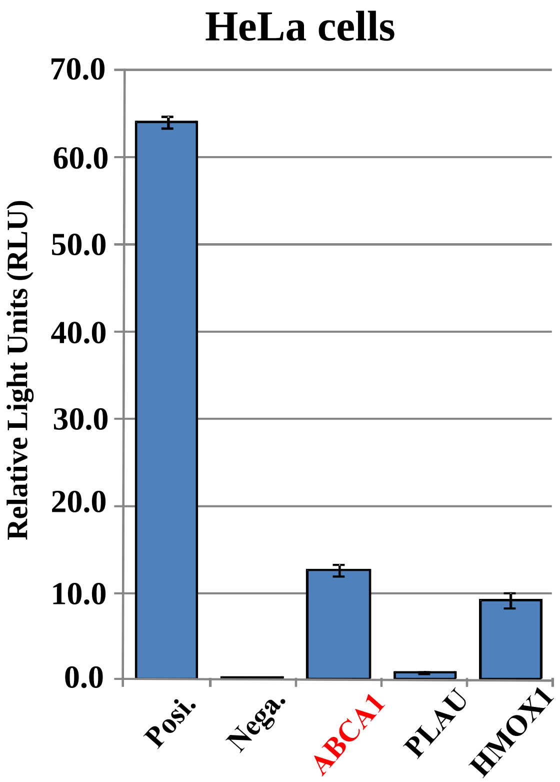
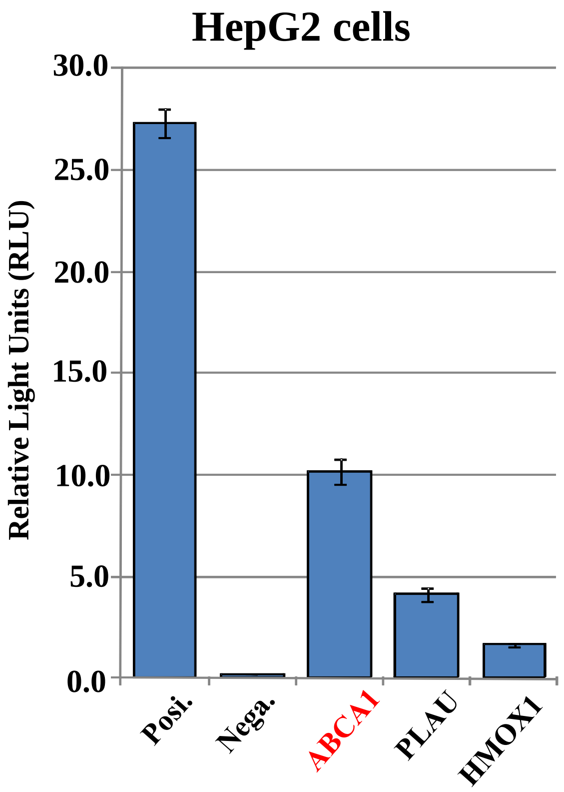
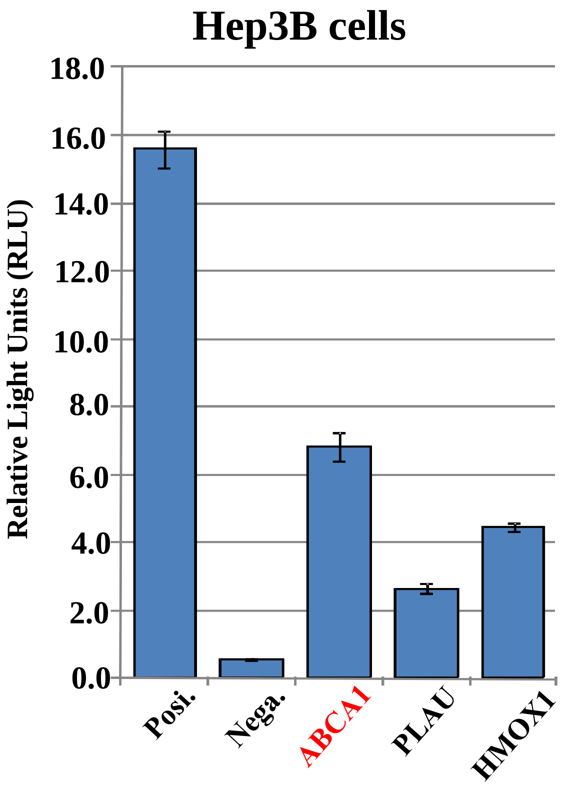
The Promoter Activities of Reporter Constructs


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 : 2010.01.29

1st Nucleotide Sequence
  File Name         : Reference Seq (ABCA1)-insert
  Sequence Size     : 1154

2nd Nucleotide Sequence
  File Name         : RDB7680F.fasta
  Sequence Size     : 671

Unit Size to Compare : 6

Percent Similarity   : 98.7
Percent Identity     : 98.3


     1’ CCCTTCAGGG -CAGATTCAT ATTTAGACTC TTCACAGTTT GACCTGAGTT TTGGCCAGAA
        **********  ********* ********** ********** ********** **********
    56″ CCCTTCAGGG ACAGATTCAT ATTTAGACTC TTCACAGTTT GACCTGAGTT TTGGCCAGAA

    60’ TAAGGTGACA TTTAGTTTGT TGGCTTGATG GATGACTTAA ATATTTAGAC ATATGGTGTG
        ********** ********** ********** ********** **********   ********
   116″ TAAGGTGACA TTTAGTTTGT TGGCTTGATG GATGACTTAA ATATTTAGAC --ATGGTGTG

   120’ TAGGCCTGCA TTCCTACTCT TGCCTTTTTT TTTGCCCCTC CAGTGTTTTG GGTAGTTTTG
        ********** ********** ********** ********** ********** **********
   174″ TAGGCCTGCA TTCCTACTCT TGCCTTTTTT TTTGCCCCTC CAGTGTTTTG GGTAGTTTTG

   180’ CTCCCCTACA GCCAAAGGCA AACAGATAAG TTGGAGGTCT GGAGTGGCTA CATAATTTTA
        ********** ********** ****** *** ********** ********** **********
   234″ CTCCCCTACA GCCAAAGGCA AACAGAGAAG TTGGAGGTCT GGAGTGGCTA CATAATTTTA

   240’ CACGACTGCA ATTCTCTGGC TGCACTTCAC AAATGTATAC AAACTAAATA CAAGTCCTGT
        ********** ********** ********** ********** ********** **********
   294″ CACGACTGCA ATTCTCTGGC TGCACTTCAC AAATGTATAC AAACTAAATA CAAGTCCTGT
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300’ GTTTTTATCA CAGGGAGGCT GATCAATATA ATGAAATTAA AAGGGGGCTG GTCCATATTG
     ********** ********** ********** ********** ********** **********
354” GTTTTTATCA CAGGGAGGCT GATCAATATA ATGAAATTAA AAGGGGGCTG GTCCATATTG

360’ TTCTGTGTTT TTG------- --TTTGTTTG TTTCTTTTTT TGTTTTTGTG GCCTCCTTCC
     ********** ***          ******** ********** ********** **********
414” TTCTGTGTTT TTGTTTGTTT GTTTTGTTTG TTTCTTTTTT TGTTTTTGTG GCCTCCTTCC

411’ TCTCAATTTA TGAAGAGAAG CAGTAAGATG TTCCTCTCGG GTCCTCTGAG GGACCTGGGG
     ********** ********** ********** ********** ********** **********
474” TCTCAATTTA TGAAGAGAAG CAGTAAGATG TTCCTCTCGG GTCCTCTGAG GGACCTGGGG

471’ AGCTCAGGCT GGGAATCTCC AAGGCAGTAG GTCGCCTATC AAAAATCAAA GTCCAGGTTT
     ********** ********** ********** ********** ********** **********
534” AGCTCAGGCT GGGAATCTCC AAGGCAGTAG GTCGCCTATC AAAAATCAAA GTCCAGGTTT

531’ GTGGGGGGAA AACAAAAGCA GCCCATTACC CAGAGGACTG TCCGCCTTCC CCTCACCCCA
     ********** ********** **** ***** **.* ***** ** ******* **** *****
594” GTGGGGGGAA AACAAAAGCA GCCCTTTACC CANAAGACTG TCTGCCTTCC CCTCCCCCCA

591’ GCCTAGGCCT TTGAAAGG
      ********* *  **.**
654” CCCTAGGCCT TGAAANGG
```

1st Nucleotide Sequence
  File Name   : Reference Seq (ABCA1)-insert
  Sequence Size   : 1154

2nd Nucleotide Sequence
  File Name   : RDB7680R.fasta (Complementary)
  Sequence Size   : 327

Unit Size to Compare : 6

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Percent Similarity   : 98.8
Percent Identity     : 98.4


  905’ ACCCCACCCA CCTCCCCCCA ACTCCCTAGA TGTGTCGTGG GCGGCTGAAC GTCGCCCGTT
       ** .****** ********** ********** ********** ********** **********
  327″ ACANCACCCA CCTCCCCCCA ACTCCCTAGA TGTGTCGTGG GCGGCTGAAC GTCGCCCGTT

  965’ TAAGGGGCGG GCCCCGGCTC CACGTGCTTT CTGCTGAGTG ACTGAACTAC ATAAACAGAG
       ********** ********** ********** ********** ********** **********
  267″ TAAGGGGCGG GCCCCGGCTC CACGTGCTTT CTGCTGAGTG ACTGAACTAC ATAAACAGAG

 1025’ GCCGGGAACG GGGCGGGGAG GAGGGAGAGC ACAGGCTTTG ACCGATAGTA ACCTCTGCGC
       ******** * ********** ********** ********** ********** **********
  207″ GCCGGGAAGG GGGCGGGGAG GAGGGAGAGC ACAGGCTTTG ACCGATAGTA ACCTCTGCGC

 1085’ TCGGTGCAGC CGAATCTATA AAAGGAACTA GTCCCGGCAA AAACCCCGTA ATTGCGAGCG
       ********** ********** ********** *** ****** ********** **********
  147″ TCGGTGCAGC CGAATCTATA AAAGGAACTA GTCTCGGCAA AAACCCCGTA ATTGCGAGCG

 1145’ AGAGTGAGTG
       **********
   87″ AGAGTGAGTG
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