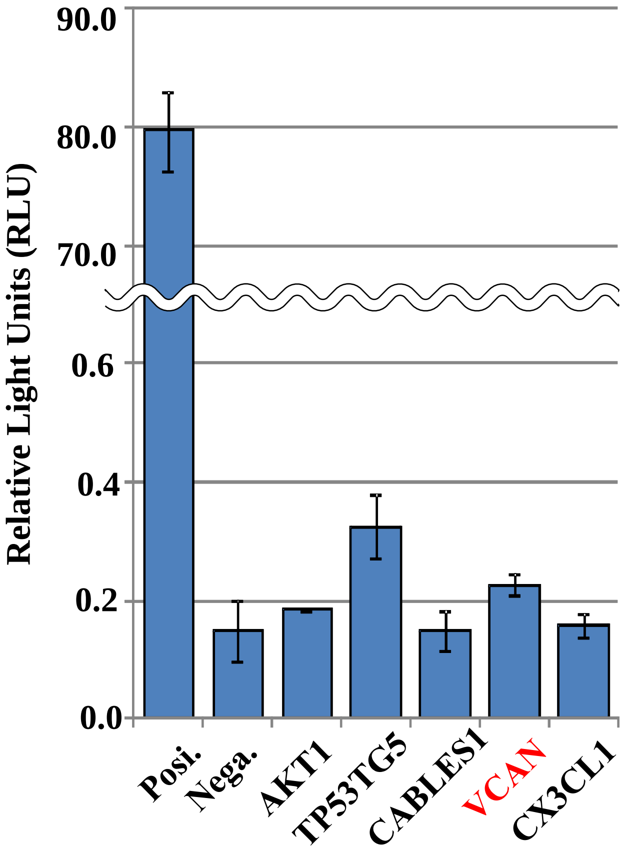
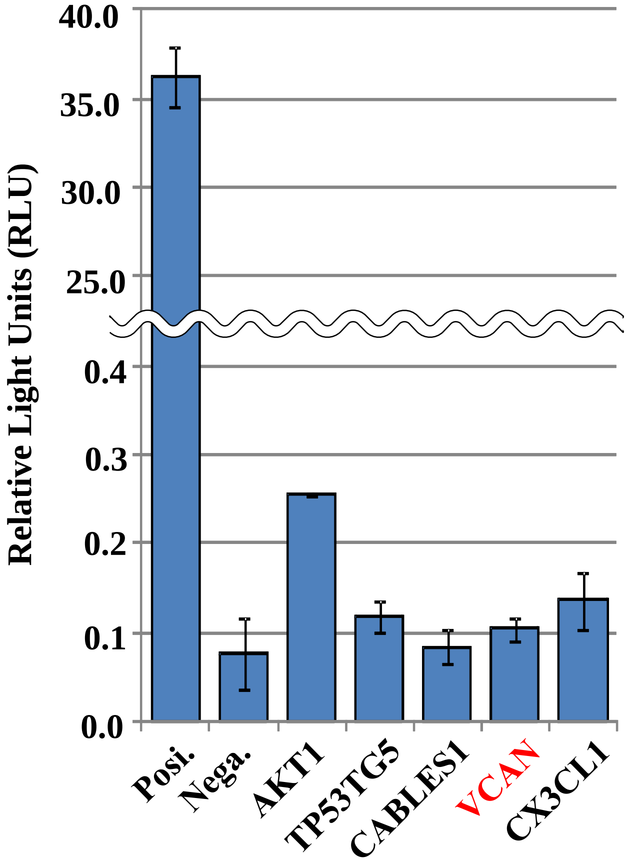
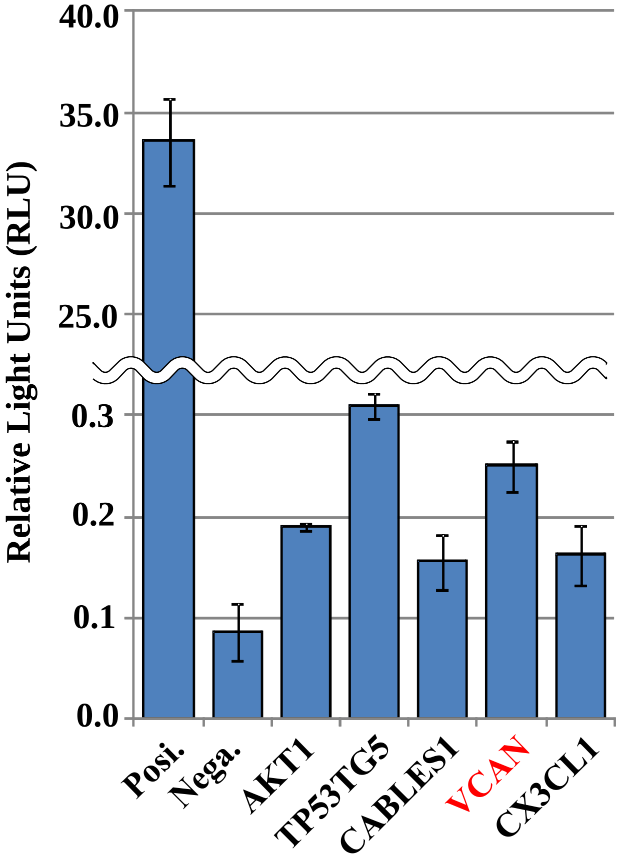
The Promoter Activities of Reporter Constructs



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    : 5428

2nd Nucleotide Sequence
  File Name        : RDB7339F.fasta
  Sequence Size    : 601

  Unit Size to Compare = 1
  Pick up Location     = 1



[99.828% / 580 bp]     INT/OPT.Score : <   2314/  2314 >

      1'                       GGCCTAACTG GCCGGTACCT GAGCTCGCTA GCCTCGAGGA
                               ********** ********** ********** **********
      1" GTGCCAGAAC ATTATACTCT GGCCTAACTG GCCGGTACCT GAGCTCGCTA GCCTCGAGGA

     41' TCTGATGTGC ACCTTGGATT TATTTTGTTC CTATTGTATA AACTCATACT TGACTTCAAA
         ********** ********** ********** ********** ********** **********
     61" TCTGATGTGC ACCTTGGATT TATTTTGTTC CTATTGTATA AACTCATACT TGACTTCAAA

    101' GAAAAGGAAA ATCCAAAGTC CCTCTTTTCT AAGGGGACAG AAATCCTTTG TGTCAACTGT
         ********** ********** ********** ********** ********** **********
    121" GAAAAGGAAA ATCCAAAGTC CCTCTTTTCT AAGGGGACAG AAATCCTTTG TGTCAACTGT

    161' TTGACCCTTT TCTCTGTAAG GTCCTATTGG AAATCTTTTG TAACACAATG CAGGGGACTC
         ********** ********** ********** ********** ********** **********
    181" TTGACCCTTT TCTCTGTAAG GTCCTATTGG AAATCTTTTG TAACACAATG CAGGGGACTC

    221' TTCCATGTGT TGATGCTGTT TACACAGTGG GGTGGGCCTG ACTGAAGAAA AAAAATCGCA
         ********** ********** ********** ********** ********** **********
    241" TTCCATGTGT TGATGCTGTT TACACAGTGG GGTGGGCCTG ACTGAAGAAA AAAAATCGCA
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281’ TATACGCATG AAAGATTATG GTCTTATTTC CGGAAAGCAT GAAAGGTGAT TGATACTTCC
     ********** ********** ********** ********** ********** **********
301″ TATACGCATG AAAGATTATG GTCTTATTTC CGGAAAGCAT GAAAGGTGAT TGATACTTCC

341’ AAGAAGTCCC TGTTACTCAG GAAAATTATC AAATATTCTA CTCAGAGATA CTTGGAAAGA
     ********** ********** ********** ********** ********** **********
361″ AAGAAGTCCC TGTTACTCAG GAAAATTATC AAATATTCTA CTCAGAGATA CTTGGAAAGA

401’ CTGAAGGAAA GGAAGAACGA AGAAAGCAGA ATCTAGACTT ATGTGGGGAG AGATTTGTGG
     ********** ********** ********** ********** ********** **********
421″ CTGAAGGAAA GGAAGAACGA AGAAAGCAGA ATCTAGACTT ATGTGGGGAG AGATTTGTGG

461’ CAGAGGAAAA GTATTCTCTT TGAATCCGAC AAGGGATTTG CCTGGGGGAA TTTCCTGTCC
     ********** ********** ********** ********** ********** **********
481″ CAGAGGAAAA GTATTCTCTT TGAATCCGAC AAGGGATTTG CCTGGGGGAA TTTCCTGTCC

521’ AGCCTTTTAT TACCAGGGTC TTTTGAAGCC GGGCTCCCCA TTGGGCAGTT CCCTGGGAGT
     ********** ****** *** ********** ********** ********** **********
541″ AGCCTTTTAT TACCAGTGTC TTTTGAAGCC GGGCTCCCCA TTGGGCAGTT CCCTGGGAGT

581’ GCAGTGGGGA ATTCTTACAC TTTCCCTCTA GGTCCCCGAA GGATCTCGTT TTCTCAGTGT

601″ T
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1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5428

2nd Nucleotide Sequence
  File Name         : RDB7339R.fasta (Complementary)
  Sequence Size     : 641

  Unit Size to Compare = 1
  Pick up Location     = 1
```

```
[99.844% / 640 bp]     INT/OPT.Score : <   2554/  2554 >

  661’ CCTTGAGCCT GACACTTCCC TTTGATGGGA CAGGCAAGCT CTGTGGGCGC GTAAACACGC
                  ******** ******** * ********** ********** **********
    1″             CCACTTCCC TTTGATGGAA CAGGCAAGCT CTGTGGGCGC GTAAACACGC

  721’ TGTAACCAAG TTCTTTGCTG ATTTTACAGT TTTGTGTGCT CCCGAGAAGA AGTGATCGTA
       ********** ********** ********** ********** ********** **********
   50″ TGTAACCAAG TTCTTTGCTG ATTTTACAGT TTTGTGTGCT CCCGAGAAGA AGTGATCGTA

  781’ CTCAATTGTC TATTGCTGGC CTGCCCCCTA AGAGCCTGGG GGCTCCTTTC CCCTAACCCA
       ********** ********** ********** ********** ********** **********
  110″ CTCAATTGTC TATTGCTGGC CTGCCCCCTA AGAGCCTGGG GGCTCCTTTC CCCTAACCCA

  841’ GAACTAGCTG CACGGGGGGC GGGGAAATGG GGGTGGGGAA GGAGTGGGAG GGCAGTGGTT
       ********** ********** ********** ********** ********** **********
  170″ GAACTAGCTG CACGGGGGGC GGGGAAATGG GGGTGGGGAA GGAGTGGGAG GGCAGTGGTT

  901’ TCCGCGAGCA GAGCGATGTT ACTGAGTGAG TCCCTGAATG GGGAGCGCTG CTGTCCCCAA
       ********** ********** ********** ********** ********** **********
  230″ TCCGCGAGCA GAGCGATGTT ACTGAGTGAG TCCCTGAATG GGGAGCGCTG CTGTCCCCAA

  961’ GCCGATTGGT ACTTCTTGTC AGGAAGAAAC GCCAAGAGGT GGGAGTGCCT GGGGAGGGAG
       ********** ********** ********** ********** ********** **********
  290″ GCCGATTGGT ACTTCTTGTC AGGAAGAAAC GCCAAGAGGT GGGAGTGCCT GGGGAGGGAG

 1021’ GCAGGCGGTC CCTACCGCAG GCGCGGGGAG CTGCCTTTCC GCCCCTCCGC CTGCTTTCCA
       ********** ********** ********** ********** ********** **********
  350″ GCAGGCGGTC CCTACCGCAG GCGCGGGGAG CTGCCTTTCC GCCCCTCCGC CTGCTTTCCA

 1081’ AGCCTGGACT CTTAGGAGTG GCTGAAGCTG CGGAGCGCTT TTGGAGCCTG TGAATGAACC
       ********** ********** ********** ********** ********** **********
  410″ AGCCTGGACT CTTAGGAGTG GCTGAAGCTG CGGAGCGCTT TTGGAGCCTG TGAATGAACC

 1141’ CTCCTCCTCT CCCTCCTCCT TCTTCTCGCT GAGTCTCCTC CTCGGCTCTG ACGGTACAGT
       ********** ********** ********** ********** ********** **********
  470″ CTCCTCCTCT CCCTCCTCCT TCTTCTCGCT GAGTCTCCTC CTCGGCTCTG ACGGTACAGT
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1201' GATATAATGA TGATGGGTGT CACAACCATC AAGATCTGGC CTCGGCGGCC AAGCTTGGCA
      ********** ********** ********** ********** ********** **********
 530″ GATATAATGA TGATGGGTGT CACAACCATC AAGATCTGGC CTCGGCGGCC AAGCTTGGCA

1261' ATCCGGTACT GTTGGTAAAG CCACCATGGA AGATGCCAAA AACATTAAGA AGGGCCCAGC
      ********** ********** ********** ********** ********** **
 590″ ATCCGGTACT GTTGGTAAAG CCACCATGGA AGATGCCAAA AACATTAAGA AG
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