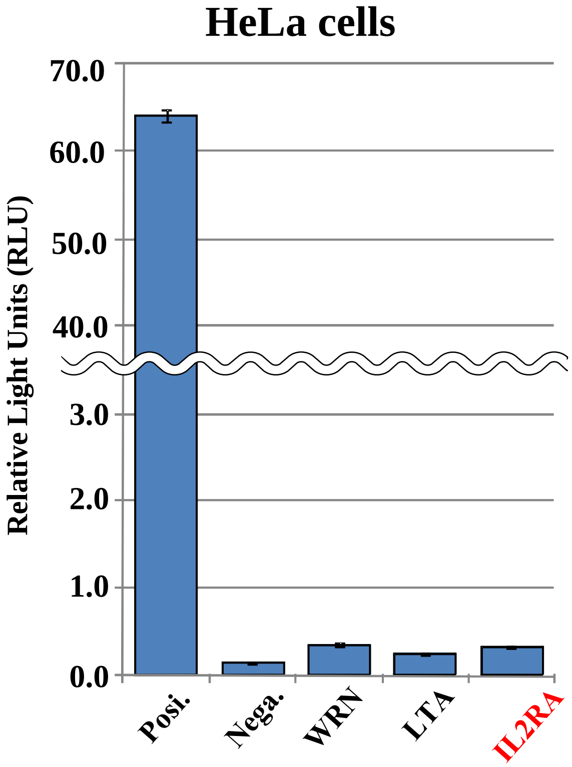
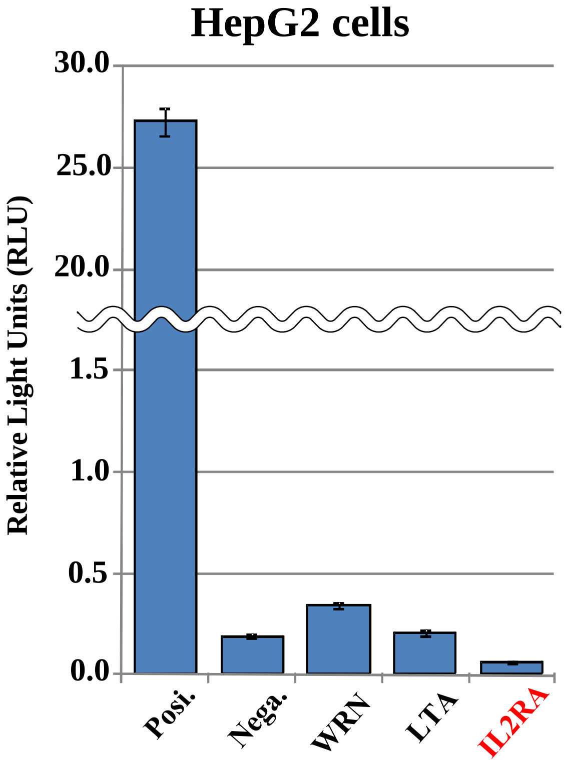
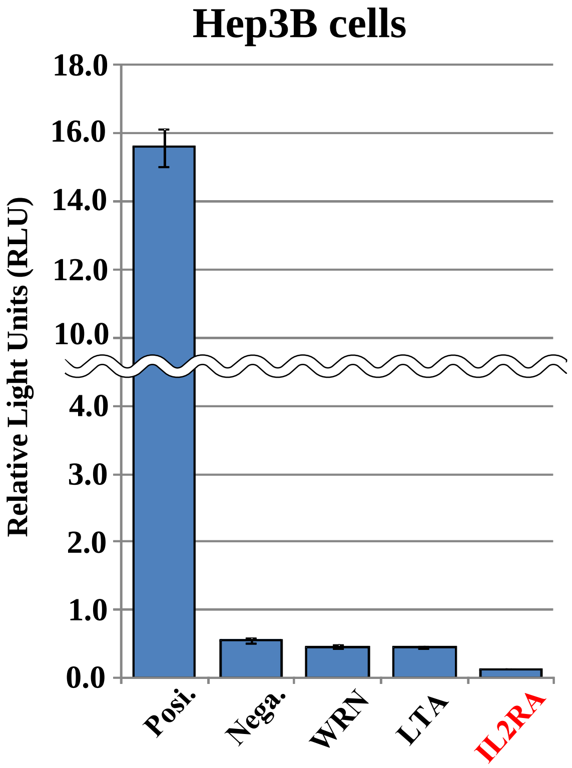
The Promoter Activities of Reporter Constructs







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 : 2009.09.25

1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5743

2nd Nucleotide Sequence
  File Name        : RDB7525F.fasta
  Sequence Size    : 614

  Unit Size to Compare = 1
  Pick up Location     = 1



[97.360% / 606 bp]     INT/OPT.Score : <    478/  2219 >

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

     43' AAGGAGCGTG ACTTTGGTGG GAGTACTAGG AGTTTCTACT GNGAGCACTT GCCCGCAGAG
         ********** ********** ********** ********** * ******** **********
     61″ AAGGAGCGTG ACTTTGGTGG GAGTACTAGG AGTTTCTACT G-GAGCACTT GCCCGCAGAG

    103' TGAGAAACGT TCCTAGAGAG GAAGTTATAC CTNGCTGTGG AATTTAAGAG AATCTTGTCA
         ********** ********** ********** ** ******* ********** **********
    120″ TGAGAAACGT TCCTAGAGAG GAAGTTATAC CT-GCTGTGG AATTTAAGAG AATCTTGTCA

    163' TATTTTGACA AGTTTTTTGA GATNGGAAGT CTCACTCTGT CGCCCAGGCT GGAGTGCAGT
         ********** ********** *** ****** ********** ********** **********
    179″ TATTTTGACA AGTTTTTTGA GAT-GGAAGT CTCACTCTGT CGCCCAGGCT GGAGTGCAGT

    223' GGCGCAATCT CAGCNTCACT GCAGCCTGCA CCTCCTCGGT TCCAGCTATT CTCTTGTCTC
         ********** **** ***** ********** ********** ********** **********
    238″ GGCGCAATCT CAGC-TCACT GCAGCCTGCA CCTCCTCGGT TCCAGCTATT CTCTTGTCTC
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283’ AGCCTNCCTG AGTAACTGGG ATTACAGGCG CCCGCCACTA CGCCTGGCTA ATTTTTNGTA
     ***** **** ********** ********** ********** ********** ****** ***
297″ AGCCT-CCTG AGTAACTGGG ATTACAGGCG CCCGCCACTA CGCCTGGCTA ATTTTT-GTA

343’ TTTTTAGTAG AAATGGGGTT TTACCATGTT GGCCAGACTG GTCTCAANAC TCCCGACCTC
     ********** ********** ********** ********** ******* ** **********
355″ TTTTTAGTAG AAATGGGGTT TTACCATGTT GGCCAGACTG GTCTCAA-AC TCCCGACCTC

403’ AGGTGATCTG CCTGCCTCAG CCTCCCAAAG TGCTGGAANT TACAGGCGTG TGCCACTGCG
     ********** ********** ********** ******** * ********** **********
414″ AGGTGATCTG CCTGCCTCAG CCTCCCAAAG TGCTGGAA-T TACAGGCGTG TGCCACTGCG

463’ CCTGGCTAAT TTTTTTTTTT TTTTTTTTTN TTTTTTTTTT TTTAG--TAG AGACGGTGGT
     ********** ********** *********. * ******** ** **   ** **********
473″ CCTGGCTAAT TTTTTTTTTT TTTTTTTTTC TCTTTTTTTT TTAAGTTAAG AGACGGTGGT

521’ TTCACCATGT CATCCAGGCT GGNTCTCAAA CTCCTGACCT CAGGTGATCC ACCCACCTTG
     ********** ********** ** ******* ********** ********** **********
533″ TTCACCATGT CATCCAGGCT GG-TCTCAAA CTCCTGACCT CAGGTGATCC ACCCACCTTG

581’ GTCTACCAAA GTGNCTCGGA TTACAGGCAT GAGCCACCAG GCCCAGTCAA CGTGATGTGT
     ********** *** ****** ****
592″ GTCTACCAAA GTG-CTCGGA TTAC




1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5743

2nd Nucleotide Sequence
  File Name        : RDB7525R.fasta (Complementary)
  Sequence Size    : 689

  Unit Size to Compare = 1
  Pick up Location     = 1
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[97.854% / 699 bp]     INT/OPT.Score : <    630/  2592 >

  901' CCTTTAAGAG AAAGAAATCT GGAAGCAAAA CACCTTATAA AATGACAATG NCACTTTCAG
                           ******** *.****.*** **********  *********
    1"                      AAAGCAAAA CNCCTTNTAA AATGACAATG -CACTTTCAG

  961' GA-GCCCAGG GCACTGTGGT GAAATGATGA TGGCTAGTAC AGNGTTATAA GCCTTGGGGA
       ** ******* ********** ********** ********** ** ******* **********
   39" GAGGCCCAGG GCACTGTGGT GAAATGATGA TGGCTAGTAC AG-GTTATAA GCCTTGGGGA

 1020' ATTATTTATG AATTCTCAGG ATCCTTCAGT TCGNCCGCAT CCTTCTCCAT TATTTGAATA
       ********** ********** ********** *** ****** ********** **********
   98" ATTATTTATG AATTCTCAGG ATCCTTCAGT TCG-CCGCAT CCTTCTCCAT TATTTGAATA

 1080' TTGGAGGCTG CCTGACCAGA ATCTNTGTCA GGACTTTGCT CCTTCATCCC AGGTGGTCCC
       ********** ********** **** ***** ********** ********** **********
  157" TTGGAGGCTG CCTGACCAGA ATCT-TGTCA GGACTTTGCT CCTTCATCCC AGGTGGTCCC

 1140' GGCTGACTCC TGAGGNACGT TACAGCCCTG AGGGGAGGAC TCAGCTTATG AAGTGCTGGG
       ********** ***** **** ********** ********** ********** **********
  216" GGCTGACTCC TGAGG-ACGT TACAGCCCTG AGGGGAGGAC TCAGCTTATG AAGTGCTGGG

 1200' TGAGACNCAC TGCCAAGAAG TGCTTGCTCA CCCTACCTTC AACGGCAGGG GAATCTCNCC
       ****** *** ********** ********** ********** ********** ******* **
  275" TGAGAC-CAC TGCCAAGAAG TGCTTGCTCA CCCTACCTTC AACGGCAGGG GAATCTC-CC

 1260' TCTCCTTTTA TGGGCGTAGC TGAAGAAAGG ATTCATAAAT GAAGTTCANA TCCTTCTCAT
       ********** ********** ********** ********** ******** * **********
  333" TCTCCTTTTA TGGGCGTAGC TGAAGAAAGG ATTCATAAAT GAAGTTCA-A TCCTTCTCAT

 1320' CAACCCCAGC CCACACCTCC AGCAATTGAA CTTGAAAAAN AAAAACCTGG TTTGAAAAAT
       ********** ********** ********** *********  ********** **********
  392" CAACCCCAGC CCACACCTCC AGCAATTGAA CTTGAAAAA- AAAAACCTGG TTTGAAAAAT

 1380' TACCGCAAAC TATATTGTCA TCAAAAAAAA NAAAAAAAAA AAAACACTTC CTATATTTGA
       ********** ********** **********  ********* ********** **********
  451" TACCGCAAAC TATATTGTCA TCAAAAAAAA -AAAAAAAAA AAAACACTTC CTATATTTGA
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1440' GATGAGAGAA GAGAGTGCTA GNGCAGTTTC CTGGCTGAAC ACGCCAGCCC AATACTTAAA
      ********** ********** * ******** ********** ********** **********
 510″ GATGAGAGAA GAGAGTGCTA G-GCAGTTTC CTGGCTGAAC ACGCCAGCCC AATACTTAAA

1500' GAGAGCAACT CCTGACTCCG ATAGAGACTG GATGGACCCA CAAATCAAGA TCTGGCCTCG
      ********** ********** ********** ********** ********** **********
 569″ GAGAGCAACT CCTGACTCCG ATAGAGACTG GATGGACCCA CAAATCAAGA TCTGGCCTCG

1560' GCGGCCAAGC TTGGCAATCC GGTACTGTTG GTAAAGCCAC CATGGAAGAT GCCAAAAACA
      ********** ********** ********** ********** ********** ****** ***
 629″ GCGGCCAAGC TTGGCAATCC GGTACTGTTG GTAAAGCCAC CATGGAAGAT GCCAAACACA

1620' TTAAGAAGGG CCCAGCGCCA TTCTACCCAC TCGAAGACGG GACCGCCGGC GAGCAGCTGC
      *
 689″ T
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