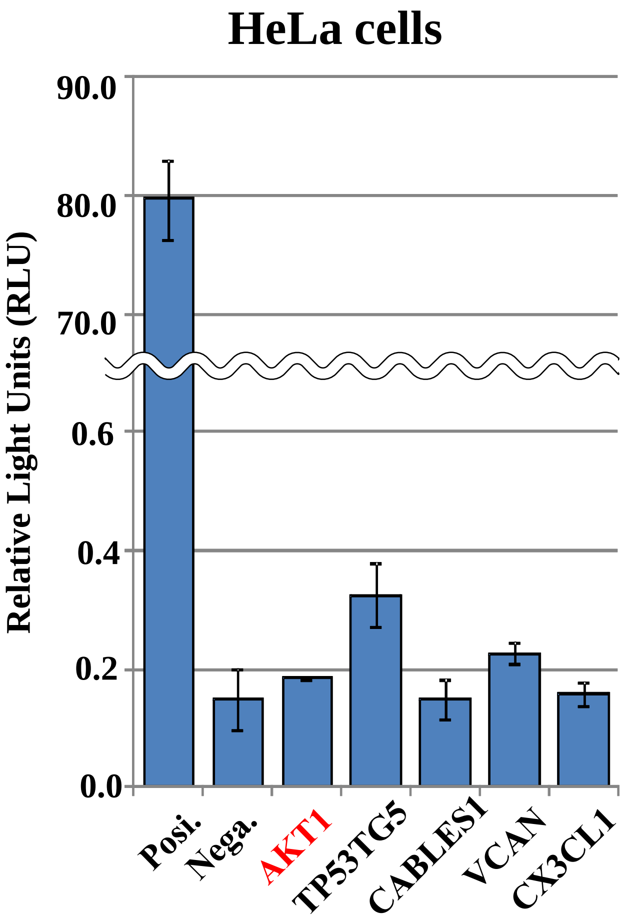
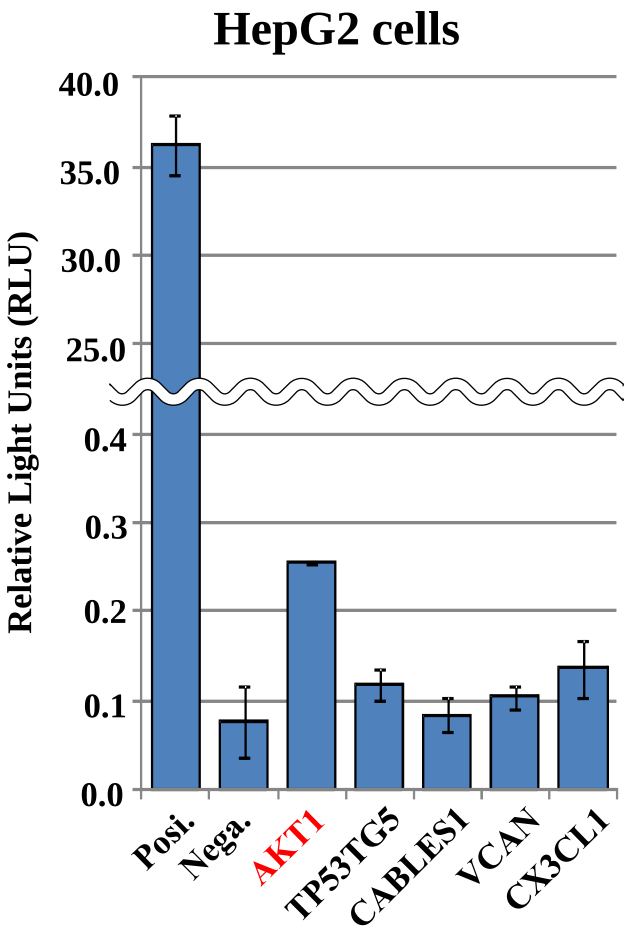
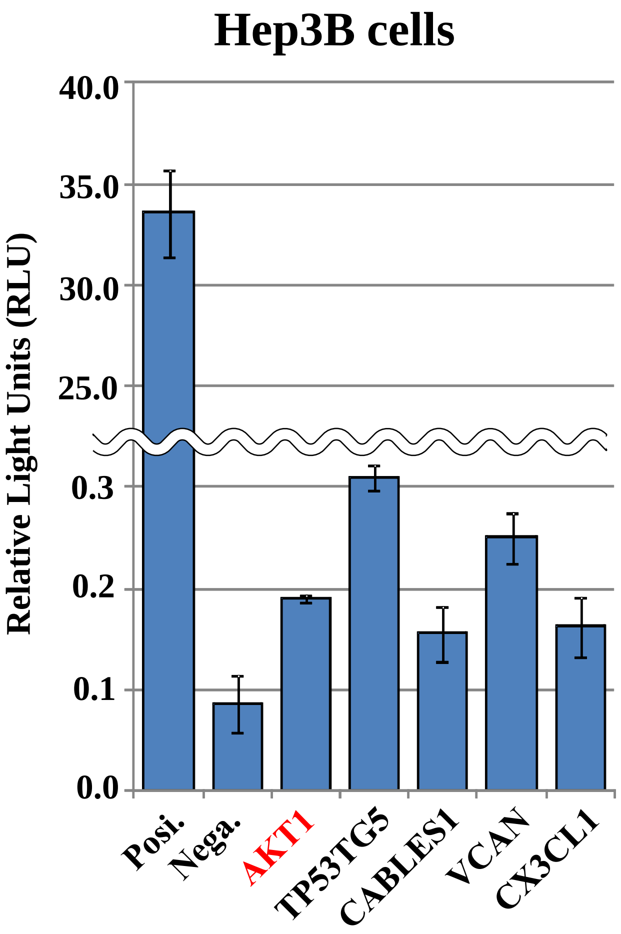
The Promoter Activities of Reporter Constructs


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    : 5394

2nd Nucleotide Sequence
  File Name        : RDB7331F.fasta
  Sequence Size    : 714

  Unit Size to Compare = 1
  Pick up Location     = 1



[98.293% / 703 bp]     INT/OPT.Score : <   1668/  2660 >

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

   43' TCCAGGTGGC CACTTCTTGA CTGCTTTGAG TCCCTCATCC GAGCGAAGGG CGGACGGAGT
       ********** ********** ********** ********** ********** **********
   61″ TCCAGGTGGC CACTTCTTGA CTGCTTTGAG TCCCTCATCC GAGCGAAGGG CGGACGGAGT

  103' CCGTTGGTGG GGGTCCGGTT GCCTCTCCCG GGAGCTGTGT AGACTTCTCA TACACCAGGG
       ********** ********** ********** ********** ********** **********
  121″ CCGTTGGTGG GGGTCCGGTT GCCTCTCCCG GGAGCTGTGT AGACTTCTCA TACACCAGGG

  163' TTCTGGAGGC AGATGGAGGA GCCCTTTCGA AA-ACAGAGT ATTTTTTTTT AAGTTGTGAC
       ********** ********** ********** ** ******* ********** **********
  181″ TTCTGGAGGC AGATGGAGGA GCCCTTTCGA AACACAGAGT ATTTTTTTTT AAGTTGTGAC

  222' TTAATAATAG TAGCAAGAAT ATGTGCTTAT GGTAAAGGCA GGCGGCAGGT ACGGAGGCTG
       ********** ********** ********** ********** ********** **********
  241″ TTAATAATAG TAGCAAGAAT ATGTGCTTAT GGTAAAGGCA GGCGGCAGGT ACGGAGGCTG
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282’ TGGGAAGTCG GGGTCCCTCC GCCCCCACAG GCAGCCCTGT GCTGGCCTGG TGTATACGTT
     ********** ********** ********** ********** ********** **********
301″ TGGGAAGTCG GGGTCCCTCC GCCCCCACAG GCAGCCCTGT GCTGGCCTGG TGTATACGTT

342’ TCTGTGCAGA CGTACACCAC CCTGTGTGAG CACAGATGTA TTTTTACACA TGGCTCTGGA
     ********** ********** ********** ********** ********** **********
361″ TCTGTGCAGA CGTACACCAC CCTGTGTGAG CACAGATGTA TTTTTACACA TGGCTCTGGA

402’ CAGCTGTCTG ACTCTGTCAG CAGCAGGCCT TGGAGGGGCT CAGGCCCGTG TGGGGGTGGG
     ********** ********** ********** ********** ********** **********
421″ CAGCTGTCTG ACTCTGTCAG CAGCAGGCCT TGGAGGGGCT CAGGCCCGTG TGGGGGTGGG

462’ GGGACATCCA GAGGTCTTTG AGTCCAGCCC TCTGCCTCCA GGCCACGCCC ACTCAGTGTC
     ********** ********** ********** ********** ********** **********
481″ GGGACATCCA GAGGTCTTTG AGTCCAGCCC TCTGCCTCCA GGCCACGCCC ACTCAGTGTC

522’ GTCAGAGCCC CCTGTGCCTG AGGCGTGCGC GGCTCGGAGC CCTGCCCTCG GAGTCCTGCG
     ********** ********** ********** ********** ********** **********
541″ GTCAGAGCCC CCTGTGCCTG AGGCGTGCGC GGCTCGGAGC CCTGCCCTCG GAGTCCTGCG

582’ GTGCCTTCCT CGAGTCTGGC CTGCTTTCCA TCCTGCTAAG TACTTGGGGC ATTTCCCTCT
     ********** ********** **** ***** ********** ********** **** *****
601″ GTGCCTTCCT CGAGTCTGGC CTGC-TTCCA TCCTGCTAAG TACTTGGGGC ATTT-CCTCT

642’ TTGGGTAAGG TGTGGTCTTC CCTGTCCTGG CATTAGACAC AAGGCAGTGG GCCTTCCTGC
     ********** ******* ** ** ** ***  ** ** ** *  ********* *** ******
659″ TTGGGTAAGG TGTGGTC-TC CC-GTTCTGC CA-TAAAC-C CAGGCAGTGG GCC-TCCTGC

702’ CATTCTAAGT GTAGCTTAAG ACAATCAGTG CAAAGCAACC CTTTGTGGGT GTCCAGCCCT
     *
714″ C
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1st Nucleotide Sequence
  File Name   : Reference Seq.gnu
  Sequence Size   : 5394

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2nd Nucleotide Sequence
  File Name         : RDB7331R (Complementary)
  Sequence Size     : 656

  Unit Size to Compare = 1
  Pick up Location     = 1



[99.391% / 657 bp]     INT/OPT.Score : <   2352/  2587 >

    601' CCTGCTTTCC ATCCTGCTAA GTACTTGGGG CATTTCCCTC TTTGGGTAAG GTGTGGTCTT
                                ***** *** ********** ********** *** .*****
      1″                       TTACTTTGGG CATTTCCCTC TTTGGGTAAG GTG-NGTCTT

    661' CCCTGTCCTG GCATTAGACA CAAGGCAGTG GGCCTTCCTG CCATTCTAAG TGTAGCTTAA
         ********** ********** *********  ********** ********** **********
     40″ CCCTGTCCTG GCATTAGACA CAAGGCAGT- GGCCTTCCTG CCATTCTAAG TGTAGCTTAA

    721' GACAATCAGT GCAAAGCAAC CCTTTGTGGG TGTCCAGCCC TTGCCTCGGG AGGCCAGAAA
         ********** ********** ********** ********** ********** **********
     99″ GACAATCAGT GCAAAGCAAC CCTTTGTGGG TGTCCAGCCC TTGCCTCGGG AGGCCAGAAA

    781' GGTGGCCTGG GGGGAGAGCG TCTAAGCTGG CTGTGGAAAG ACCCATGTTG GGATCCATTC
         ********** ********** ********** ********** ********** **********
    159″ GGTGGCCTGG GGGGAGAGCG TCTAAGCTGG CTGTGGAAAG ACCCATGTTG GGATCCATTC

    841' CACAGAGGTC GTCAGGGGTC TCTGCCTGGC CTGGAGGTCC CAGAGAGGAC CCTCCTCCCC
         ********** ********** ********** ********** ********** **********
    219″ CACAGAGGTC GTCAGGGGTC TCTGCCTGGC CTGGAGGTCC CAGAGAGGAC CCTCCTCCCC

    901' TCAGGAAGGC CCATCTGGAA GGGTAGCAGA GGACTGCTCA CAGGAAGAGC ATGCGAAGTG
         ********** ********** ********** ********** ********** **********
    279″ TCAGGAAGGC CCATCTGGAA GGGTAGCAGA GGACTGCTCA CAGGAAGAGC ATGCGAAGTG

    961' CTCTTTCTGG GGATGCCTGT AGTTGGTGAT GTGGGAACTG GGTTTTGAGG GATGCCTAGG
         ********** ********** ********** ********** ********** **********
    339″ CTCTTTCTGG GGATGCCTGT AGTTGGTGAT GTGGGAACTG GGTTTTGAGG GATGCCTAGG
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1021’ AGTTCATCCA TCAGAGGGGA AATGAGGAAG CCATGCAGGA TCAATGGATA AAGTGTGCTC
      ********** ********** ********** ********** ********** **********
 399″ AGTTCATCCA TCAGAGGGGA AATGAGGAAG CCATGCAGGA TCAATGGATA AAGTGTGCTC

1081’ AGGTGAGGGT TGGCTGGTGG GCCGCTGCAG GGCGGGGGCC TGTCCAGTGC TCCCCCACTT
      ********** ********** ********** ********** ********** **********
 459″ AGGTGAGGGT TGGCTGGTGG GCCGCTGCAG GGCGGGGGCC TGTCCAGTGC TCCCCCACTT

1141’ ACTTGCTGCC TCCCGACTGC TGTAATTATG GGTCTGTAAC CACCCTGGAC TGGATCAAGA
      ********** ********** ********** ********** ********** **********
 519″ ACTTGCTGCC TCCCGACTGC TGTAATTATG GGTCTGTAAC CACCCTGGAC TGGATCAAGA

1201’ TCTGGCCTCG GCGGCCAAGC TTGGCAATCC GGTACTGTTG GTAAAGCCAC CATGGAAGAT
      ********** ********** ********** ********** ********** **********
 579″ TCTGGCCTCG GCGGCCAAGC TTGGCAATCC GGTACTGTTG GTAAAGCCAC CATGGAAGAT

1261’ GCCAAAAACA TTAAGAAGGG CCCAGCGCCA TTCTACCCAC TCGAAGACGG GACCGCCGGC
      ********** ********
 639″ GCCAAAAACA TTAAGAAG
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