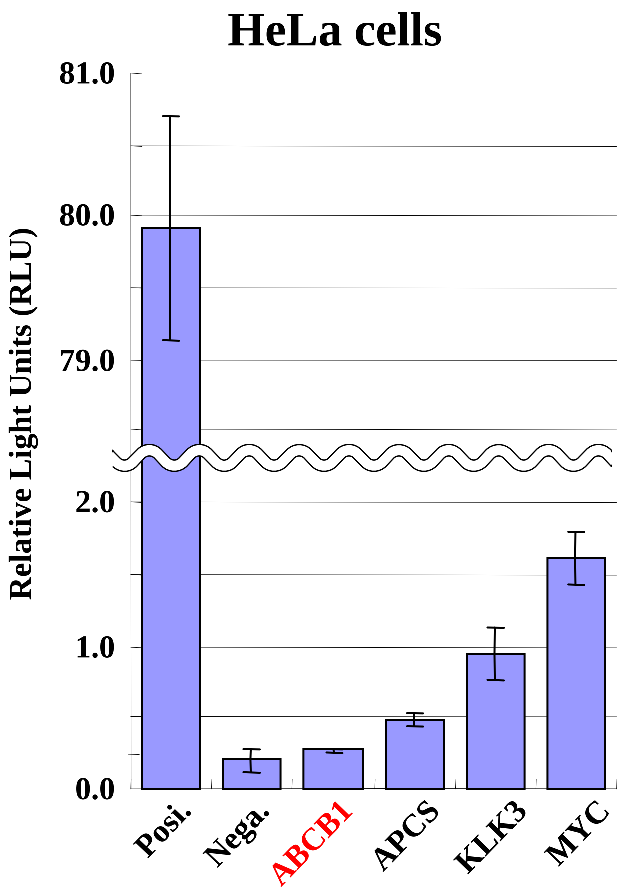
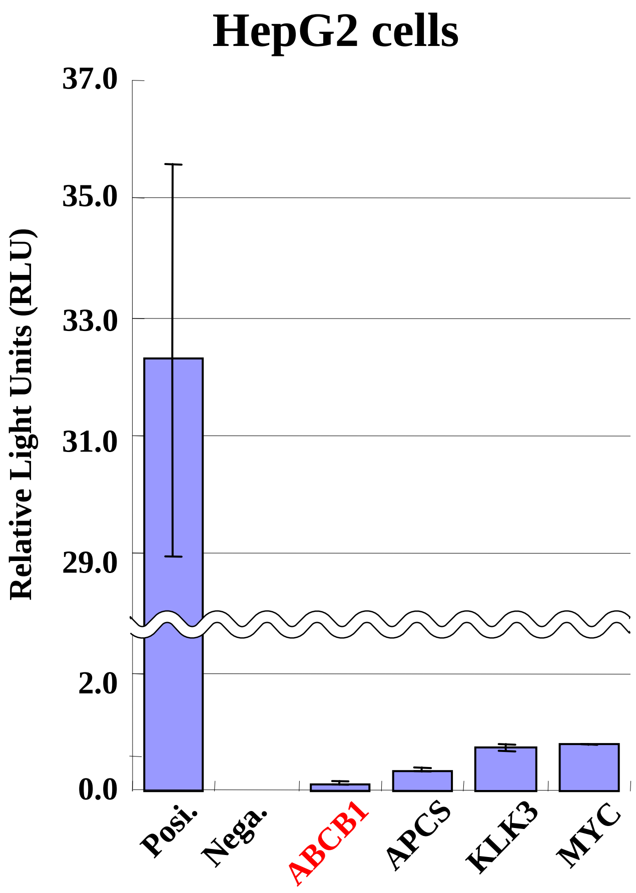
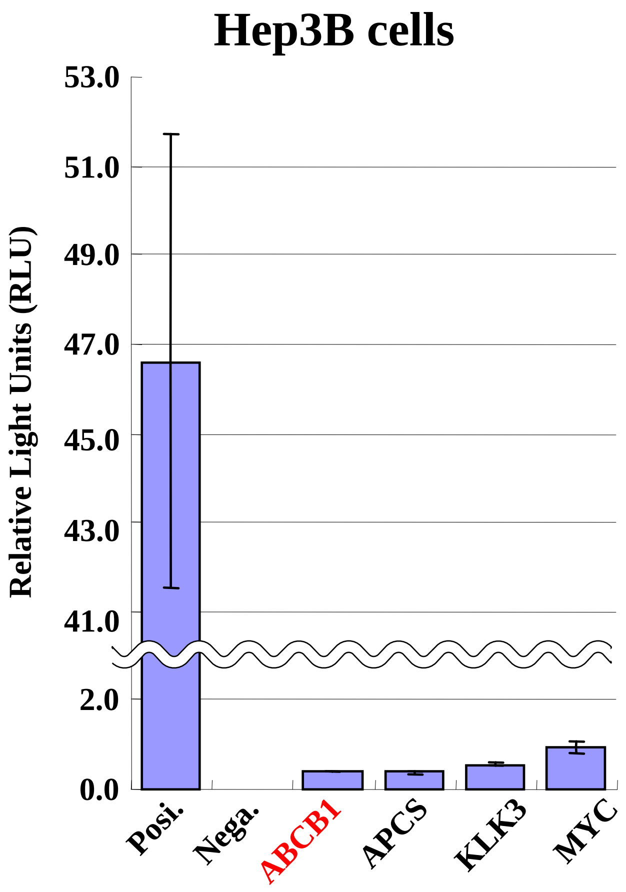
The Promoter Activities of Reporter Constructs


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     : 5461

2nd Nucleotide Sequence
  File Name         : RDB7315F.fasta
  Sequence Size     : 684

  Unit Size to Compare = 1
  Pick up Location     = 1



[98.622% / 653 bp]     INT/OPT.Score : <   2408/  2518 >

    1’                                  GGCCTAACTG GCCGGTACCT GAGCTCGCTA
                                        ********** ********** **********
    1″ NNNNATTTGC AGGTGCCAGA ACATTTCTCT GGCCTAACTG GCCGGTACCT GAGCTCGCTA

   31’ GCCTCGAGGA TCAAATGACC CTAAATCCCT CACTAACCTA CCCCTGCCCT CACTAAACTT
       ********** ********** ********** ********** ********** **********
   61″ GCCTCGAGGA TCAAATGACC CTAAATCCCT CACTAACCTA CCCCTGCCCT CACTAAACTT

   91’ AATAATAAAT GCTGGTATAT CCAGTGCATT GTTGGCACCG TGGGACCAGA AGGTAGTGAC
       ********** ********** ********** ********** ********** **********
  121″ AATAATAAAT GCTGGTATAT CCAGTGCATT GTTGGCACCG TGGGACCAGA AGGTAGTGAC

  151’ CCCCCTGGAC CCAGCTTTCA CTATCTTGTG TGTGTCTATT ATTTCTCAAC CTGCCGATCC
       ********** ********** ********** ********** ********** **********
  181″ CCCCCTGGAC CCAGCTTTCA CTATCTTGTG TGTGTCTATT ATTTCTCAAC CTGCCGATCC

  211’ GCCTAAGAAC AAAGAGAGAG CCCCGTTGCA TTGCAGGCTG CTGGCCAGAT CCCACAATAC
       ********** ********** ********** ********** ********** **********
  241″ GCCTAAGAAC AAAGAGAGAG CCCCGTTGCA TTGCAGGCTG CTGGCCAGAT CCCACAATAC
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271’ ATACACAGAT TCCAAAATGC ATTCTTAACT CTTAAAAGAT TTTGGTTACT TATCACTATT
     ********** ********** ********** ********** ********** **********
301″ ATACACAGAT TCCAAAATGC ATTCTTAACT CTTAAAAGAT TTTGGTTACT TATCACTATT

331’ CTGTCTACTT TTCTGTAATT GAGAAAAGTA TTTGTCAACT CATTTTTTCT CTCTGTGACA
     ********** ********** ********** ********** ********** **********
361″ CTGTCTACTT TTCTGTAATT GAGAAAAGTA TTTGTCAACT CATTTTTTCT CTCTGTGACA

391’ GCTCAGTCAT TTACAAAGTT TTATTTTATA CTTTACTCCT TCCTTCAATT TGTGCTAAAA
     ********** ********** ********** ********** ********** **********
421″ GCTCAGTCAT TTACAAAGTT TTATTTTATA CTTTACTCCT TCCTTCAATT TGTGCTAAAA

451’ CATTGTGAAA ATTAACATTT CTTTGGAACA CAACTTTTTC ATTATAAATT AAATACTGAT
     *** ****** ********** ********** ********** ********** **********
481″ CATAGTGAAA ATTAACATTT CTTTGGAACA CAACTTTTTC ATTATAAATT AAATACTGAT

511’ ATAATTGCAA AGTAAACAAA TGAATTTCCA TAAAGCTAAT TTATCTTTAT ATTTTCCATA
     ********** ********** ********** ********** ********** **********
541″ ATAATTGCAA AGTAAACAAA TGAATTTCCA TAAAGCTAAT TTATCTTTAT ATTTTCCATA

571’ CTTATTACTT CAAATTCTTG TTACATTTTC AA-TTTTGTT TGAAATATCA TAT-GGTATT
     *********  ***** ** * ********** ** ******* ********** *** ******
601″ CTTATTACTC CAAATACTAG TTACATTTTC AATTTTTGTT TGAAATATCA TATGGGTATT

629’ TT-AAATTGA AATTT-ACTA ATTATTTTTT AGCCAGTGGA TAAAGAGAAA TTAAAAATTT
     ** **** ** ***** **** ***
661″ TTAAAATGGA AATTTAACTA ATTT
```

1st Nucleotide Sequence
  File Name : Reference Seq.gnu
  Sequence Size : 5461

2nd Nucleotide Sequence
  File Name : RDB7315R.fasta (Complementary)
  Sequence Size : 713

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  Unit Size to Compare = 1
  Pick up Location     = 1



[91.933% / 719 bp]     INT/OPT.Score : <   1850/  2401 >

    601' AATTTTGTTT GAAATATCAT ATGGTATTTT AAATTGAAAT TTACTAATTA TTTTTTAGCC
                                                 **  ***   *  *    ****
      1″                                         AAA TTAAGGAGAA AAATTTAAAA

    661' AGTGGATAAA GAGAAATTAA AAATTTGAAC AAATTAATTC AATTTTTACT TCACTTCTCA
         *     *  *    *** *  ******   * *****  **  *  *** **   *  **   *
     24″ AAAATTTGGA ACCAAAATTT AAATTT---C AAATT-TTTT ACCTTTCAC- -CTTTTTCAA

    721' TTTGAAGG-- -TCTTCCCAG -TAACCTA-C CAAAAGAAGT CTCTCTCTTT TTTTTTTTTT
         ********    * * *****  ** **** * ********** ******* ** **********
     78″ TTTGAAGGTT CTTTCCCCAG TTACCCTACC CAAAAGAAGT CTCTCTCCTT TTTTTTTTTT

    776' TTTTTAGCTT AGATTCTAAT CTTCATTCTG CCTATTCTGG -CTAAACTTC TCAA-CTCTG
         ********** ********** *****.**** **********  ********* **** *****
    138″ TTTTTAGCTT AGATTCTAAT CTTCANTCTG CCTATTCTGG CCTAAACTTC TCAACCTCTG

    834' GCTA-TTTTT CAATTATA-C CCCAATCCCT AAGCCATGTA ACTCTTCGAG GTTTTTGTTT
         **** ***** ******** * ********** ********** ********** **********
    198″ GCTATTTTTT CAATTATACC CCCAATCCCT AAGCCATGTA ACTCTTCGAG GTTTTTGTTT

    892' GTTTTTTCAA CTGCTCATTA AGACGTCCTA CACCTTAGCA AAAAGATCAC ACATATTTCT
         ********** ********** ********** ********** ********** **********
    258″ GTTTTTTCAA CTGCTCATTA AGACGTCCTA CACCTTAGCA AAAAGATCAC ACATATTTCT

    952' TCAATGCTTT GGAGCCATAG TCATGTACTC AAAATTTATT TTATCTCTAC TCCCACCCTT
         ********** ********** ********** ********** ****** *** **********
    318″ TCAATGCTTT GGAGCCATAG TCATGTACTC AAAATTTATT TTATCTATAC TCCCACCCTT

   1012' CCTCCACCCA AACTTATCCT TGGGTTTTCA CTGATTAGTG CTTTCAAGCC TGCCTGCCTT
         ********** ********** ********** ********** ********** **********
    378″ CCTCCACCCA AACTTATCCT TGGGTTTTCA CTGATTAGTG CTTTCAAGCC TGCCTGCCTT
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1072' AGTTCATGTA GCTCCTCCTC TGGTACTGGG ATAAACACTT GTATTACCAT TTTAAAGGCT
      ********** ********** ********** ********** ********** **********
 438″ AGTTCATGTA GCTCCTCCTC TGGTACTGGG ATAAACACTT GTATTACCAT TTTAAAGGCT

1132' ATCATTACTC TTTACCTGTG AAGAGTAGAA CATGAAGAAA TCTACTTTAT TCAGATATTC
      ********** ********** ********** ********** ********** **********
 498″ ATCATTACTC TTTACCTGTG AAGAGTAGAA CATGAAGAAA TCTACTTTAT TCAGATATTC

1192' TCCAGATTCC TAAAGATTAG AGATCATTTC TCATTCTCCT AGGAGTACTC ACTTCAGGAA
      ********** ********** ********** ********** ********** **********
 558″ TCCAGATTCC TAAAGATTAG AGATCATTTC TCATTCTCCT AGGAGTACTC ACTTCAGGAA

1252' GCAACCAGAA TCAAGATCTG GCCTCGGCGG CCAAGCTTGG CAATCCGGTA CTGTTGGTAA
      ********** ********** ********** ********** ********** **********
 618″ GCAACCAGAA TCAAGATCTG GCCTCGGCGG CCAAGCTTGG CAATCCGGTA CTGTTGGTAA

1312' AGC-CACCAT GGAAGATGCC AAAAACATTA A-GAAGGGCC CAGCGCCATT CTACCCACTC
      *** ****** ********** ********** * ****
 678″ AGCACACCAT GGAAGATGCC AAAAACATTA ATGAAG
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