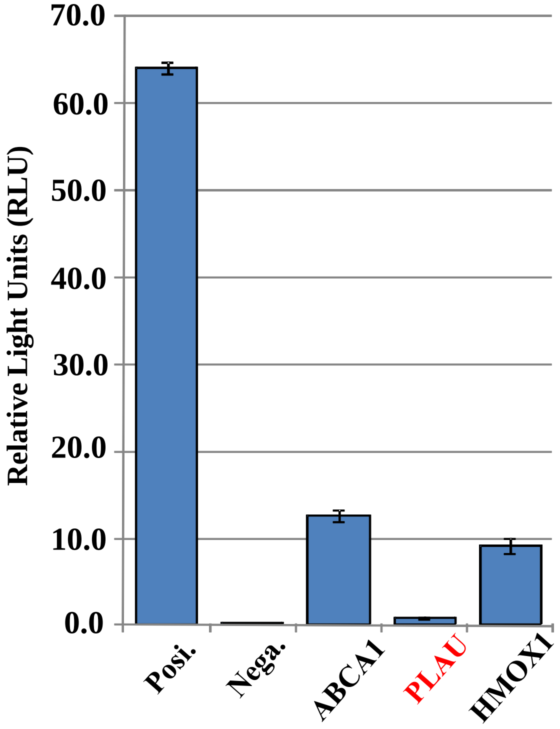
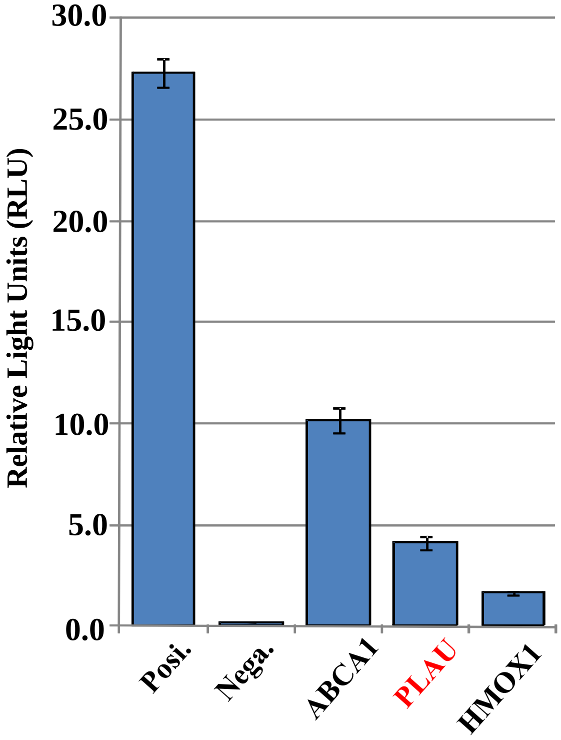
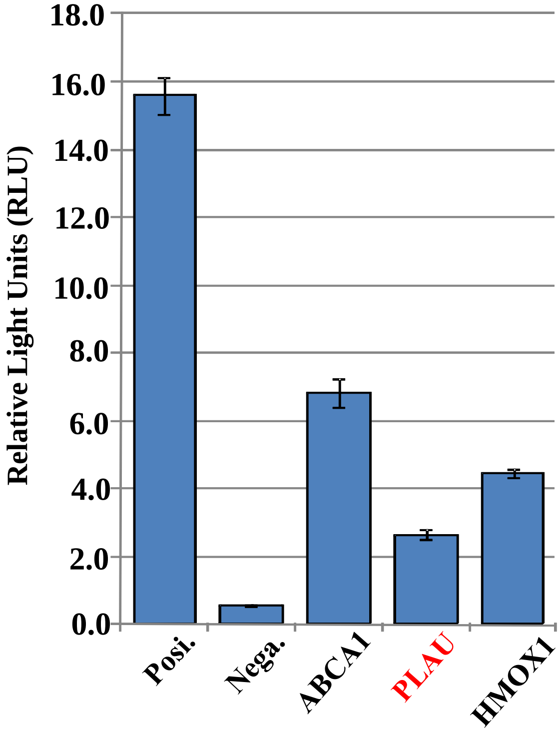
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

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

ABCA1: pGL4-phABCA1 (RDB# 7680)
PLAU: pGL4-phPLAU (RDB# 7487)
HMOX1: pGL4-phHMOX1 (RDB# 7485)

2010, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.08.17

1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5671

2nd Nucleotide Sequence
  File Name        : RDB7487F.fasta
  Sequence Size    : 740

  Unit Size to Compare = 1
  Pick up Location     = 1



[97.151% / 737 bp]     INT/OPT.Score : <    404/  2661 >

      1'                      G GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT
                              * ********** ********** ********** **********
      1" GGTGCCAGAA CATTTCTCTG GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT

     42' -GGTTCAAAA TGACCCCAAG CCCTGGTTCC TGACACTAGG GGAAAGNAGA TGGGGGTGAC
          ********* ********** ********** ********** ****** *** **********
     61" GGGTTCAAAA TGACCCCAAG CCCTGGTTCC TGACACTAGG GGAAAG-AGA TGGGGGTGAC

    101' AGAATCACAG AATCCCTGCT ATGTTCCTCC AAGTGTGNCC CAGAGATGCG TGTGTGTGTG
         ********** ********** ********** ******* ** *********   *********
    120" AGAATCACAG AATCCCTGCT ATGTTCCTCC AAGTGTG-CC CAGAGATGC- -GTGTGTGTG

    161' TGTGTGTATA CACAAATGTC TGCTTATCNC TCAGGCAGGA AGGGTGGATG CAGTCATTTA
         ********** ********** ******** * ********** ********** **********
    177" TGTGTGTATA CACAAATGTC TGCTTATC-C TCAGGCAGGA AGGGTGGATG CAGTCATTTA

    221' CACATGGTCT GTTTTTCTGN GAGGACAATT TTATTTGATA AACAATTGTT TCTATCTGAA
         ********** *********  ********** ********** ********** **********
    236" CACATGGTCT GTTTTTCTG- GAGGACAATT TTATTTGATA AACAATTGTT TCTATCTGAA
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281’ TAGAATAAAC NAAGGCTCTA TGATGAAGTA AAACACTAAA TACACATGCA TTAAAAAATG
     ********** ********* ********** ********** ********** **********
295″ TAGAATAAAC -AAGGCTCTA TGATGAAGTA AAACACTAAA TACACATGCA TTAAAAAATG

341’ CNATAATTAT CTTTTTGGAA TGGGCTATAC AGAGATGTGC TTTTTAAAAT GTNTAAGAGT
     * ******** ********** ********** ********** ********** ** *******
354″ C-ATAATTAT CTTTTTGGAA TGGGCTATAC AGAGATGTGC TTTTTAAAAT GT-TAAGAGT

401’ GTAAAAGGAC AAACAGTGAA AAATAAATCT TCCTCTTATT TTGNTCCTCC AGTCTCCCAA
     ********** ********** ********** ********** *** ****** **********
412″ GTAAAAGGAC AAACAGTGAA AAATAAATCT TCCTCTTATT TTG-TCCTCC AGTCTCCCAA

461’ TTCCTCTACT CAGAGGTGAG AACAGAACTT CCACNACCCT CCAGAACCTC CACAGTTAGA
     ********** ********** ********** **** ***** ********** **********
471″ TTCCTCTACT CAGAGGTGAG AACAGAACTT CCAC-ACCCT CCAGAACCTC CACAGTTAGA

521’ ACTGTCTACA TGTTTCCATT GTCTTNTACT TTTATTCTTG CCTGCACAAA TAAATGAATT
     ********** ********** ***** **** ********** ********** **********
530″ ACTGTCTACA TGTTTCCATT GTCTT-TACT TTTATTCTTG CCTGCACAAA TAAATGAATT

581’ GCTCATTATG GAAACTNTCC CAAAAGACCC GTTAACACTT CAATAGGAAG CACCAACAGT
     ********** ******. ** ********** ********** ********** **********
589″ GCTCATTATG GAAACTC-CC CAAAAGACCC GTTAACACTT CAATAGGAAG CACCAACAGT

641’ TTATGCCNCT AGGACTTTGT TCCCACAATC CTGTAACATC ATATCACGAC ACCTAACCNC
     ******* ** ********** ********** ********** ********** ********
648″ TTATGCC-CT AGGACTTTGT TCCCACAATC CTGTAACATC ATATCACGAC ACCTAACC--

701’ AATCCTTATC AAGCCCTGTC AAAAACGGAC TTTAAACCAA GCTGCAAATN TTTCAGTAAT
      ** ****** **********  ********* ******
705″ CATTCTTATC AAGCCCTGTC -AAAACGGAC TTTAAAA
```

1st Nucleotide Sequence

File Name : Reference Seq.GNU

Sequence Size : 5671

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2nd Nucleotide Sequence
  File Name        : RDB7487R.fasta (Complementary)
  Sequence Size    : 724

  Unit Size to Compare = 1
  Pick up Location     = 1



[96.770% / 743 bp]     INT/OPT.Score : <    568/  2650 >

   781' CTGATAGCAC CATCAAACAA NACCCCCTTA CTGCCGAAAG CAATAAGCCC GGCTTTGTTC
                                         ******** **** ** ** **********
     1"                                  GCCGAAAG CAAT-AGGCC GGCTTTGTTC

   841' CATCCACTGG TNTGTGTTGG TGATATCTGG GGACTGCCAC TGAACAGACG CACAGAGGGA
        *** ****** * *** .*** ******** * ***** .*** * .******* ***** .***
    28" CAT-CACTGG T-TGT-NTGG TGATATCT-G GGACT-NCAC T-NACAGACG CACAG-NGGA

   901' GCNCCCTACA GGCAGGGGTT TTTCTGTCTG TGCTTCTGGG AGAGTATGTC TCGNTACATT
        ** ******* ********** ********** ********** ********** *** ******
    81" GC-CCCTACA GGCAGGGGTT TTTCTGTCTG TGCTTCTGGG AGAGTATGTC TCG-TACATT

   961' TGTCGCGTTG ATGAAGACTT CACAGCTCCA TCAGCTGCGG GCAANGGGGG TCTGAGGCAG
        ********** ********** ********** ********** **** ***** **********
   139" TGTCGCGTTG ATGAAGACTT CACAGCTCCA TCAGCTGCGG GCAA-GGGGG TCTGAGGCAG

  1021' TCTTAGGCAA GTTGGGGCCC AGCGGGGAGA AGTTGNCAGA AGAACTGATT AGAGGACCCC
        ********** ********** ********** ***** **** ********** **********
   198" TCTTAGGCAA GTTGGGGCCC AGCGGGGAGA AGTTG-CAGA AGAACTGATT AGAGGACCCC

  1081' AGGAGGCTTC AGAGCTGGGC GAGGTANGAG AGTCTCCTGT GCGCCTTCTC TCCTCTCTGC
        ********** ********** ****** *** ********** ********** **********
   257" AGGAGGCTTC AGAGCTGGGC GAGGTA-GAG AGTCTCCTGT GCGCCTTCTC TCCTCTCTGC

  1141' AATTCGGGGA CTCCTTGNCA CTGGGGCAGG CCCCCGGCCA GGTGCATGGG AGGAAGCACG
        ********** ******* ** ********** ********** ********** **********
   316" AATTCGGGGA CTCCTTG-CA CTGGGGCAGG CCCCCGGCCA GGTGCATGGG AGGAAGCACG
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1201' GAGAATTTNA CAAGCCTCTC GATTCCTCAG TCCAGACGCT GTTGGGTCCC CTCCGCTGGN
      ******** * ********** ********** ********** ********** *********
 375″ GAGAATTT-A CAAGCCTCTC GATTCCTCAG TCCAGACGCT GTTGGGTCCC CTCCGCTGG-

1261' AGATCGCGCT TCCCCCAAAT CTTTGTGAGC GTTGCGGAAG CACGCGGGGT NCCGGGTCGC
      ********** ********** ********** ********** **********  *********
 433″ AGATCGCGCT TCCCCCAAAT CTTTGTGAGC GTTGCGGAAG CACGCGGGGT -CCGGGTCGC

1321' TGAGCGCTGC AAGACAGGGG AGGGAGCCGG GCGGGAGAGG GNAGGGGCGG CGCCGGGGCG
      ********** ********** ********** ********** * ******** **********
 492″ TGAGCGCTGC AAGACAGGGG AGGGAGCCGG GCGGGAGAGG G-AGGGGCGG CGCCGGGGCG

1381' GGCCCTGATA TAGAGCAGGC GCCGCGGGTC GCNAGCACAG TGCGGAGACC GCAGCCCCGG
      ********** ********** ********** ** ******* ********** **********
 551″ GGCCCTGATA TAGAGCAGGC GCCGCGGGTC GC-AGCACAG TGCGGAGACC GCAGCCCCGG

1441' AGCCCGGGCC AGGGTCCACC TGTCCCCGCA ATCAAGATCT GGCCTCGGCG GCCAAGCTTG
      ********** ********** ********** ********** ********** **********
 610″ AGCCCGGGCC AGGGTCCACC TGTCCCCGCA ATCAAGATCT GGCCTCGGCG GCCAAGCTTG

1501' GCAATCCGGT ACTGTTGGTA AAGCCACCAT GGAAGATGCC AAAAACATTA AGAAGGGCCC
      ********** ********** ********** ********** ********** *****
 670″ GCAATCCGGT ACTGTTGGTA AAGCCACCAT GGAAGATGCC AAAAACATTA AGAAG
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