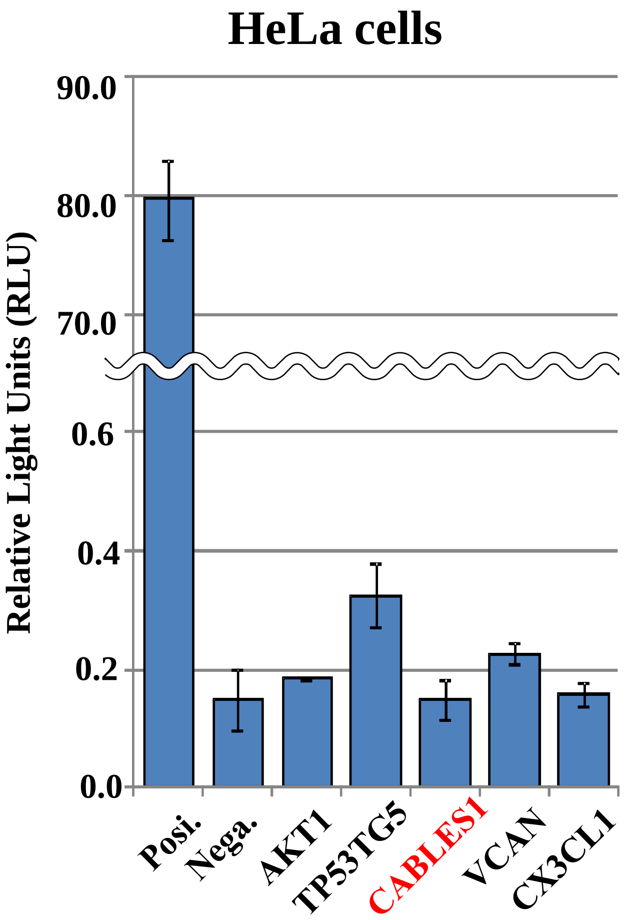
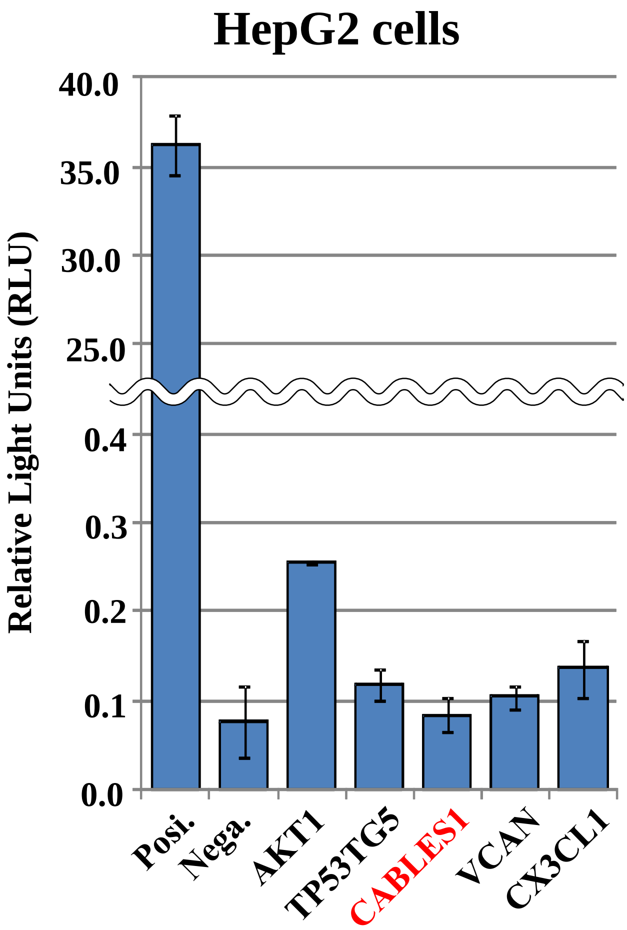
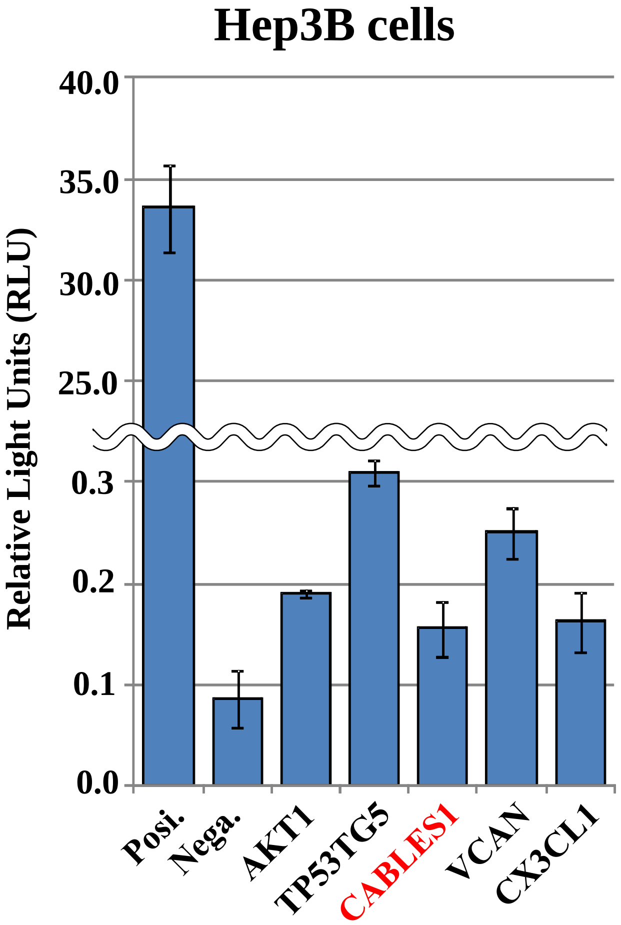
The Promoter Activities of Reporter Constructs


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    : 5464

2nd Nucleotide Sequence
  File Name        : RDB7337F.fasta
  Sequence Size    : 685

  Unit Size to Compare = 1
  Pick up Location     = 1



[99.850% / 666 bp]     INT/OPT.Score : <   2658/  2658 >

     1'                      G GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT
                             * ********** ********** ********** **********
     1" GGTGCCAGAA CATTTCTCTG GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT

    42' CATGTCAGCA AGGGATTTGA ACTTTAGAGA ATTGAGTTTT CTCACCAAGT CATGTAGAGC
        ********** ********** ********** ********** ********** **********
    61" CATGTCAGCA AGGGATTTGA ACTTTAGAGA ATTGAGTTTT CTCACCAAGT CATGTAGAGC

   102' AGGGATCCCT TCTAACGGAA GCCCATCCTC TCCCACTCTG CTCTCTTGCC TTTTGACACG
        ********** ********** ********** ********** ********** **********
   121" AGGGATCCCT TCTAACGGAA GCCCATCCTC TCCCACTCTG CTCTCTTGCC TTTTGACACG

   162' TGTGACATTT TATCTAAACA AATTTTGTGA CCTTCCTGAA CAAAACAGGT TGTTTTAGGA
        ********** ********** ********** ********** ********** **********
   181" TGTGACATTT TATCTAAACA AATTTTGTGA CCTTCCTGAA CAAAACAGGT TGTTTTAGGA

   222' TGGGCCAGTG TTTCTGGACA CCTGTACTGT TCAACACTTG CACTGTCTAA GAACATACGC
        ********** ********** ********** ********** ********** **********
   241" TGGGCCAGTG TTTCTGGACA CCTGTACTGT TCAACACTTG CACTGTCTAA GAACATACGC
```

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282’ TGATATTCAT GTCATTTACC CATCCAGCCC CTGTTGGTGG GAAGCTGCTA TGTGTGTACA
     ********** ********** ********** ********** ********** **********
301″ TGATATTCAT GTCATTTACC CATCCAGCCC CTGTTGGTGG GAAGCTGCTA TGTGTGTACA

342’ GAATGACTAA ACCAGACTTT TTTATTTGAC CCTGTTTGCT ACAAACGTAA TTGAATAATT
     ********** ********** ********** ********** ********** **********
361″ GAATGACTAA ACCAGACTTT TTTATTTGAC CCTGTTTGCT ACAAACGTAA TTGAATAATT

402’ GGGGCCTGGC AGATCGGAAG CAATAGGAAC AATATATTTC AATCCAGTAC TCTGTGAGCA
     ********** ********** ********** ********** ********** **********
421″ GGGGCCTGGC AGATCGGAAG CAATAGGAAC AATATATTTC AATCCAGTAC TCTGTGAGCA

462’ GCAGCATTTC ACAGAGCCAG AAATAATTTA GCCTGTAGAG CTTATTAAGA AGTGCAATGT
     ********** ********** ********** ********** ********** **********
481″ GCAGCATTTC ACAGAGCCAG AAATAATTTA GCCTGTAGAG CTTATTAAGA AGTGCAATGT

522’ TCGTTATGCG TAACTTCAGT TCTGTTAGAG CCAAGAAAAT AAAAGTCAAG GCTGAAATAT
     ********** ********** ********** ********** ********** **********
541″ TCGTTATGCG TAACTTCAGT TCTGTTAGAG CCAAGAAAAT AAAAGTCAAG GCTGAAATAT

582’ AAGGAAATGA ATAAGATACA TGGAGGCTGG TGAGATCTGG AATAAAAAAA ATATTTACAT
     ********** ********** ********** ********** ********** **********
601″ AAGGAAATGA ATAAGATACA TGGAGGCTGG TGAGATCTGG AATAAAAAAA ATATTTACAT

642’ AGGAGTTCAG CTTTGATTTT ATATTGTCAC AAATTGGTAC CAGATGCCTG CATTTCAGAC
     ********** * ******** *****
661″ AGGAGTTCAG CCTTGATTTT ATATT
```

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1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5464

2nd Nucleotide Sequence
  File Name        : RDB7337R.fasta (Complementary)
  Sequence Size    : 691
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  Unit Size to Compare = 1
  Pick up Location     = 1



[99.421% / 691 bp]     INT/OPT.Score : <   2616/  2730 >

   601' ATGGAGGCTG GTGAGATCTG GAATAAAAAA AATATTTACA TAGGAGTTCA GCTTTGATTT
                                                                       **
     1″                                                                TT

   661' TATATTGTCA CAAATTGGTA CCAGATGCCT GCATTTCAGA CAGACTCCTG AGCTGATCCC
        ********** **** ***** ********** ********** ********** **********
     3″ TATATTGTCA CAAAATGGTA CCAGATGCCT GCATTTCAGA CAGACTCCTG AGCTGATCCC

   721' AGAGTGTGAG TTGGGAAACA AATCACTTTG CCATTTGGAA GGCTGATTGA TATTTTAGGA
        ********** ********** ********** ********** ********** **********
    63″ AGAGTGTGAG TTGGGAAACA AATCACTTTG CCATTTGGAA GGCTGATTGA TATTTTAGGA

   781' GTTTCTTTTT GTTTTCAAAG GGAAAATAAT GCATATTATA GACCTAGCAA ACAGAACTTT
        ********** ********** ********** ******** * ********** **********
   123″ GTTTCTTTTT GTTTTCAAAG GGAAAATAAT GCATATTACA GACCTAGCAA ACAGAACTTT

   841' TGTAAATGGC AATTAACAGA AGATGCCCAA GTGAGGAAGT CTCCAGTTTC TTTTTATAAC
        ********** ********** ********** * ******** ********** **********
   183″ TGTAAATGGC AATTAACAGA AGATGCCCAA GGGAGGAAGT CTCCAGTTTC TTTTTATAAC

   901' CCTGGCAAAA GTAATGGAGG TGACATTTTA TTAGCATTGG CATCTCCCGC TTACAATGGG
        ********** ********** ********** ********** ********** **********
   243″ CCTGGCAAAA GTAATGGAGG TGACATTTTA TTAGCATTGG CATCTCCCGC TTACAATGGG

   961' AGCTAGTTCA GCCTTGTTGA GCCGTGTCCA GAGCTGGTAG CTTCATTTCC ATTTTCCTTC
        ********** ********** ********** ********** ********** **********
   303″ AGCTAGTTCA GCCTTGTTGA GCCGTGTCCA GAGCTGGTAG CTTCATTTCC ATTTTCCTTC

  1021' AACCTCAGGG AGAAACACAA GGGTATTTCT GTCTGGGGCG GCAGGACCTC ATGTGGTCTC
        ********** ********** ********** ********** ********** **********
   363″ AACCTCAGGG AGAAACACAA GGGTATTTCT GTCTGGGGCG GCAGGACCTC ATGTGGTCTC
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1081’ CACGTGGCAG GATCCTAGAA TCACGGGGTG GCAGTACATA TTTTCCCCTA TGGCTTTAAG
      ********** ********** ********** ********** ********** **********
 423″ CACGTGGCAG GATCCTAGAA TCACGGGGTG GCAGTACATA TTTTCCCCTA TGGCTTTAAG

1141’ AAAATGGCTT TTCATTTTGA GTCTTAGGTT TGGTCTCAAC AGTGCTTGCT TAGCCTCCAG
      ********** ********** ********** ********** ********** **********
 483″ AAAATGGCTT TTCATTTTGA GTCTTAGGTT TGGTCTCAAC AGTGCTTGCT TAGCCTCCAG

1201’ GCCATTTTTC TTCCTGGTGT TTGAATGACT CATAAAATGA GTTTGGAGTG GTCTGAAGCC
      ********** ********** ********** ********** ********** **********
 543″ GCCATTTTTC TTCCTGGTGT TTGAATGACT CATAAAATGA GTTTGGAGTG GTCTGAAGCC

1261’ TCTATCAAGA TCTGGCCTCG GCGGCCAAGC TTGGCAATCC GGTACTGTTG GTAAAG-CCA
      ********** ********** ********** ********** ********** ****** ***
 603″ TCTATCAAGA TCTGGCCTCG GCGGCCAAGC TTGGCAATCC GGTACTGTTG GTAAAGACCA

1320’ CCATGGAAGA TGCCAAAAAC ATTAAGAAGG GCCCAGCGCC ATTCTACCCA CTCGAAGACG
      ********** ********** *********
 663″ CCATGGAAGA TGCCAAAAAC ATTAAGAAG
```