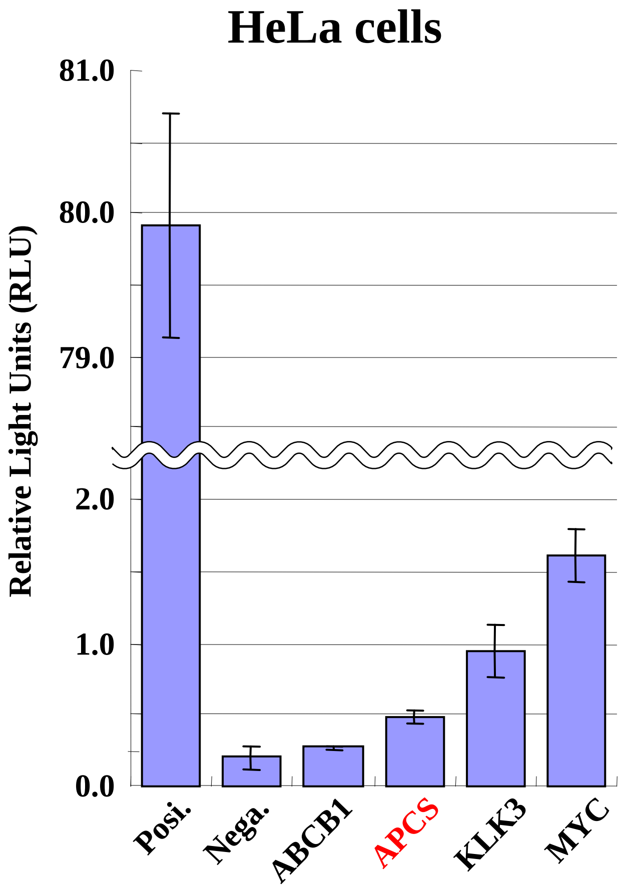
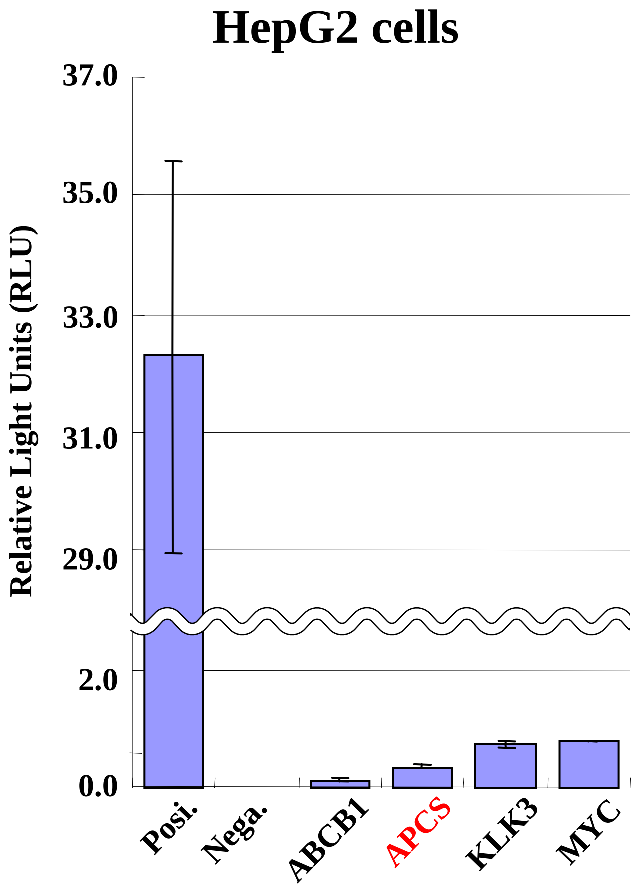
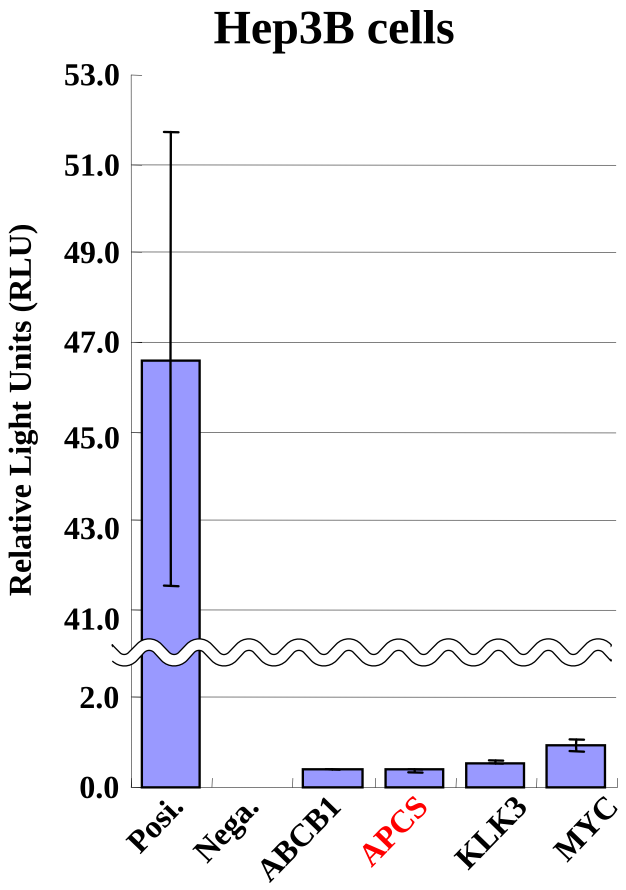
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

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

ABCB1: pGL4-phABCB1 (RDB#7315)
APCS: pGL4-phAPCS (RDB# 7317)
KLK3: pGL4-phKLK3 (RDB# 7324)
MYC: pGL4-phMYC (RDB#7325)

2009, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.03.01

1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5405

2nd Nucleotide Sequence
  File Name         : RDB7317F.fasta
  Sequence Size     : 622

  Unit Size to Compare = 1
  Pick up Location     = 1



[99.834% / 602 bp]     INT/OPT.Score : <    2402/  2402 >

     1’                      G GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT
                             * ********** ********** ********** **********
     1″ GGTGCCAGAA CATTTCTCTG GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT

    42’ CTTGGTGGCA GTGATTGTGT CATTGAAAAG GCTGATTAGG TCTGTGGTGA GCTAACAGAA
        ********** ********** ********** ********** ********** **********
    61″ CTTGGTGGCA GTGATTGTGT CATTGAAAAG GCTGATTAGG TCTGTGGTGA GCTAACAGAA

   102’ GAGAGAGTGA ACAAGAGGCT AAACAGTAGG ATGAGAAACA AGACACCATA TAATTCAGGG
        ********** ********** ********** ********** ********** **********
   121″ GAGAGAGTGA ACAAGAGGCT AAACAGTAGG ATGAGAAACA AGACACCATA TAATTCAGGG

   162’ ATGAGAGAGA AAGAAATAAT GTGGCTAGAA AGAAGAACTT CAGTTTGATA TCTCAGAGGC
        ********** ********** ********** ********** ********** **********
   181″ ATGAGAGAGA AAGAAATAAT GTGGCTAGAA AGAAGAACTT CAGTTTGATA TCTCAGAGGC

   222’ AGAGAAGGTT TGAGTGGTGG TTAATAAACT GTACAGAGAG AGAATGAAGG AGACATAGAA
        ********** ********** ********** ********** ********** **********
   241″ AGAGAAGGTT TGAGTGGTGG TTAATAAACT GTACAGAGAG AGAATGAAGG AGACATAGAA
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   282’ AGAATGAAGG TGGAGATCTC TGGGGCTGTG AGAGAGCCAG TGACCACTGA ATCCCCAGCA
        ********** ********** ********** ********** ********** **********
   301″ AGAATGAAGG TGGAGATCTC TGGGGCTGTG AGAGAGCCAG TGACCACTGA ATCCCCAGCA

   342’ CCTAGTGTAG TAACTGAGAG CTAGTGAATA AATGTATTAG TGGGGTCATC ACCAAAGATG
        ********** ********** ********** ********** ********** **********
   361″ CCTAGTGTAG TAACTGAGAG CTAGTGAATA AATGTATTAG TGGGGTCATC ACCAAAGATG

   402’ GATTAGATAT ACACTCAATG ACCAAGGACT CAAAGAAGAG GAGAGAAAAA CTTGGGGAGA
        ********** ********** ********** ********** ********** **********
   421″ GATTAGATAT ACACTCAATG ACCAAGGACT CAAAGAAGAG GAGAGAAAAA CTTGGGGAGA

   462’ TGCTGACATC TCTGCAGGTA GCATGAAGTA ACCAGAAAAC AAGTCGTAAT GAGAAATGGA
        ********** ********** ********** ********** ********** **********
   481″ TGCTGACATC TCTGCAGGTA GCATGAAGTA ACCAGAAAAC AAGTCGTAAT GAGAAATGGA

   522’ AAGATCTAGG ATAAGGAAGC ACCATGATAT GCAAACGAAA AAAAAGCACT GAGTAGAAGT
        ********** ********** ********** ********** ********** **********
   541″ AAGATCTAGG ATAAGGAAGC ACCATGATAT GCAAACGAAA AAAAAGCACT GAGTAGAAGT

   582’ AGCAGAAAAA TACTAAGCTT CATGGGGACA GAAAGTTTAT TCTCCAAGTC CCTCTTTCCC
        ********** ***** **** *
   601″ AGCAGAAAAA TACTAGGCTT CC




1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5405

2nd Nucleotide Sequence
  File Name        : RDB7317R.fasta (Complementary)
  Sequence Size    : 647

  Unit Size to Compare = 1
  Pick up Location     = 1
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[98.762% / 646 bp]     INT/OPT.Score : <   2184/  2506 >

 601' TCATGGGGAC AGAAAGTTTA TTCTCCAAGT CCCTCTTTCC CCTTAGCTTT GCC-TGGATG
                                                         *** *** ******
    1″                                                  TTTT GCCTTGGATG

 660' TATTAC-TTG ATGTTGAATT AGTCAAAGTT GAAGGCACTT TTTAGGGTCT TCAGCAGAAA
      ****** *** ********** ***** **** **  ****** ********** **********
  15″ TATTACTTTG ATGTTGAATT AGTCATAGTT GAGAGCACTT TTTAGGGTCT TCAGCAGAAA

 719' GCAGAATCCT AGAATATCCT ACA-AATACA AGACAACTTG AGAACTATAA AAGAAAGAAA
      ********** ********** *** *****  ********** **********  *********
  75″ GCAGAATCCT AGAATATCCT ACATAATACT AGACAACTTG AGAACTATAA TAGAAAGAAA

 778' AGGCCTTGTT CCCATAGCCC ACAAGAGGGC TGAGCTCAGC GATACACTCT GTGTGGCTCA
      ********** ********** ********** ********** ********** **********
 135″ AGGCCTTGTT CCCATAGCCC ACAAGAGGGC TGAGCTCAGC GATACACTCT GTGTGGCTCA

 838' GGAGCTTCTG GCAGAGCACA GAGCCATCAG AGAGGGGGCC CAGAGAGCAG AGAGAGGCTC
      ********** ********** ********** ********** ********** **********
 195″ GGAGCTTCTG GCAGAGCACA GAGCCATCAG AGAGGGGGCC CAGAGAGCAG AGAGAGGCTC

 898' TGCTGACATG GCCAGCCCAG CGCCTCATCC CATCCATAAC CCTGCTGCCC TGCAATGACT
      ********** ********** ********** ********** ********** **********
 255″ TGCTGACATG GCCAGCCCAG CGCCTCATCC CATCCATAAC CCTGCTGCCC TGCAATGACT

 958' CTCTTCCCAG CAATAAAATC TGGGTCACAG GAGTTGGAGC TCTAGCCATC ACTTGTCTCT
      ********** ********** ********** ********** ********** **********
 315″ CTCTTCCCAG CAATAAAATC TGGGTCACAG GAGTTGGAGC TCTAGCCATC ACTTGTCTCT

1018' AATAAATAAC TCCCATTGAT TTTCCAGCTC AGGGCTCACC ACTCCTTCAC CGTAAGCGCC
      ********** ********** ********** ********** ********** **********
 375″ AATAAATAAC TCCCATTGAT TTTCCAGCTC AGGGCTCACC ACTCCTTCAC CGTAAGCGCC

1078' AGGAGGCAGA CCTGGAAAAT CACTCACATA TTATTGGTGC TCTTCCTCCC CCATCCTCAC
      ********** ********** ********** ********** ********** **********
 435″ AGGAGGCAGA CCTGGAAAAT CACTCACATA TTATTGGTGC TCTTCCTCCC CCATCCTCAC
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1138' CCAAGGTGCA TATAAACCCT GAATAACCTG AAGTCTAAGG GCATGAATAT CAGACGCTAG
      ********** ********** ********** ********** ********** **********
 495" CCAAGGTGCA TATAAACCCT GAATAACCTG AAGTCTAAGG GCATGAATAT CAGACGCTAG

1198' GGGGACAATC AAGATCTGGC CTCGGCGGCC AAGCTTGGCA ATCCGGTACT GTTGGTAAAG
      ********** ********** ********** ********** ********** **********
 555" GGGGACAATC AAGATCTGGC CTCGGCGGCC AAGCTTGGCA ATCCGGTACT GTTGGTAAAG

1258' CCACCATGGA AGATGCCAAA AACATTAAGA AGGGCCCAGC GCCATTCTAC CCACTCGAAG
      ********** ********** ********** ***
 615" CCACCATGGA AGATGCCAAA AACATTAAGA AGG
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