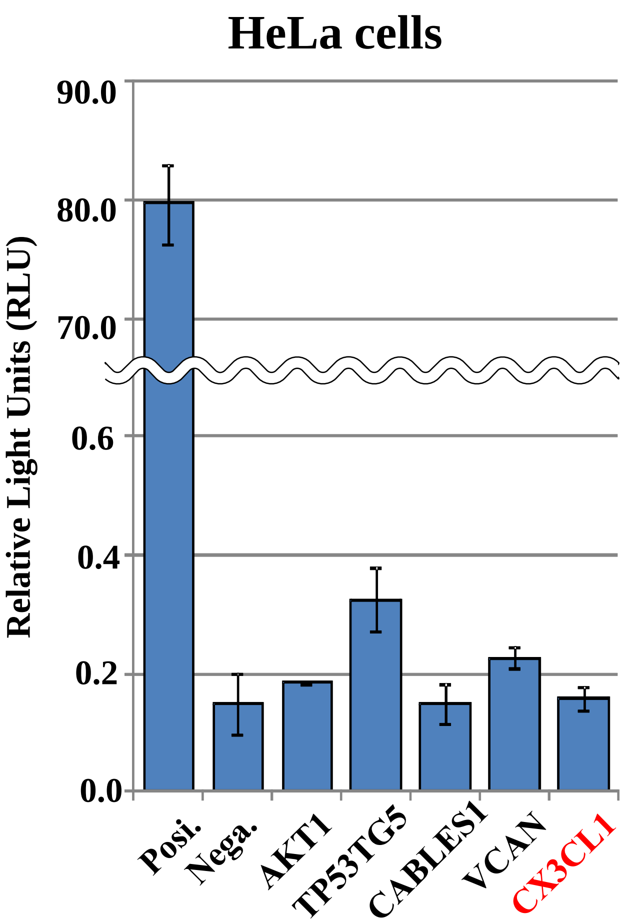
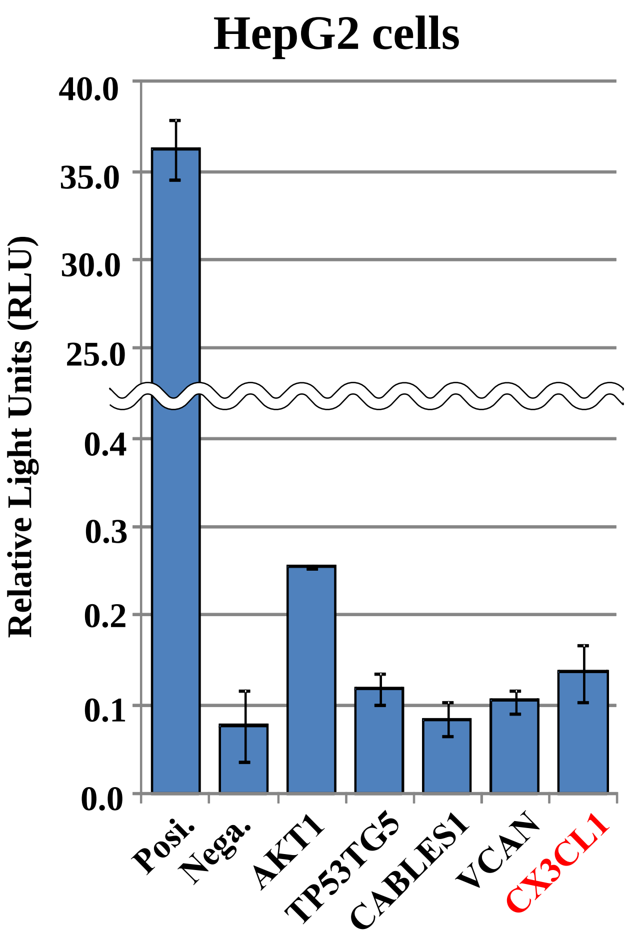
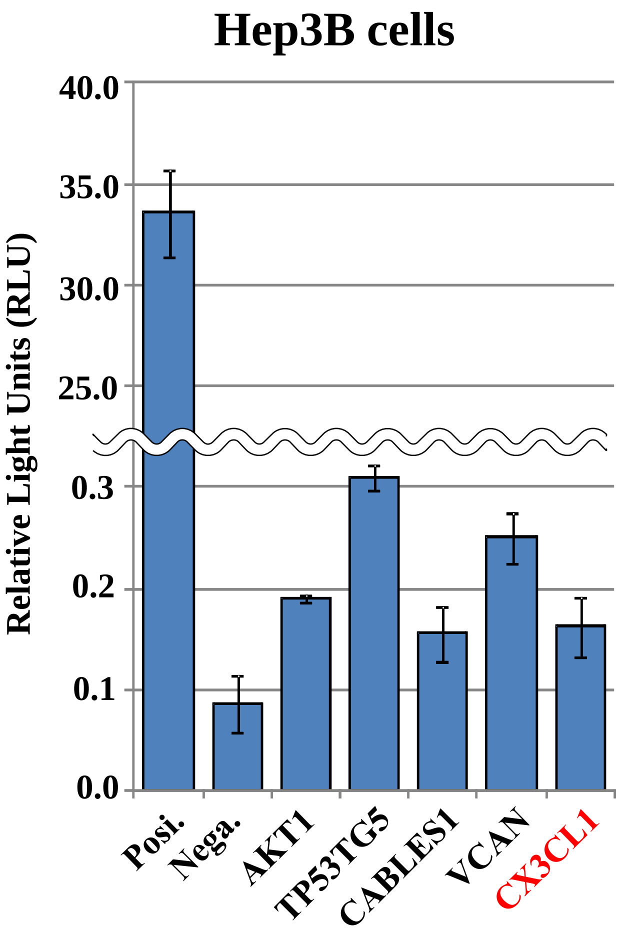
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

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

AKT1: pGL4-phAKT1 (RDB# 7331)
TP53TG5: pGL4-phTP53TG5 (RDB# 7336)
CABLES1: pGL4-phCABLES1 (RDB# 7337)
VCAN: pGL4-phVCAN (RDB#7339)
CX3CL1: pGL4-phCX3CL1 (RDB#7340)

2010, 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    : 5478

2nd Nucleotide Sequence
  File Name        : RDB7340F.fasta
  Sequence Size    : 587

  Unit Size to Compare = 1
  Pick up Location     = 1



[99.824% / 569 bp]     INT/OPT.Score : <   2270/  2270 >

     1'                    GG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATT
                           ** ********** ********** ********** **********
     1″ GTGCCAGAAC ATTTCTCTGG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATT

    43' GGAGACACCA GTACAGCTCA GTCCTATACC AAGGCAGAGC TGCTGACTCT TCTGGAGTCT
        ********** ********** ********** ********** ********** **********
    61″ GGAGACACCA GTACAGCTCA GTCCTATACC AAGGCAGAGC TGCTGACTCT TCTGGAGTCT

   103' CAGGGATTGT TGCCACTGCC TTTAGGGAAG GCTGCCATGA AGGCAGACTG TGTTCTAATG
        ********** ********** ********** ********** ********** **********
   121″ CAGGGATTGT TGCCACTGCC TTTAGGGAAG GCTGCCATGA AGGCAGACTG TGTTCTAATG

   163' TGCTCCCAAG GCTGGCAAGC CTCTGCACCC TTCGGTGAGA GCCTGTTGGA GGGCCGGTGC
        ********** ********** ********** ********** ********** **********
   181″ TGCTCCCAAG GCTGGCAAGC CTCTGCACCC TTCGGTGAGA GCCTGTTGGA GGGCCGGTGC

   223' TGGGAAGCCC TCTCCCCATT GCACTAGCCC AATGCTCTCT TTGGGCAGAT AGAGAACTCA
        ********** ********** ********** ********** ********** **********
   241″ TGGGAAGCCC TCTCCCCATT GCACTAGCCC AATGCTCTCT TTGGGCAGAT AGAGAACTCA
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283’ GGCCCCACGA GAGGCAAGCC TTATCCAAGC CACGGCTACA GAGTTGAGGA GCCAAGAGCC
     ********** ********** ********** ********** ********** **********
301″ GGCCCCACGA GAGGCAAGCC TTATCCAAGC CACGGCTACA GAGTTGAGGA GCCAAGAGCC

343’ ACAGAGTTAT CGGGGATGGG TTGGCAGCCA CCTTGTTCTT TGGGCTAACA GGGGCCAGAG
     ********** ********** ********** ********** ********** **********
361″ ACAGAGTTAT CGGGGATGGG TTGGCAGCCA CCTTGTTCTT TGGGCTAACA GGGGCCAGAG

403’ CAGAGGTGGG AGTGGGTGCA AAGCAGGGAG CGGGAGACCG GGAGGTGGAG GCAGGGAGGC
     ********** ********** ********** ********** ********** **********
421″ CAGAGGTGGG AGTGGGTGCA AAGCAGGGAG CGGGAGACCG GGAGGTGGAG GCAGGGAGGC

463’ CAGGGCTCTC TCCTGGGTCC TGAGCTGTCC ACATTCTGCT CATCATGGTG GTGGGAGGGG
     ********** ********** ********** ********** ********** **********
481″ CAGGGCTCTC TCCTGGGTCC TGAGCTGTCC ACATTCTGCT CATCATGGTG GTGGGAGGGG

523’ AGTTCTCCAC TCTGATGCTG TGGATAACCT GGGGTGGCTC CGGGCCTCAG TTTCCCCATC
     *** ****** ********** ********** ********** *******
541″ AGTCCTCCAC TCTGATGCTG TGGATAACCT GGGGTGGCTC CGGGCCT
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1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5478

2nd Nucleotide Sequence
  File Name        : RDB7340R.fasta (Complementary)
  Sequence Size    : 671

  Unit Size to Compare = 1
  Pick up Location     = 1


[99.701% / 670 bp]     INT/OPT.Score : <   2654/  2658 >
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 661' GGCTCTGGAG ATGCATAGAT CAACAAGGTC CCCCA-GGAG CTTGGGATTC TAAGAGGGGA
                                    ** ***** **** ********** **********
   1″                              TTC CCCCAGGGAG CTTGGGATTC TAAGAGGGGA

 720' AATTTAGGGG TCCATCCTGA TGTGGGCGAG GCATTCTCTG GATCAAAGAA GAGCTTGTCA
      ********** ****** *** ********** ********** ********** **********
  34″ AATTTAGGGG TCCATCTTGA TGTGGGCGAG GCATTCTCTG GATCAAAGAA GAGCTTGTCA

 780' GACCCAGGAT GGAGGGGCCC TGAGTCTCTC CCGGCCCCTT GGCGCCCCGC TCTCTATTCC
      ********** ********** ********** ********** ********** **********
  94″ GACCCAGGAT GGAGGGGCCC TGAGTCTCTC CCGGCCCCTT GGCGCCCCGC TCTCTATTCC

 840' ACGGCCTGCT GGCCTTTTGT GTGTTGCCCA CTTAGGATCA AGGGCCCCAG GCCAGATCCT
      ********** ********** ********** ********** ********** **********
 154″ ACGGCCTGCT GGCCTTTTGT GTGTTGCCCA CTTAGGATCA AGGGCCCCAG GCCAGATCCT

 900' AGGGCATGTT CCCAGCTTGT GGCAGGAGAG GAGGCCTTTG TACCCAGGCA GGCCCAGTCC
      ********** ********** ********** ********** ********** **********
 214″ AGGGCATGTT CCCAGCTTGT GGCAGGAGAG GAGGCCTTTG TACCCAGGCA GGCCCAGTCC

 960' AGCCTCCCGG GGAAGGTCCC AGTATGACAA GCCTAGGATG GTGAGAAGCC CAGGGACACA
      ********** ********** ********** ********** ********** **********
 274″ AGCCTCCCGG GGAAGGTCCC AGTATGACAA GCCTAGGATG GTGAGAAGCC CAGGGACACA

1020' AAGCCGGCTT GGTTCCTTGG CAACATCCTG AGGAATCCAG CGGCTGCACA CTGGCTCCCT
      ********** ********** ********** ********** ********** **********
 334″ AAGCCGGCTT GGTTCCTTGG CAACATCCTG AGGAATCCAG CGGCTGCACA CTGGCTCCCT

1080' TCCTCTCCCC TCCCACCCTC CTGCCTGCGG GGGCTGGAGG CGGAGGCAGC CAACCCCATT
      ********** ********** ********** ********** ********** **********
 394″ TCCTCTCCCC TCCCACCCTC CTGCCTGCGG GGGCTGGAGG CGGAGGCAGC CAACCCCATT

1140' ATAAAAAGCC ACAGATCTCT GGCGGCGGCA AGGGGACAGC ACTGAGCTCT GCCGCCTGGC
      ********** ********** ********** ********** ********** **********
 454″ ATAAAAAGCC ACAGATCTCT GGCGGCGGCA AGGGGACAGC ACTGAGCTCT GCCGCCTGGC

1200' TCTAGCCGCC TGCCTGGCCC CCGCCGGGAC TCTTGCCCAC CCTCAGCCAT GGCTCCGATA
      ********** ********** ********** ********** ********** **********
 514″ TCTAGCCGCC TGCCTGGCCC CCGCCGGGAC TCTTGCCCAC CCTCAGCCAT GGCTCCGATA
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1260' TCTCTGTCGT GGCTGCTCAT CAAGATCTGG CCTCGGCGGC CAAGCTTGGC AATCCGGTAC
      ********** ********** ********** ********** ********** **********
 574″ TCTCTGTCGT GGCTGCTCAT CAAGATCTGG CCTCGGCGGC CAAGCTTGGC AATCCGGTAC

1320' TGTTGGTAAA GCCACCATGG AAGATGCCAA AAACATTAAG AAGGGCCCAG CGCCATTCTA
      ********** ********** ********** ********
 634″ TGTTGGTAAA GCCACCATGG AAGATGCCAA AAACATTA
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