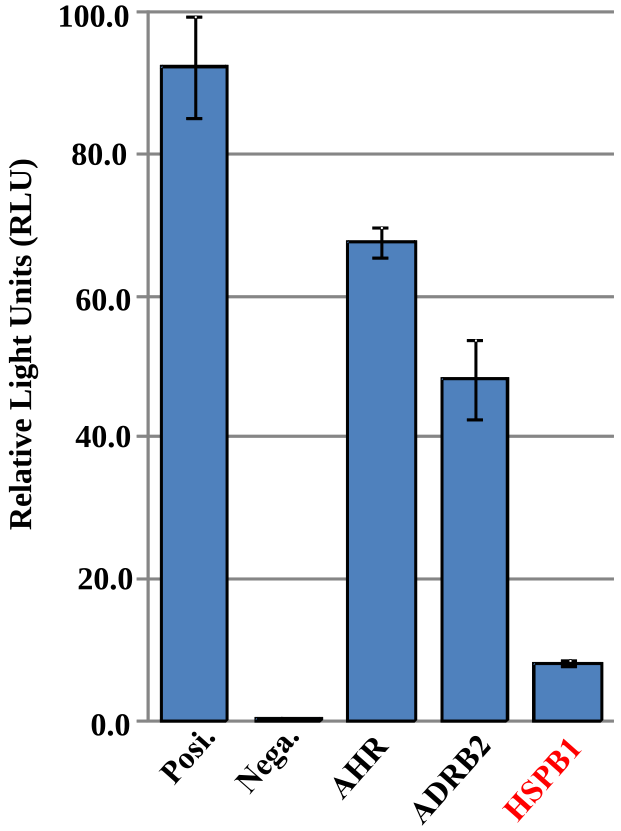
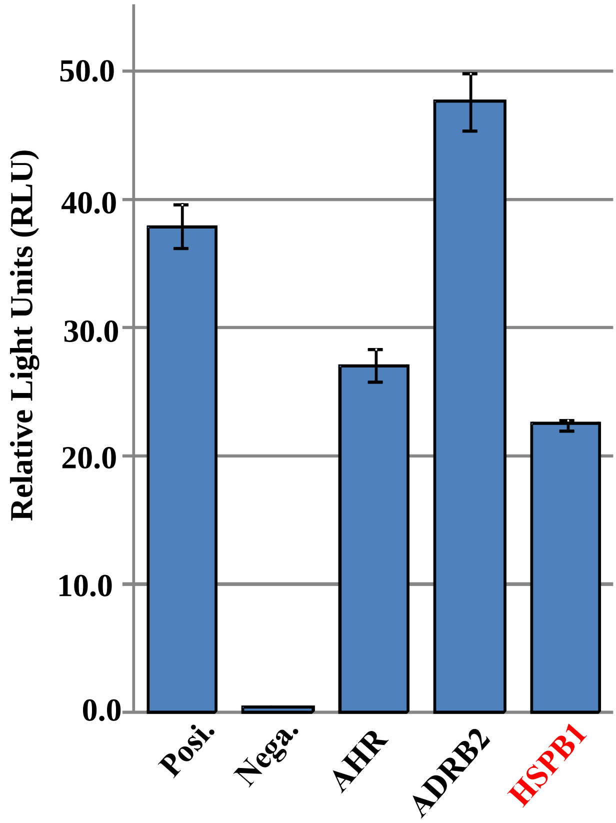
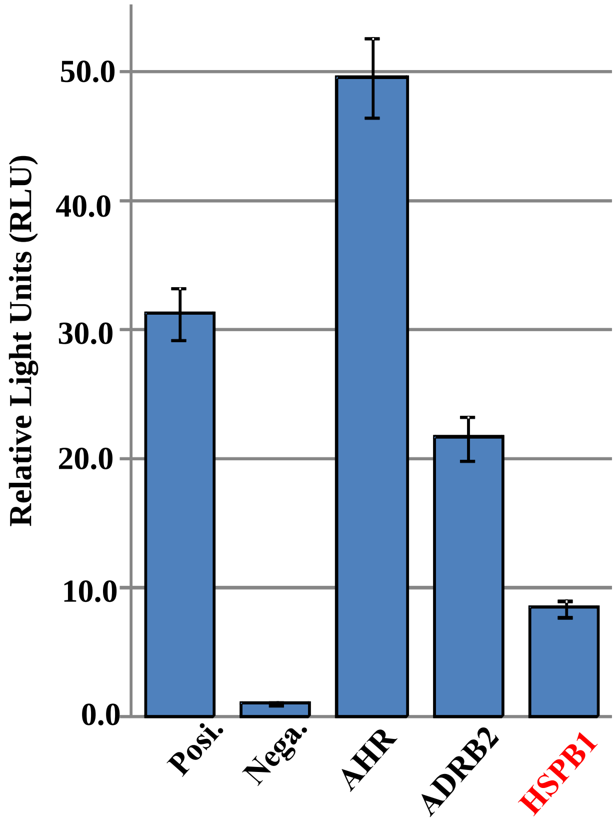
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

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

AHR: pGL4-ph AHR (RDB# 7724)
ADRB2: pGL4-ph ADRB2 (RDB# 7532)
HSPB1: pGL4-ph HSPB1 (RDB# 7530)

2010, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.10.29

1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5756

2nd Nucleotide Sequence
  File Name        : RDB7530F.fasta
  Sequence Size    : 810

  Unit Size to Compare = 1
  Pick up Location     = 1



[97.044% / 812 bp]     INT/OPT.Score : <    394/  2925 >

     1'               GGCCTAA CTGGCCGGTA CCTGAGCTCG CTAGCCTCGA GGATGTTGCC
                      ******* ********** ********** ********** **********
     1″ CCGAACTTTC TCTGGCCTAA CTGGCCGGTA CCTGAGCTCG CTAGCCTCGA GGATGTTGCC

    48' CAGGCTTGTT CCAGCCTTCT GGCTTCAAGT AATCCTCCCA CNATCAGCCT CCCAAAGTGC
        ********** ********** ********** ********** * ******** **********
    61″ CAGGCTTGTT CCAGCCTTCT GGCTTCAAGT AATCCTCCCA C-ATCAGCCT CCCAAAGTGC

   108' TAAGATTACA GATGTCAGCC ACTGCACCCA GCNCAGTAAT ATAATTTTAT GGGACCACCT
        ********** ********** ********** ** ******* ********** **********
   120″ TAAGATTACA GATGTCAGCC ACTGCACCCA GC-CAGTAAT ATAATTTTAT GGGACCACCT

   168' TCATATTTGC TGTCCCTTGC TGANCTTACA CATCTTTATG CAATGCATGA CTGTTACCAT
        ********** ********** *** ****** ********** ********** **********
   179″ TCATATTTGC TGTCCCTTGC TGA-CTTACA CATCTTTATG CAATGCATGA CTGTTACCAT

   228' CATTATCATC TCTANTTTTC CAGATGGGGA AACTGAGGCA CAAAGAATCT AACTTGCACA
        ********** **** ***** ********** ********** ********** **********
   238″ CATTATCATC TCTA-TTTTC CAGATGGGGA AACTGAGGCA CAAAGAATCT AACTTGCACA
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288' AGTTCNATCT GCTTAGTGAT GGAACAAAGA TGTGAATTCA GGCAGTCTGG CTTCAANAGT
     ***** **** ********** **** ***** ********** ********** ****** ***
297" AGTTC-ATCT GCTTAGTGAT GGAAGAAAGA TGTGAATTCA GGCAGTCTGG CTTCAA-AGT

348' CCACACGCCT AACAACCACA CCAGATTACT AGATTGCTTT TTTCTTTNTT TCTTTTTTTT
     ********** ********** ********** ********** *******.**   ********
355" CCACACGCCT AACAACCACA CCAGATTACT AGATTGCTTT TTTCTTTTTT CTTTTTTTTT

408' TTTTTGAGAT GGAGTCTCAC TCTGTCACCC AGGCTGGANG TACAGTGGTG AGATCTCGGC
     ********** ********** ********** ******** * ********** **********
415" TTTTTGAGAT GGAGTCTCAC TCTGTCACCC AGGCTGGA-G TACAGTGGTG AGATCTCGGC

468' TCACTGCAAC CTCTGCCTTC TGGGTTCAAN GCAATTCTCC TGCCTCAGCC TCCCCAGCAG
     ********** ********** *********  ********** ********** **********
474" TCACTGCAAC CTCTGCCTTC TGGGTTCAA- GCAATTCTCC TGCCTCAGCC TCCCCAGCAG

528' CTGCGATTAC AGGCGCCCGC NCACCACACC CAGCTAATTT TTGTATTTTT AGTAGAGATG
     ********** **********  ********* ********** ********** **********
533" CTGCGATTAC AGGCGCCCGC -CACCACACC CAGCTAATTT TTGTATTTTT AGTAGAGATG

588' GGGTTTCACC ANTGTTGGCC AGGCTGGTCT CAAACTCCTG ACCTCTGGTG ATCCTCCCAC
     ********** * ******** ********** ********** ********** **********
592" GGGTTTCACC A-TGTTGGCC AGGCTGGTCT CAAACTCCTG ACCTCTGGTG ATCCTCCCAC

648' CTNCGGTCTC CCAAAGTGCT GGGATTACAG GCGTGAGCCA CCACGCCCAG CCCNAGACTG
     ** ******* ********** ********** ********** ********** *** ******
651" CT-CGGTCTC CCAAAGTGCT GGGATTACAG GCGTGAGCCA CCACGCCCAG CCC-AGACTG

708' CTTTATTTTT GTATTTGTAT TTATTCATTT ACTTATTTTG AGACNAGGGT TTTGCTCTGT
     ********** ********** ********** ********** **** ****  **********
709" CTTTATTTTT GTATTTGTAT TTATTCATTT ACTTATTTTG AGAC-AGGG- TTTGCTCTGT

768' AGCCCAGGCT GAAGTGCAGT GGTGCAATCC AGCTCNACCA CAGCCTCTAC TCACCGGGGT
     ********** **** *****  ******* * ****  ****  ****
767" AGCCCAGGCT GAAG-GCAGT -GTGCAAT-C AGCT--ACCA AAGCCCTTT
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1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5756

2nd Nucleotide Sequence
  File Name        : RDB7530R.fasta (Complementary)
  Sequence Size    : 790

  Unit Size to Compare = 1
  Pick up Location     = 1



[97.506% / 802 bp]     INT/OPT.Score : <    461/  2954 >

    781' GTGCAGTGGT GCAATCCAGC TCNACCACAG CCTCTACTCA CCGGGGTTCA AAGGATCCTC
                                                             **.*******
      1″                                                   TC AANGATCCTC

    841' CTGCTTCAGC CTCNTGGAGT AGCTGGGGCC ACAGGCATGC ACCACCATGC CCAGCTAATT
         **********  * .* **** ******* ** ********** ********** ******** *
     13″ CTGCTTCAGC TTTCT-GAGT AGCTGGGCCC ACAGGCATGC ACCACCATGC CCAGCTAAAT

    901' TTTANAATAT TTTTTGGTAG AAGTAGGGTC TCACTATGTT GCCCAGACTG GTCTCNAAAC
         **** ***** ********** ********** ********** ********** ***** ****
     72″ TTTA-AATAT TTTTTGGTAG AAGTAGGGTC TCACTATGTT GCCCAGACTG GTCTC-AAAC

    961' TCCTAGCCTC AAGGGACCCT TCTGCCTTGG CCTCCCAAAG TGCTGANGAT TACAGGCATG
         ********** ********** ********** ********** ****** *** **********
    130″ TCCTAGCCTC AAGGGACCCT TCTGCCTTGG CCTCCCAAAG TGCTGA-GAT TACAGGCATG

   1021' AGCCATGCAC CCAGCCCCTT TTTAAAATTT TTTTGAGNAG ACAAGACTTT GATCTGTTGC
         ********** ********** ********** ******* ** ********** **********
    189″ AGCCATGCAC CCAGCCCCTT TTTAAAATTT TTTTGAG-AG ACAAGACTTT GATCTGTTGC

   1081' CTAGGCTGGA GTGCAGTGGT GAGATCATNA GCTCACTGCA GCCTCAACTC CTGGGCTCAA
         ********** ********** ******** * ********** ********** **********
    248″ CTAGGCTGGA GTGCAGTGGT GAGATCAT-A GCTCACTGCA GCCTCAACTC CTGGGCTCAA
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1141' GCACCAGACT CCTTTTATCN ACATTCTATC TCACACGCGT GTGGTTCCAA TCCTGCCTCT
      ********** *********  ********** ********** ********** **********
 307″ GCACCAGACT CCTTTTATC- ACATTCTATC TCACACGCGT GTGGTTCCAA TCCTGCCTCT

1201' GCCACTTCTC NAGTTGTATG CCCCAACCCA ACCTGTCTGG CTCTGTCCTC CTTAACAGAA
      **********  ********* ********** ********** ********** **********
 366″ GCCACTTCTC -AGTTGTATG CCCCAACCCA ACCTGTCTGG CTCTGTCCTC CTTAACAGAA

1261' GNGACGGCCC TGGCCACGGG CCACAGCCAG CAACGCTTAA GCACCAGGGC CGNGCGAGTG
      * ******** ********** ********** ********** ********** ** *******
 425″ G-GACGGCCC TGGCCACGGG CCACAGCCAG CAACGCTTAA GCACCAGGGC CG-GCGAGTG

1321' CCCTGCCGTG GCACGGCTCC AGCGTCGCGC TCTCGAATTC ATTNTGCTTT CCTTAACGAG
      ********** ********** ********** ********** *** ****** **********
 483″ CCCTGCCGTG GCACGGCTCC AGCGTCGCGC TCTCGAATTC ATT-TGCTTT CCTTAACGAG

1381' AGAAGGTTCC AGATGAGGGC TGAACCCTCT TCGCNCCCGC CCACGGCCCC TGAACGCTGG
      ********** ********** ********** **** ***** ********** **********
 542″ AGAAGGTTCC AGATGAGGGC TGAACCCTCT TCGC-CCCGC CCACGGCCCC TGAACGCTGG

1441' GGGAGGAGTG CATGGGGAGG GGCGGNCCCT CAAACGGGTC ATTGCCATTA ATAGAGACCT
      ********** ********** ***** **** ********** ********** **********
 601″ GGGAGGAGTG CATGGGGAGG GGCGG-CCCT CAAACGGGTC ATTGCCATTA ATAGAGACCT

1501' CAAACACCGC CTGCTANAAA ATACCCGACT GGAGGAGCAT AAAAGCGCAG CCGAGATCAA
      ********** ****** *** ********** ********** ********** **********
 660″ CAAACACCGC CTGCTA-AAA ATACCCGACT GGAGGAGCAT AAAAGCGCAG CCGAGATCAA

1561' GATCTGGCCT CGGCGGCCAA GCTTGGCAAT CCGGTACTGT TGGTAAAGCC ACCATGGAAG
      ********** ********** ********** ********** ********** **********
 719″ GATCTGGCCT CGGCGGCCAA GCTTGGCAAT CCGGTACTGT TGGTAAAGCC ACCATGGAAG

1621' ATGCCAAAAA CATTAAGAAG GGCCCAGCGC CATTCTACCC ACTCGAAGAC GGGACCGCCG
      ********** **
 779″ ATGCCAAAAA CA
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