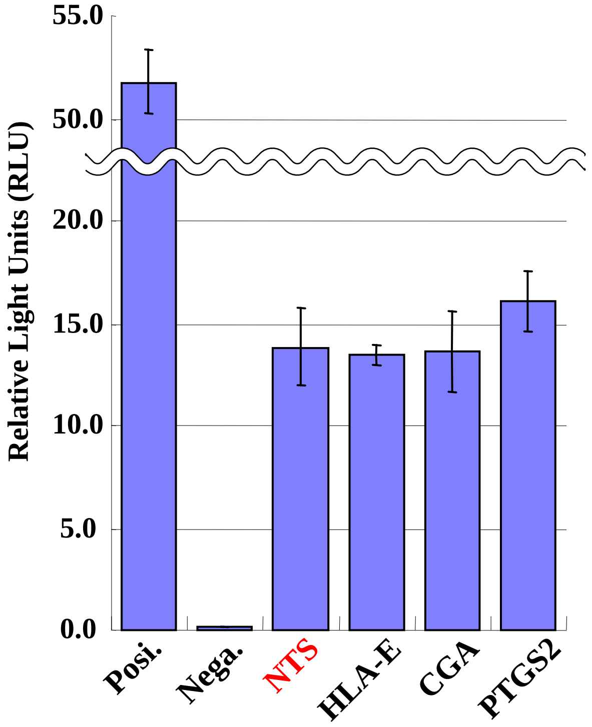
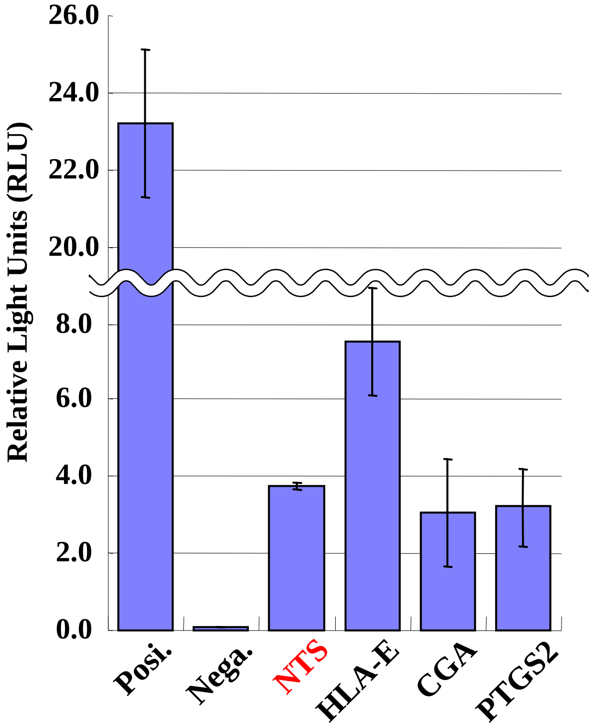
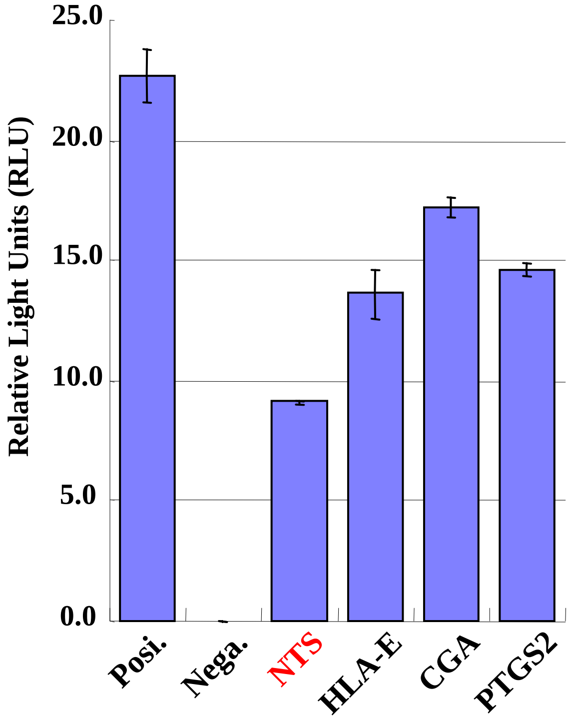
The Promoter Activities of Reporter Constructs



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 : 2009.07.02

1st Nucleotide Sequence
  File Name         : Reference Seq.GNU
  Sequence Size     : 5480

2nd Nucleotide Sequence
  File Name         : RDB7308F.fasta
  Sequence Size     : 497

  Unit Size to Compare = 1
  Pick up Location     = 1



[97.951% / 488 bp]     INT/OPT.Score : <    289/  1802 >

      1'                     GG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATC
                             ** ********** ********** ********** **********
      1″ GTGCCAGAAC ATTTCTCTGG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATC

     43' CCCATGTATC TTGAAATGCT TACTACANAG AAGAAAGTTT TACTCTAAAA GGCATTTTGA
         ********** ********** ******* ** ********** ********** **********
     61″ CCCATGTATC TTGAAATGCT TACTACA-AG AAGAAAGTTT TACTCTAAAA GGCATTTTGA

    103' ACAATTTTCT TTTGAGAANC TCAGACAAAG AATGGGTATC AGTGTAACTC ATGAAATACA
         ********** ******** * ********** ********** ********** **********
    120″ ACAATTTTCT TTTGAGAA-C TCAGACAAAG AATGGGTATC AGTGTAACTC ATGAAATACA

    163' TGAAGACTAN TCATAGAAAA GTGACTTTGG TGAATGGTGG TTATTTAGGA TTGTCTCCTT
         *********  ********** ********** ********** ********** **********
    179″ TGAAGACTA- TCATAGAAAA GTGACTTTGG TGAATGGTGG TTATTTAGGA TTGTCTCCTT

    223' NTCCAAAAGT ACAATCTCTT TTTTTATGGT GAAAAGAGTA TTATAACAGG GNAAAGAAAG
          ********* ********** ********** ********** ********** * ********
    238″ -TCCAAAAGT ACAATCTCTT TTTTTATGGT GAAAAGAGTA TTATAACAGG G-AAAGAAAG
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    283’ CCGATGCAAT AGTAAAAACT GTTGAGAAGG GAATTATACA AANGAGTGAG ACATGGCATC
         ********** ********** ********** ********** ** ******* **********
    296″ CCGATGCAAT AGTAAAAACT GTTGAGAAGG GAATTATACA AA-GAGTGAG ACATGGCATC

    343’ AAGAATGAAT TCAAAAAGAG CAGAAAAATA TAGNGCATAA AAAGAGATAA TGTACAGAAA
         ********** ********** ********** *** ****** ********** **********
    355″ AAGAATGAAT TCAAAAAGAG CAGAAAAATA TAG-GCATAA AAAGAGATAA TGTACAGAAA

    403’ AAAAGTCAGT GATACAACAA CACANAATTT TTACCTGCTA GAATGTAAGT AATTTAGAGC
         ********** ********** **** ***** ********** ******* ** **********
    414″ AAAAGTCAGT GATACAACAA CACA-AATTT TTACCTGCTA GAATGTACGT AATTTAGAGC

    463’ TGGATTTTAT AAACANTGAA ATTGTTTTTC TAATACATTC AACCAAAAGT CAGCACACAT
         ********** ***** **** ******
    473″ TGGATTTTAT AAACA-TGAA ATTGTT
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1st Nucleotide Sequence
  File Name         : Reference Seq.GNU
  Sequence Size     : 5480

2nd Nucleotide Sequence
  File Name         : RDB7308R.fasta (Complementary)
  Sequence Size     : 685

  Unit Size to Compare = 1
  Pick up Location     = 1


[97.564% / 698 bp]     INT/OPT.Score : <    278/  2540 >

    661’ CTGATTCTCT GTCTCTATTC CNATCTTATT CCAGCATGGA TTATTTAAAA CCTGTATTAG
            * ***** ********** * ******** ********** ****** *** **********
      1″   AAATCTCT GTCTCTATTC C-ATCTTATT CCAGCATGGA TTATTTTAAA CCTGTATTAG

    721’ TTTTGGAACC ACNTAAACAT TTGCTCAGAA GTTTGAATTA CCAGAGAAGC ACCCTAACTC
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      ********** ** ******* ********** ***** **** ********** **********
  58″ TTTTGGAACC AC-TAAACAT TTGCTCAGAA GTTTG-ATTA CCAGAGAAGC ACCCTAACTC

 781' TTCNAAGAAC TTCCAAGCCT AAGGAATCAC TGATTTCATG CATTCATCCT GGAGNATTTT
      *** ****** ********** ********** ********** ********** **** *****
 116″ TTC-AAGAAC TTCCAAGCCT AAGGAATCAC TGATTTCATG CATTCATCCT GGAG-ATTTT

 841' CCTTAAAAAT TAGAAATAAC AGATCTCATG TTTCACAAAA TCAAANATGA CAACTTTTGG
      ********** ********** ********** ********** ***** **** **********
 174″ CCTTAAAAAT TAGAAATAAC AGATCTCATG TTTCACAAAA TCAAA-ATGA CAACTTTTGG

 901' AGTGGGGGAA TGAGAAGTGG GAAAAGGATG ATACTGNGGG GTTCTTTGTC AGTATGCTGT
      ********** ********** ********** ****** *** ********** **********
 233″ AGTGGGGGAA TGAGAAGTGG GAAAAGGATG ATACTG-GGG GTTCTTTGTC AGTATGCTGT

 961' ATGTATGCTG TATGTCAGTG CAGTTGANAT GACTCCTTCT GTGCGTCAGA AATCCAAAGC
      ********** ********** ******* ** ********** ********** **********
 292″ ATGTATGCTG TATGTCAGTG CAGTTGA-AT GACTCCTTCT GTGCGTCAGA AATCCAAAGC

1021' AGCAGCAGCA GCAATTAGNG GAAGATCGTC ACTTTCACTC AAGGTTCAGA AATGGGGGAG
      ********** ******** * ********** ********** ********** **********
 351″ AGCAGCAGCA GCAATTAG-G GAAGATCGTC ACTTTCACTC AAGGTTCAGA AATGGGGGAG

1081' GAGAGCAGGN GGGGACAAAG GAAAAGGGGA GGAGAAAGCA GGGCAAAGAG GGGAGGGATG
      *********  ********** ********** ********** ********** **********
 410″ GAGAGCAGG- GGGGACAAAG GAAAAGGGGA GGAGAAAGCA GGGCAAAGAG GGGAGGGATG

1141' NGAGGTGAAG ATAGGGCACA TCCTGCAAAG ATAATGTCTG TACAATCAAT GNACATCATC
       ********* ********** ********** ********** ********** * ********
 469″ -GAGGTGAAG ATAGGGCACA TCCTGCAAAG ATAATGTCTG TACAATCAAT G-ACATCATC

1201' CTCCTGCTTA TATATATAGG GGAATGGCCA GAGCACCTCT CANTAGTTCA CTCACTTTCA
      ********** ********** ********** ********** ** ******* **********
 527″ CTCCTGCTTA TATATATAGG GGAATGGCCA GAGCACCTCT CA-TAGTTCA CTCACTTTCA

1261' AAGCCAGCTG AAGGAAAGAA TCAAGATCTG GCCTCGGCGG CCAAGCTTGG CAATCCGGTA
      ********** ******** * ********** ********** ********** **********
 586″ AAGCCAGCTG AAGGAAAG-A TCAAGATCTG GCCTCGGCGG CCAAGCTTGG CAATCCGGTA
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1321’ CTGTTGGTAA AGCCACCATG GAAG-ATGCC AAAAACATTA AGAAGGGCCC AGCGCCATTC
      ********** ********** **** ***** ********** *
 645″ CTGTTGGTAA AGCCACCATG GAAGTATGCC AAAAACATTA A
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