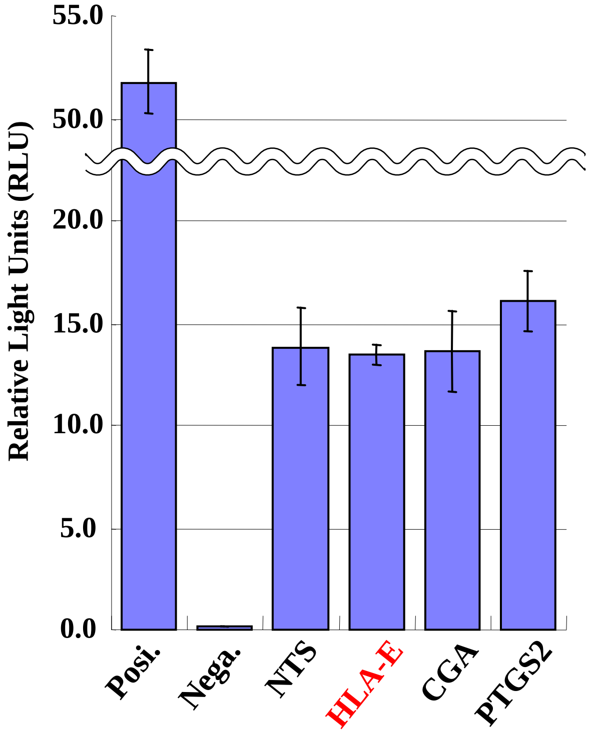
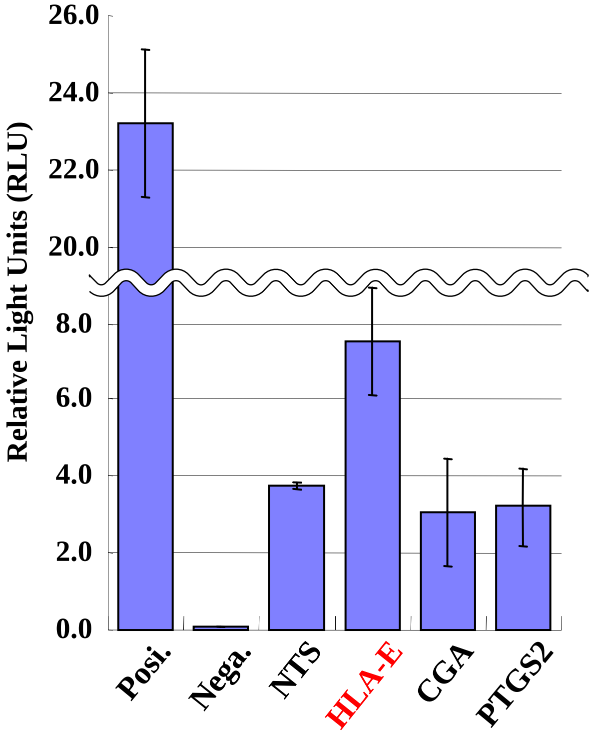
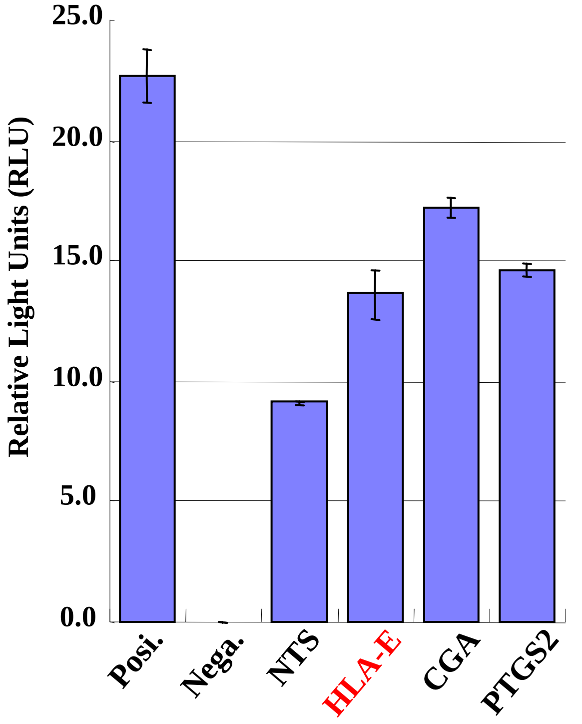
The Promoter Activities of Reporter Constructs


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 : 2009.06.12

1st Nucleotide Sequence
  File Name         : Reference Seq.GNU
  Sequence Size     : 5425

2nd Nucleotide Sequence
  File Name         : RDB7388F.fasta
  Sequence Size     : 519

  Unit Size to Compare = 1
  Pick up Location     = 1



[91.720% / 471 bp]     INT/OPT.Score : <    359/  1518 >

     1’                 GGCCT AACTGGCCGG TACCTGAGCT CGCTAGCCTC GAGGATTCTC
                        ***** ********** ********** ********** **********
     1″ CCAGAACATT TCTCTGGCCT AACTGGCCGG TACCTGAGCT CGCTAGCCTC GAGGATTCTC

    46’ AGCCTCCAGA GTTGCTGGAA TTACAGGCGC GCACNCACCA CACCCGGCTA ATTTTTGTAT
        ********** ********** ********** **** ***** ********** **********
    61″ AGCCTCCAGA GTTGCTGGAA TTACAGGCGC GCAC-CACCA CACCCGGCTA ATTTTTGTAT

   106’ TGTTAGTAGA GACAGGGTTT CATCANTGTT GGCCAGGTTA GTCTTGAACT CCTGACCTCG
        ********** ********** ***** **** ********** ********** **********
   120″ TGTTAGTAGA GACAGGGTTT CATCA-TGTT GGCCAGGTTA GTCTTGAACT CCTGACCTCG

   166’ TGATCTGCCT GCCTCGNGCC TACCAAAATG CTGCGATTAC AGGCGTGAGC CACCGTTCCC
        ********** ****** *** ********** ********** ********** **********
   179″ TGATCTGCCT GCCTCG-GCC TACCAAAATG CTGCGATTAC AGGCGTGAGC CACCGTTCCC

   226’ GGCCTATNAC GTTGTTTATT TTGGAAAAAT TAAAAATTAA GTTTTTTTTC ATTAAAGANT
        ******* ** ********** ********** ********** ********** ******** *
   238″ GGCCTAT-AC GTTGTTTATT TTGGAAAAAT TAAAAATTAA GTTTTTTTTC ATTAAAGA-T
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286' ATGTTATTTC CGATCAAGAG ATCAAGACCA TCCTGG-CCA ACATGGTGAA NACCCCGTCT
     ********** ********** ********** ****** *** **********  *********
296" ATGTTATTTC CGATCAAGAG ATCAAGACCA TCCTGGACCA ACATGGTGAA -ACCCCGTCT

345' CTACTAAAAA CACAAAAATT AG-CTGGGTG TGGTGGCACA CGNCCTGTAG TT-CCAGTTA
     ********** ********** ** ******* ********** **.******* ** *******
355" CTACTAAAAA CACAAAAATT AGACTGGGTG TGGTGGCACA CGACCTGTAG TTACCAGTTA

403' CTGGGGAGGC TGAGGCAGGA G-AATCG--C TTGAACCNCG GGAGAAGGAG GTTGCAGTGA
     ******        *** *** * *****  *   *   *. * ** **** *  *  *  *  *
415" CTGGGG---- GAGGGCTGGA GAAATCGAAC GAGGGGCCAG GGCGAAGCAC G-AGGGGAAA

460' GCCGAGATCA TGCCACTGCA CTCCAGCCNT GGGGACAGAG CAAGACTCTG ACTCAAAAAA
     *  ***
470" GGGGAGGGAT GGACAAGGGG AANAGCAAGA AAAATTGATT NACCAAACTC




1st Nucleotide Sequence
  File Name          : Reference Seq.GNU
  Sequence Size      : 5425

2nd Nucleotide Sequence
  File Name          : RDB7388R.fasta (Complementary)
  Sequence Size      : 405

  Unit Size to Compare = 1
  Pick up Location     = 1



[97.805% / 410 bp]     INT/OPT.Score : <    403/  1519 >

841' GACANGGGTT TCTCCATATT GGTCGGGCTG GTCTCGAACT CCCAACCTCA GGTGANTCAG
                                                                 .****
  1"                                                            TTTCAG
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 901’ CCCGCCTTGG CCTCCCAAAG TGCTGAGATT ACAGG-CGTG AGCCACCNGC GCCCAGCCAG
      ********** ********** ********** ***** **** ******* ** **********
   7″ CCCGCCTTGG CCTCCCAAAG TGCTGAGATT ACAGGTCGTG AGCCACC-GC GCCCAGCCAG

 960’ GACTAATTTC TAAGAGTGTG CAGAGATACC GAAACCTANA AAGTTTAAGA ACTGCTGATT
      ********** ********** ********** ******** * ********** **********
  66″ GACTAATTTC TAAGAGTGTG CAGAGATACC GAAACCTA-A AAGTTTAAGA ACTGCTGATT

1020’ GCTGGGAAAC TCTGCAGTTT CCCGTTCCTN CTCGTAACCT GGTCATGTGT CCTTCTTCCT
      ********** ********** *********  ********** ********** **********
 125″ GCTGGGAAAC TCTGCAGTTT CCCGTTCCT- CTCGTAACCT GGTCATGTGT CCTTCTTCCT

1080’ GGATACTCAT GACGCAGACT NCAGTTCTCA TTCCCAATGG GTGTCGGGTT TCTAGAGAAG
      ********** **********  ********* ********** ********** **********
 184″ GGATACTCAT GACGCAGACT -CAGTTCTCA TTCCCAATGG GTGTCGGGTT TCTAGAGAAG

1140’ CCAATCAGCG TNCGCCACGA CTCCCGACTA TAAAGTCCCC ATCCGGACTC AAGAAGTTCT
      ********** * ******** ********** ********** ********** **********
 243″ CCAATCAGCG T-CGCCACGA CTCCCGACTA TAAAGTCCCC ATCCGGACTC AAGAAGTTCT

1200’ CANGGACTCA GAGGCTGGGA TCATGATCAA GATCTGGCCT CGGCGGCCAA GCTTGGCAAT
      ** ******* ********** ********** ********** ********** **********
 302″ CA-GGACTCA GAGGCTGGGA TCATGATCAA GATCTGGCCT CGGCGGCCAA GCTTGGCAAT

1260’ CCGGTACTGT TGGTAAAGCC ACCATGGAAG ATGCCAAAAA CATTAAGAAG GGCCCAGCGC
      ********** ********** ********** ********** *** *
 361″ CCGGTACTGT TGGTAAAGCC ACCATGGAAG ATGCCAAAAA CATAA
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