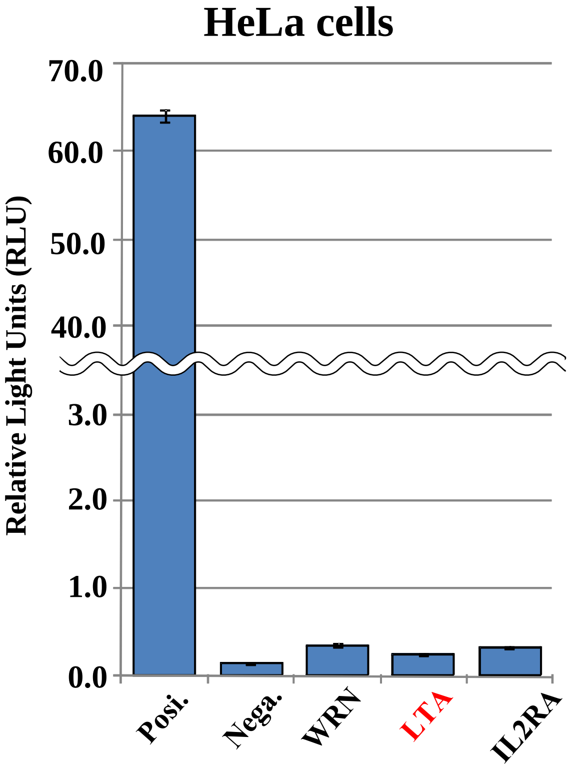
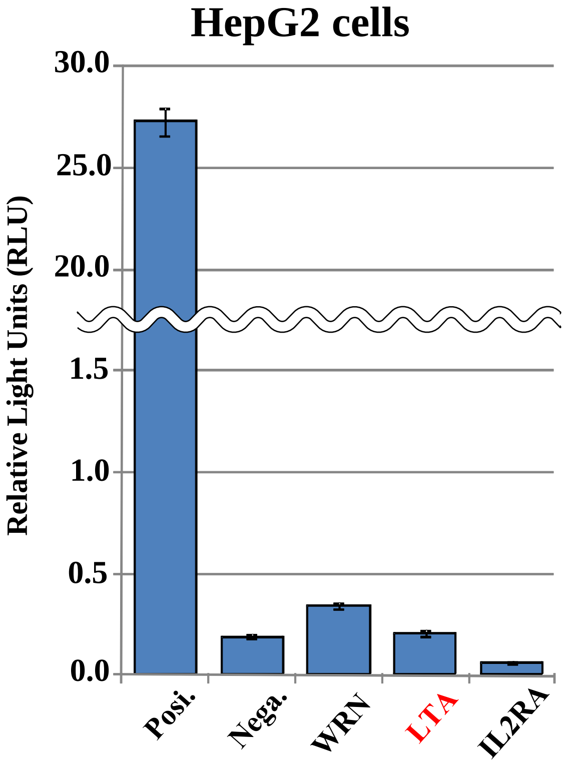
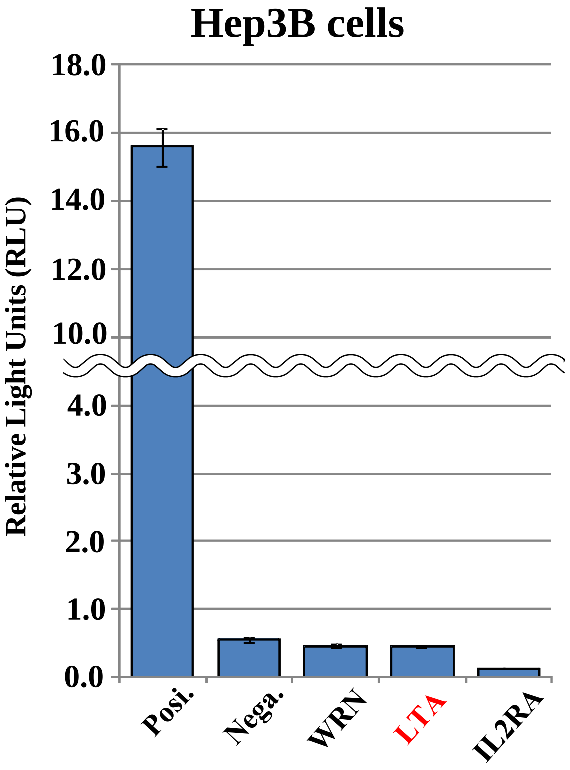
The Promoter Activities of Reporter Constructs







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

WRN: pGL4-phWRN (RDB# 7569)
LTA: pGL4-phLTA (RDB# 7486)
IL2RA: pGL4-phIL2RA (RDB# 7525)

2010, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.08.27

1st Nucleotide Sequence
  File Name         : Reference Seq.GNU
  Sequence Size     : 5677

2nd Nucleotide Sequence
  File Name         : RDB7486F.fasta
  Sequence Size     : 563

  Unit Size to Compare = 1
  Pick up Location     = 1



[96.964% / 560 bp]     INT/OPT.Score : <    328/  2019 >

     1'               GGCCTAA CTGGCCGGTA CCTGAGCTCG CTAGCCTCGA GGATGCTGGG
                      ******* ********** ********** ********** **********
     1" AACATTTGTC TCTGGCCTAA CTGGCCGGTA CCTGAGCTCG CTAGCCTCGA GGATGCTGGG

    48' TGGTGGCTAC ATACAGATGG AAAAATTNCA TCAGCTGTAC ACTTAAGAGG TGTCCACCTC
        ********** ********** ******* ** ********** ********** **********
    61" TGGTGGCTAC ATACAGATGG AAAAATT-CA TCAGCTGTAC ACTTAAGAGG TGTCCACCTC

   108' ATACCTAAGT TACATATCNA ATAAAAAGGA AAAAAATTTT GGAAACTTTT TTTTTTTTTT
        ********** ******** * ********** ********** ******   ** **********
   120" ATACCTAAGT TACATATC-A ATAAAAAGGA AAAAAATTTT GGAAAC--TT TTTTTTTTTT

   168' TTGAGACAGN AGTCTTGCTC TGTCCCCCAG GCTGGAATAC AGTGGTGCGA TCTTGACTCA
        *********  ********** ********** ********** ********** **********
   177" TTGAGACAG- AGTCTTGCTC TGTCCCCCAG GCTGGAATAC AGTGGTGCGA TCTTGACTCA

   228' NCTGCAGCCT CCGCCTCCCA GGTTCAAATA ATTCTCCAGC CTCAGCCTCC CNGAGTAGCT
         ********* ********** ********** ********** ********** * ********
   236" -CTGCAGCCT CCGCCTCCCA GGTTCAAATA ATTCTCCAGC CTCAGCCTCC C-GAGTAGCT
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288’ GGGACTGCAG ATGCGCACCA GCACGCCTGG CTAATTTTTG TANTTTATTA TAGAGATGGG
     ********** ********** ********** ********** ** ******* **********
294″ GGGACTGCAG ATGCGCACCA GCACGCCTGG CTAATTTTTG TA-TTTATTA TAGAGATGGG

348’ GTTTCACCAT GTTGGCCAGC TGGTCTCAAA CTCNCTGACC TCAAGTAATC CGCCCACCTC
     ********** ********** ********** *** ****** ********** **********
353″ GTTTCACCAT GTTGGCCAGC TGGTCTCAAA CTC-CTGACC TCAAGTAATC CGCCCACCTC

408’ AGACTCCCAA AGTGCCAGGA TTACNAGGTG TGAGCCACTG CACCAGGCCT GGAACAATTT
     ********** ********** **** ***** ********** ********** **********
412″ AGACTCCCAA AGTGCCAGGA TTAC-AGGTG TGAGCCACTG CACCAGGCCT GGAACAATTT

468’ TAAAATAATG TATTGNGCTC TGCAAATGCA GCTTCAGAAC AAGTCCCTTA GCTGTCCCCA
     ********** ***** **** ********** ********** ******* ** **********
471″ TAAAATAATG TATTG-GCTC TGCAAATGCA GCTTCAGAAC AAGTCCCCTA GCTGTCCCCA

528’ CCCCACNCCT AAGTCACCA- CCCTT-AAGC CTCACCCATG TGGAATTCTG AAACTTCCTN
     ****  .*** *********  ***** **** ***
530″ CCCCCACCCT AAGTCACCAC CCCTTAAAGC CTCC
```

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Date : 2009.08.17

1st Nucleotide Sequence
  File Name         : Reference Seq.GNU
  Sequence Size     : 5677

2nd Nucleotide Sequence
  File Name         : RDB7486R.fasta (Complementary)
  Sequence Size     : 677

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

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[97.238% / 688 bp]     INT/OPT.Score : <    575/  2501 >

  841' ACAAGAGGCA AACACCAGAA TGTCCCCGAT GAAGGGGATA TATAATGGAC NCTTCTTGAT
                                       ********* **********  *********
    1″                                  AAGGGGATA TATAATGGAC -CTTCTTGAT

  901' GTGAAACCTG CCAGATGGGC TGGAAAGTCC GTATACTGGG ANCAAGTATG ATTTGAGTTG
       ********** ********** ***** **** ******* ** *.******** **********
   29″ GTGAAACCTG CCAGATGGGC TGGAAGGTCC GTATACT-GG AACAAGTATG ATTTGAGTTG

  961' TTTGGG-ACA AGGACAGGGG TACAAGAGAA GGANAATGGG CAAAGAGAGA AGCCTGTACT
       ****** *** ********** ********** *** ****** ********** **********
   88″ TTTGGGAACA AGGACAGGGG TACAAGAGAA GGA-AATGGG CAAAGAGAGA AGCCTGTACT

 1020' CAGCCAAGGG TGCAGAGATG TTATNATATG ATTGCTCTTC AGGGAACCGG GCCTCCAGCT
       ********** ********** **** ***** ********** ********** **********
  147″ CAGCCAAGGG TGCAGAGATG TTAT-ATATG ATTGCTCTTC AGGGAACCGG GCCTCCAGCT

 1080' CACACCCCAG CTGCTNCAAC CGCCTCCTCT CTGAATTGAC TGTCCCTTCT TTGGAACTCT
       ********** ***** **** * ******** ********** ********** **********
  206″ CACACCCCAG CTGCT-CAAC CACCTCCTCT CTGAATTGAC TGTCCCTTCT TTGGAACTCT

 1140' AGGCCTNGAC CCCACTCCCT GGCCCTCCCA GCCCACGATT CCCCTGACCC GACTCCCNTT
       ****** *** ********** ********** ********** ********** ******* **
  265″ AGGCCT-GAC CCCACTCCCT GGCCCTCCCA GCCCACGATT CCCCTGACCC GACTCCC-TT

 1200' TCCCAGAACT CAGTCGCCTG AACCCCCAGC CTGTGGTTCT CTCCTAGGNC CTCAGCCTTT
       ********** ********** ********** ********** ******** * **********
  323″ TCCCAGAACT CAGTCGCCTG AACCCCCAGC CTGTGGTTCT CTCCTAGG-C CTCAGCCTTT

 1260' CCTGCCTTTG ACTGAAACAG CAGTATCTTC TAAGCCCTGN GGGGCTTCCC CGGGCCCCAG
       ********** ********** ********** *********  ********** **********
  382″ CCTGCCTTTG ACTGAAACAG CAGTATCTTC TAAGCCCTG- GGGGCTTCCC CGGGCCCCAG

 1320' CCCCGACCTA GAACCCGCCC GCTGCCTGCC NACGCTGCCA CTGCCGCTTC CTCTATAAAG
       ********** ********** **********  ********* ********** **********
  441″ CCCCGACCTA GAACCCGCCC GCTGCCTGCC -ACGCTGCCA CTGCCGCTTC CTCTATAAAG

 1380' GGACCTGAGC GTCCGGGCCC ANGGGGCTCC ACACAGCAGG TGAGGCTCTC CTGCCCCATC
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      ********** ********** * ********  ********* ********** **********
 500″ GGACCTGAGC GTCCGGGCCC A-GGGGCTCC GCACAGCAGG TGAGGCTCTC CTGCCCCATC

1440' TCCTTGGGCT GCCCGTGCTT CGTGCTTTGG ACTACCGATC AAGATCTGGC CTCGGCGGCC
      ********** ********** ********** ********** ********** **********
 559″ TCCTTGGGCT GCCCGTGCTT CGTGCTTTGG ACTACCGATC AAGATCTGGC CTCGGCGGCC

1500' AAGCTTGGCA ATCCGGTACT GTTGGTAAAG CCACCATGGA A-GATGCCAA A-AACATTAA
      ********** ********** ********** ********** *  ******* * *******
 619″ AAGCTTGGCA ATCCGGTACT GTTGGTAAAG CCACCATGGA ACAATGCCAA ACAACATTA
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