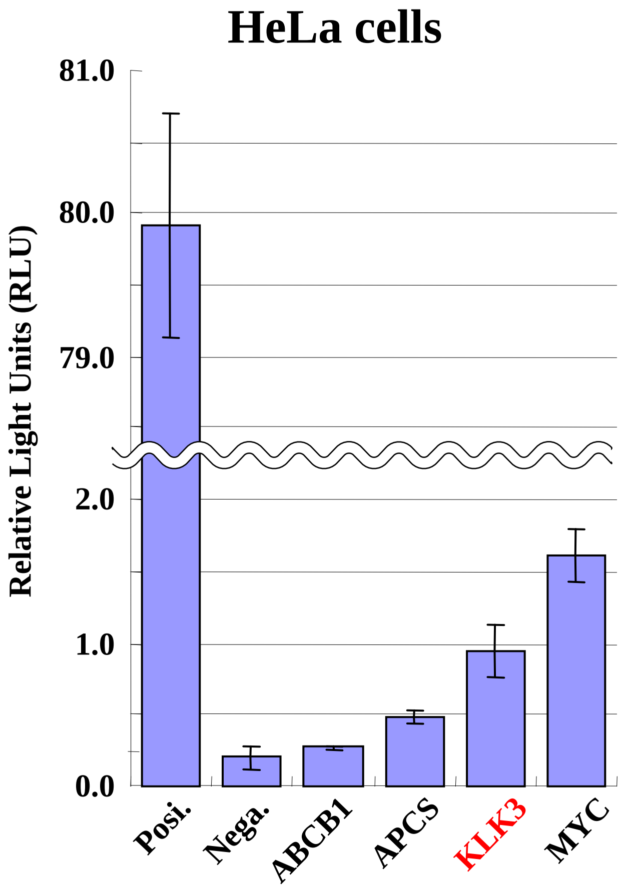
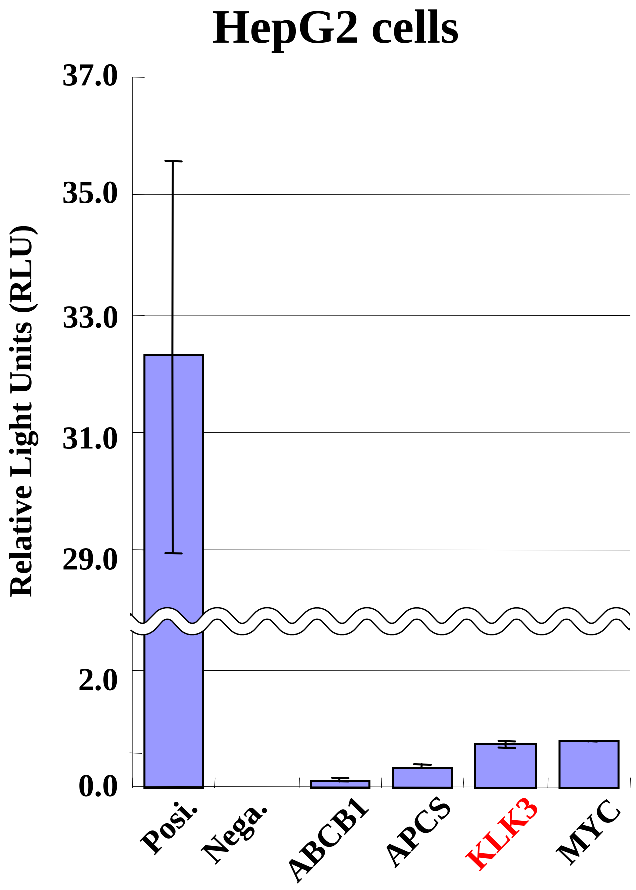
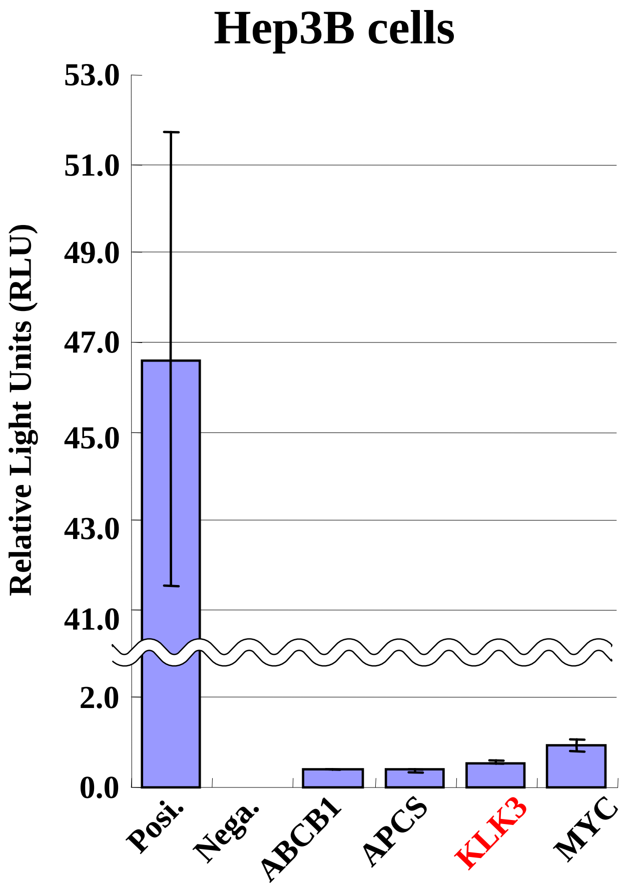
The Promoter Activities of Reporter Constructs


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 : 2010.03.02

1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5424

2nd Nucleotide Sequence
  File Name        : RDB7324F.fasta
  Sequence Size    : 672

  Unit Size to Compare = 1
  Pick up Location     = 1



[98.009% / 653 bp]     INT/OPT.Score : <    1138/   2467 >

     1'                    GG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATC
                           ** ********** ********** ********** **********
     1" GTGCCAGAAC ATTTCTCTGG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATC

    43' CTGACCAACA TGGTGAAACT CTGTCTCTAC TAAAAAAAAA AAAAATAGAA AAATTAGCCG
        ********** ********** ********** ********** ********** **********
    61" CTGACCAACA TGGTGAAACT CTGTCTCTAC TAAAAAAAAA AAAAATAGAA AAATTAGCCG

   103' GGCGTGGTGG CACACGGCAC CTGTAATCCC AGCTACTGAG GAGGCTGAGG CAGGAGAATC
        ********** ********** ********** ********** ********** **********
   121" GGCGTGGTGG CACACGGCAC CTGTAATCCC AGCTACTGAG GAGGCTGAGG CAGGAGAATC

   163' ACTTGAACCC AGAAGGCAGA GGTTGCAATG AGCCGAGATT GCGCCACTGC ACTCCAGCCT
        ********** ********** ********** ********** ********** **********
   181" ACTTGAACCC AGAAGGCAGA GGTTGCAATG AGCCGAGATT GCGCCACTGC ACTCCAGCCT

   223' GGGTGACAGA GTGAGACTCT GTCTCAAAAA AAAAAAA-TT TTTTTTTTTT TTTTGTAGAG
        ********** ********** ********** ******* ** ********** ******* **
   241" GGGTGACAGA GTGAGACTCT GTCTCAAAAA AAAAAAATTT TTTTTTTTTT TTTTGTAAAG
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282’ ATGGATCTTG CTTTGTTTCT CTGGTTGGCC TTGAACTCCT GGCTTCAAGT GATCCTCCTA
     ********** ********** ********** ********** ********** **********
301″ ATGGATCTTG CTTTGTTTCT CTGGTTGGCC TTGAACTCCT GGCTTCAAGT GATCCTCCTA

342’ CCTTGGCCTC GGAAAGTGTT GGGATTACAG GCGTGAGCCA CCATGACTGA CCTGTCGTTT
     ********** ********** ********** ********** ********** **********
361″ CCTTGGCCTC GGAAAGTGTT GGGATTACAG GCGTGAGCCA CCATGACTGA CCTGTCGTTT

402’ AATCTTGAGG TACATAAACC TGGCTCCTAA AGGCTAAATA TTTTGTTGGA GAAGGGGCAT
     ********** ********** ********** ********** ********** **********
421″ AATCTTGAGG TACATAAACC TGGCTCCTAA AGGCTAAATA TTTTGTTGGA GAAGGGGCAT

462’ TGGATTTTGC ATGAGGATGA TTCTGACCTG GGAGGGCAGG TCAGCAGGCA TCTCTGTTGC
     ********** ********** ********** ********** ****** *** **********
481″ TGGATTTTGC ATGAGGATGA TTCTGACCTG GGAGGGCAGG TCAGCAAGCA TCTCTGTTGC

522’ ACAGATAGAG TGCAC-AGGT CTGGAGAACA AGGAGT-GGG GGGTTA-TTG GAATTCCACA
     ********** ** ** **** ********** * *.** *** ****** *** **********
541″ ACAGATAGAG TGTACAAGGT CTGGAGAACA AAGNGTGGGG GGGTTATTTG GAATTCCACA

579’ -TTG-TTTGC TGCACGTTGG -ATTTTGAAA TGCTAGGGAA CTTTGGGAGA CTCATATTTC
      *** ***** **********  ********* ********** *** ****** **********
601″ TTTGTTTTGC TGCACGTTGG AATTTTGAAA TGCTAGGGAA CTTGGGGAGA CTCATATTTC

636’ TGGGCTAGAG GATCTGTGGA CCACAAGATC TTTTTATGAT GACAGTAGCA ATGTATCTGT
     ********** *
661″ TGGGCTAGAG GG
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1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5424

2nd Nucleotide Sequence
  File Name         : RDB7324R.fasta (Complementary)
  Sequence Size     : 742
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Unit Size to Compare = 1
Pick up Location     = 1



[98.248% / 742 bp]     INT/OPT.Score : <   1244/  2800 >

 541’ CTGGAGAACA AGGAGTGGGG GGTTATTGGA ATTCCAC-AT TG-TTTGCTG CA-CG-TTGG
                                        **** ** ** ******* ** ** ****
   1″                                   CCACAAT TGTTTTGCTG CACCGTTTGG

 597’ A-TTTTGAAA TGCTAGGG-A ACTTT-GGGA GACTCATATT TCTGGGCTAG AGGATCTGTG
      * ******** ******** * ***** **** ********** ********** **********
  28″ ATTTTTGAAA TGCTAGGGAA ACTTTGGGGA GACTCATATT TCTGGGCTAG AGGATCTGTG

 654’ GACCACAAGA TCTTTTTATG ATGACAGTAG CAATGTATCT GTGGAGCTGG ATTCT-GGGT
        **** *** ********** ********** ********** ********** ***** ****
  88″ ACCCACCAGA TCTTTTTATG ATGACAGTAG CAATGTATCT GTGGAGCTGG ATTCTGGGGT

 713’ TGGGAGTGCA AGGAAAAGAA TGTACTAAAT GCCAAGACAT CTATTTCAGG AGCATGAGGA
      ********** ********** ********** ********** ********** **********
 148″ TGGGAGTGCA AGGAAAAGAA TGTACTAAAT GCCAAGACAT CTATTTCAGG AGCATGAGGA

 773’ ATAAAAGTTC TAGTTTCTGG TCTCAGAGTG GTGCAGGGAT CAGGGAGTCT CACAATCTCC
      ********** ********** ********** ********** ********** **********
 208″ ATAAAAGTTC TAGTTTCTGG TCTCAGAGTG GTGCAGGGAT CAGGGAGTCT CACAATCTCC

 833’ TGAGTGCTGG TGTCTTAGGG CACACTGGGT CTTGGAGTGC AAAGGATCTA GGCACGTGAG
      ********** ********** ********** ********** ********** **********
 268″ TGAGTGCTGG TGTCTTAGGG CACACTGGGT CTTGGAGTGC AAAGGATCTA GGCACGTGAG

 893’ GCTTTGTATG AAGAATCGGG GATCGTACCC ACCCCCTGTT TCTGTTTCAT CCTGGGCGTG
      ********** ********** ********** ********** ********** ******* **
 328″ GCTTTGTATG AAGAATCGGG GATCGTACCC ACCCCCTGTT TCTGTTTCAT CCTGGGCATG

 953’ TCTCCTCTGC CTTTGTCCCC TAGATGAAGT CTCCATGAGC TAC-AGGGCC TGGTGCATCC
      ********** ********** ********** ********** *** ****** **********
 388″ TCTCCTCTGC CTTTGTCCCC TAGATGAAGT CTCCATGAGC TACAAGGGCC TGGTGCATCC
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1012’ AGGGTGATCT AGTAATTGCA GAACAGCAAG TGCTAGCTCT CCCTCCCCTT CCACAGCTCT
      ********** ********** ********** ********** ********** **********
 448″ AGGGTGATCT AGTAATTGCA GAACAGCAAG TGCTAGCTCT CCCTCCCCTT CCACAGCTCT

1072’ GGGTGTGGGA GGGGGTTGTC CAGCCTCCAG CAGCATGGGG AGGGCCTTGG TCAGCCTCTG
      ********** ********** ********** ********** ********** **********
 508″ GGGTGTGGGA GGGGGTTGTC CAGCCTCCAG CAGCATGGGG AGGGCCTTGG TCAGCCTCTG

1132’ GGTGCCAGCA GGGCAGGGGC GGAGTCCTGG GGAATGAAGG TTTTATAGGG CTCCTGGGGG
      ********** ********** ********** ********** ********** **********
 568″ GGTGCCAGCA GGGCAGGGGC GGAGTCCTGG GGAATGAAGG TTTTATAGGG CTCCTGGGGG

1192’ AGGCTCCCCA GCCCCAAGCT TACCACCTGC ACATCAAGAT CTGGCCTCGG CGGCCAAGCT
      ********** ********** ********** ********** ********** **********
 628″ AGGCTCCCCA GCCCCAAGCT TACCACCTGC ACATCAAGAT CTGGCCTCGG CGGCCAAGCT

1252’ TGGCAATCCG GTACTGTTGG TAAAGCCACC ATGGAAGATG CCAAAAACAT TAAGAAGGGC
      ********** ********** ********** ********** ********** *****
 688″ TGGCAATCCG GTACTGTTGG TAAAGCCACC ATGGAAGATG CCAAAAACAT TAAGA
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