAA AATTACGT-A CAAAGTGACA GCGTACTCTC TTTTCATGGG CTGACCTTGT

1081’ CGTCACCATN CACCTGAAAA TGGCTCCAAA CAAAAATGAC CTAAGGGTTG AAACAAGATA
      *********  ********** ********** ********** ********** **********
 147″ CGTCACCAT- CACCTGAAAA TGGCTCCAAA CAAAAATGAC CTAAGGGTTG AAACAAGATA

1141’ NAGATCAAAT TGACGTCATG GTAAAAATTG ACGTCATGGT AATTACACCA ANGTACCCTT
       ********* ********** ********** ********** ********** * ********
 206″ -AGATCAAAT TGACGTCATG GTAAAAATTG ACGTCATGGT AATTACACCA A-GTACCCTT

1201’ CAATCATTGG ATGGAATTTC CTGTTGATCC CAGGGCTTAG ATNGCAGGTG GAAACACTCT
      ********** ********** ********** ********** ** ******* **********
 264″ CAATCATTGG ATGGAATTTC CTGTTGATCC CAGGGCTTAG AT-GCAGGTG GAAACACTCT

1261’ GCTGGTATAA AAGCAGGTGA GGACTTCATT AACTGCAGTT ACTGAGAACT CATAAGACGA
      ********** ********** ********** ********** ********** **********
 323″ GCTGGTATAA AAGCAGGTGA GGACTTCATT AACTGCAGTT ACTGAGAACT CATAAGACGA

1321’ AGCTAAAATC CCTCTTCGAT CAAGATCTGG CCTCGGCGGC CAAGCTTGGC AATCCGGTAC
      ********** ********
 383″ AGCTAAAATC CCTCTTCG
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