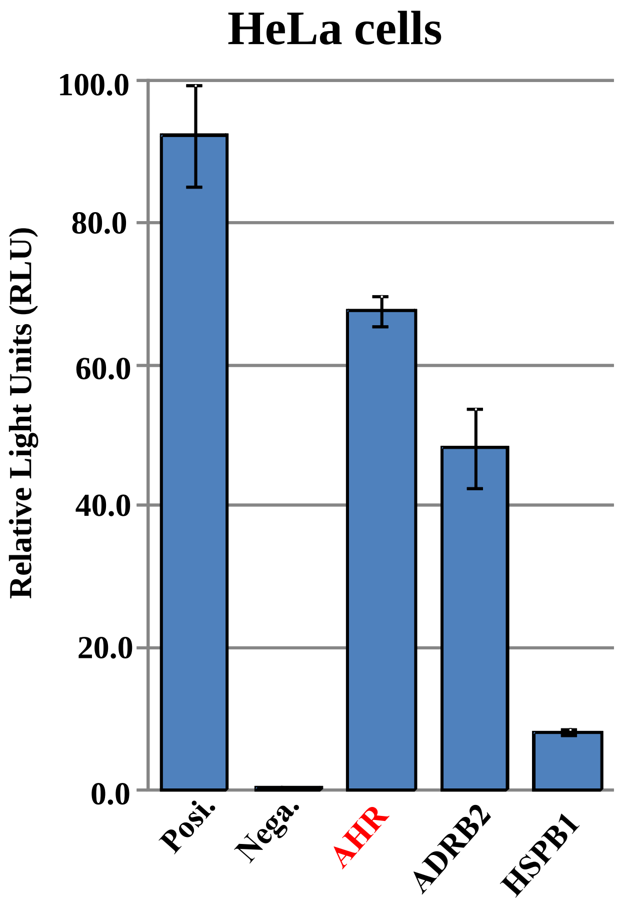
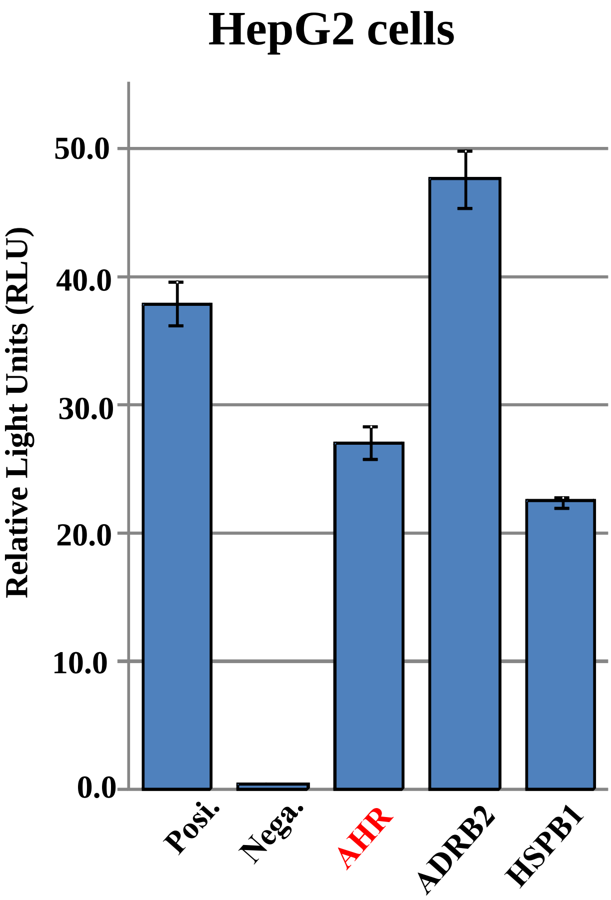
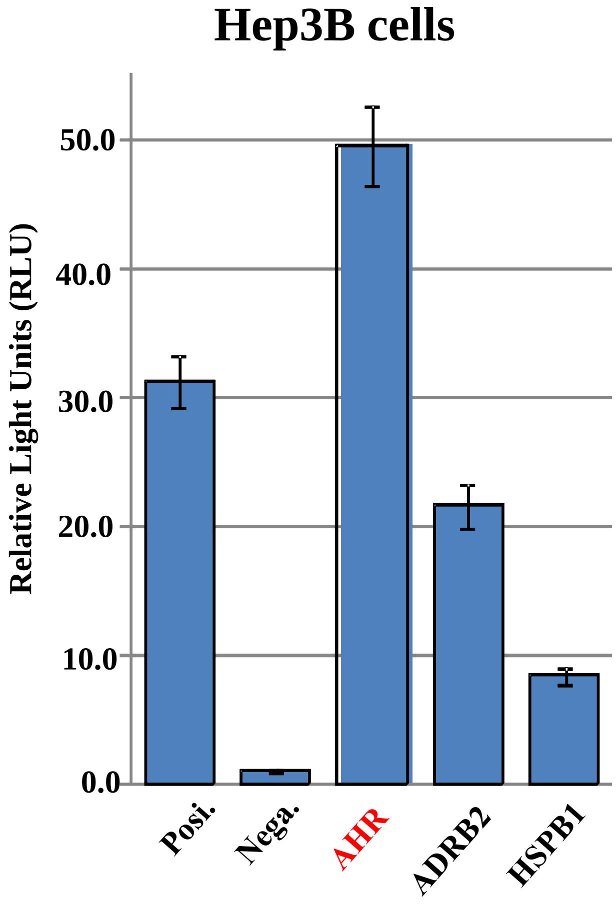
The Promoter Activities of Reporter Constructs



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 : 2009.11.19

1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5730

2nd Nucleotide Sequence
  File Name         : RDB7724F.fasta
  Sequence Size     : 607

  Unit Size to Compare = 1
  Pick up Location     = 1



[97.819% / 596 bp]     INT/OPT.Score : <    321/  2209 >

     1'                       GGCCTAACTG GCCGGTACCT GAGCTCGCTA GCCTCGAGGA
                              ********** ********** ********** **********
     1" AGGTGCCAGA ACATTTCTCT GGCCTAACTG GCCGGTACCT GAGCTCGCTA GCCTCGAGGA

    41' TGGGTGGATG TCCATCTACT TCCTTGTTGT CACTTCCCAG NATCACTTTC ACTTTATGCT
        ********** ********** ********** **********  ********* **********
    61" TGGGTGGATG TCCATCTACT TCCTTGTTGT CACTTCCCAG -ATCACTTTC ACTTTATGCT

   101' CTTCTAAAAT TAAAACAAAG ATCATCGACC ANCAAAACAC AATTGTTCTT TTGTAGCTCA
        ********** ********** ********** * ******** ********** **********
   120" CTTCTAAAAT TAAAACAAAG ATCATCGACC A-CAAAACAC AATTGTTCTT TTGTAGCTCA

   161' TGCTAGAATA CCCTCTTTGT TANCATCTCC TTCATTTTTC TGATCCAAAA TTTAGTAGCC
        ********** ********** ** ******* ********** ********** **********
   179" TGCTAGAATA CCCTCTTTGT TA-CATCTCC TTCATTTTTC TGATCCAAAA TTTAGTAGCC

   221' TACTATATCT CACNCCACTG TCCTTCTTTC CTCCAGCTAT GGTAGAGAAC TGCTCCTCCA
        ********** *** ****** ********** ********** ********** **********
   238" TACTATATCT CAC-CCACTG TCCTTCTTTC CTCCAGCTAT GGTAGAGAAC TGCTCCTCCA
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281’ ACTTNTATGT ACATTTGAAT CACCTGGGAG TTCCTGTGAA CTTCGGGTTC TGATTNTAAT
     **** ***** ********** ********** ********** ********** ***** ****
297″ ACTT-TATGT ACATTTGAAT CACCTGGGAG TTCCTGTGAA CTTCGGGTTC TGATT-TAAT

341’ AAGGACACCC AAAGAGTCTG CATTTCCTGT AACTCTCAAA AGAAGCNTGT GGAGTACTCT
     ********** ********** ********** ********** ****** *** **********
355″ AAGGACACCC AAAGAGTCTG CATTTCCTGT AACTCTCAAA AGAAGC-TGT GGAGTACTCT

401’ GAATAGCAAA GCACTGTAAG TGCTGTTTCT GTTAGTANTC TAATCTATTA GTCCTAATCT
     ********** ********** ********** ******* ** ********** **********
414″ GAATAGCAAA GCACTGTAAG TGCTGTTTCT GTTAGTA-TC TAATCTATTA GTCCTAATCT

461’ CCCATTTATG CTTTGGCACT CATTCCCTNC CTGCTTTCGG TATCTTAATA TCTATCATTC
     ********** ********** ******** * ********** ********** **********
473″ CCCATTTATG CTTTGGCACT CATTCCCT-C CTGCTTTCGG TATCTTAATA TCTATCATTC

521’ CTTCACTCTT CCCTCAGGTN TCCCTACATA GTTTATCTCT ACCCCCTCTA AGCCGCTCAG
     ********** *********  ********** ********** ********** **********
532″ CTTCACTCTT CCCTCAGGT- TCCCTACATA GTTTATCTCT ACCCCCTCTA AGCCGCTCAG

581’ TATCGCCCAT NTAAAGAACT AAACCAAAAC TAGAAAACCC TCATTTAACC CTTCACTCCC
     ********** . ** *
591″ TATCGCCCAT TAAAGGG




1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5730

2nd Nucleotide Sequence
  File Name        : RDB7724R.fasta (Complementary)
  Sequence Size    : 733

  Unit Size to Compare = 1
  Pick up Location     = 1
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[95.984% / 747 bp]     INT/OPT.Score : <    616/  2640 >

  841' TTCTCNAACT AATTTGAATT TCTCAACAGT ATTCAATATT GTTAATTACT CCCAATNATT
                                            ***.* *** *.****  .**** ***
    1″                                   TCATANT GTT-ANTACT -NCAAT-ATT

  901' TTTCCACATG GTCCTCCATG ACACAATACA TAATAGTCCC CTTATTANTC TATATTCCTG
       *** ****** ***.****** ********** ********** ******* ** **********
   25″ TTT-CACATG GTCNTCCATG ACACAATACA TAATAGTCCC CTTATTA-TC TATATTCCTG

  961' TCTATTGTAA AGACTTCCCC CGCACACCAA AAAAGGTCNA AGGAAACTCC TAGCCTTCAA
       ********** ********** ********** ******** * ********** **********
   83″ TCTATTGTAA AGACTTCCCC CGCACACCAA AAAAGGTC-A AGGAAACTCC TAGCCTTCAA

 1021' GTCTCAACTC AAATCTGGCC TTCTGAAGCN CTTCCCAACT AGGAAAATAT ACAGTCCCAT
       ********** ********** *********  ********** ********** **********
  142″ GTCTCAACTC AAATCTGGCC TTCTGAAGC- CTTCCCAACT AGGAAAATAT ACAGTCCCAT

 1081' TGGTTGTCTA CCAGTTGTCT NACCAGTTAA TTGTAATTCT TAGCCACAAG TTAGCTGACC
       ********** **********  ********* ********** ********** **********
  201″ TGGTTGTCTA CCAGTTGTCT -ACCAGTTAA TTGTAATTCT TAGCCACAAG TTAGCTGACC

 1141' CACCGTCTCT CNAAACAGGT GAAGTTAAGC TCAATATTTG GCATATCTTG ATATACTTTG
       ********** * ******** ********** ********** ********** **********
  260″ CACCGTCTCT C-AAACAGGT GAAGTTAAGC TCAATATTTG GCATATCTTG ATATACTTTG

 1201' TANCAGTCTA GCTACAATAA GTTTGCCTAT GCACGAAGAT GGCTACCGGC GGGNGGGGGG
       ** ******* ********** ********** ********** ********** ***  *****
  319″ TA-CAGTCTA GCTACAATAA GTTTGCCTAT GCACGAAGAT GGCTACCGGC GGG--GGGGG

 1261' CGTCCTTACG TCCTACGTCA TCACGTGCCG GGATGAGGGT GGGGNCCCTC AAGGAAGACG
       ********** ********** ********** ********** **** ***** **********
  376″ CGTCCTTACG TCCTACGTCA TCACGTGCCG GGATGAGGGT GGGG-CCCTC AAGGAAGACG

 1321' GAATGGAATC CAGATGGGCG GGGGCAAGCA GGACGNGGGC GGGGCTACGC GGGATCT---
       ********** ********** ********** ***** **** ********** *******
  435″ GAATGGAATC CAGATGGGCG GGGGCAAGCA GGACG-GGGC GGGGCTACGC GGGATCTGGG
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1378’ -------GGG CGGGGCGGGG CCGGTGAGGG GTCGGGNGGT GCTCCTGCTA TTCAGCCGGT
             *** ********** ********** ****** *** ********** **********
 494″ CGGGGCGGGG CGGGGCGGGG CCGGTGAGGG GTCGGG-GGT GCTCCTGCTA TTCAGCCGGT

1431’ GCGCGCGGCG GCGGGAGGCA GTGGCTGNGG GAGTCCCGTC GACGCTCTGT TCCGAGAGCG
      ********** ********** ******* ** ********** ********** **********
 553″ GCGCGCGGCG GCGGGAGGCA GTGGCTG-GG GAGTCCCGTC GACGCTCTGT TCCGAGAGCG

1491’ TGCCCCGGAC CGCCAGCTCA GAACAGGGGC AGCCGTGTAA TCAAGATCTG GCCTCGGCGG
      ********** ********** ********** ********** ********** **********
 612″ TGCCCCGGAC CGCCAGCTCA GAACAGGGGC AGCCGTGTAA TCAAGATCTG GCCTCGGCGG

1551’ CCAAGCTTGG CAATCCGGTA CTGTTGGTAA AGCCACCATG GAAGATGCCA AAAACATTAA
      ********** ********** ********** ********** ********** **********
 672″ CCAAGCTTGG CAATCCGGTA CTGTTGGTAA AGCCACCATG GAAGATGCCA AAAACATTAA

1611’ GAAGGGCCCA GCGCCATTCT ACCCACTCGA AGACGGGACC GCCGGCGAGC AGCTGCACAA
      **
 732″ GA
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