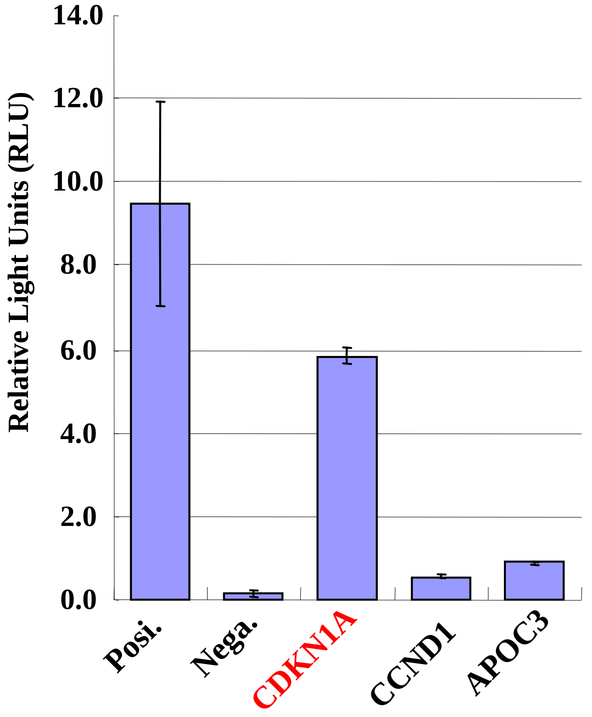
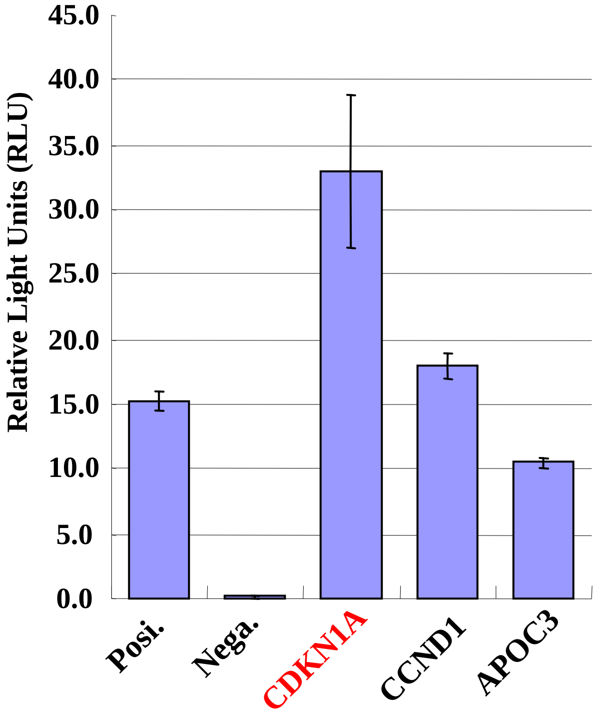
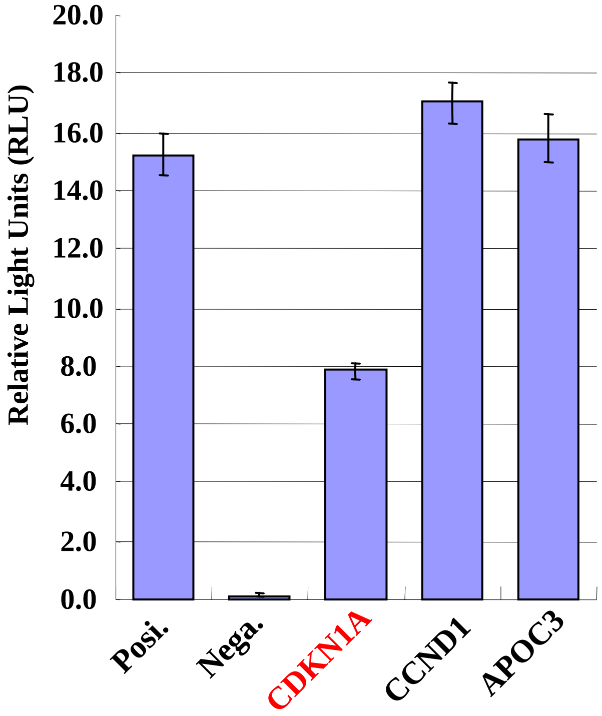
# The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

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

**CDKN1A: pGL4-phCDKN1A (RDB#7302)**
**CCND1: pGL4-phCCND1(RDB#7299)**
**APOC3:pGL4-phAPOC3 (RDB#7303)**

**2009, DNA Bank, RIKEN BioResource Center**

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.06.25

1st Nucleotide Sequence
  File Name         : Reference Seq.GNU
  Sequence Size     : 5469

2nd Nucleotide Sequence
  File Name         : RDB7302F.fasta
  Sequence Size     : 631

  Unit Size to Compare = 1
  Pick up Location     = 1



[96.135% / 621 bp]     INT/OPT.Score : <    384/  2216 >

      1’                    GG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGAT-
                            ** ********** ********** ********** *********
      1″ GTGCCAGAAC ATGTCTCTGG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATG

     42’ AT-GGGAGCG GAT-AGACAC ATCNACTCAT -TTCTGTGTC TGTCAGAAGA ACCAGTAGAC
         ** ******* *** ****** ** .******  ********* ********** **********
     61″ ATGGGGAGCG GATGAGACAC ATGCACTCAT GTTCTGTGTC TGTCAGAAGA ACCAGTAGAC

     99’ ACTTCCAGAA TTGTCNCTTT ATTTATGTCA TCTCCATAAA CCATCTGCAA ATGAGGGTTA
         ********** ***** **** ********** ********** ********** **********
    121″ ACTTCCAGAA TTGTC-CTTT ATTTATGTCA TCTCCATAAA CCATCTGCAA ATGAGGGTTA

    159’ TTTGGCNATT TTTGTCATTT TGGAGCCACA GAAATAAAGG ATGACAAGCA GAGAGCCNCC
         ****** *** ********** ********** ********** ********** ******* **
    180″ TTTGGC-ATT TTTGTCATTT TGGAGCCACA GAAATAAAGG ATGACAAGCA GAGAGCC-CC

    219’ GGGCAGGAGG CAAAAGTCCT GTGTTCCAAC TATAGTCATT TCTTTGCTNG CATGATCTGA
         ********** ********** ********** ********** ******** * **********
    238″ GGGCAGGAGG CAAAAGTCCT GTGTTCCAAC TATAGTCATT TCTTTGCT-G CATGATCTGA
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279' GTTAGGTCAC CAGACTTCTC TGAGCCCCAG TTTCCCCAGN CAGTGTATAC GGGCTATGTG
     ********** ********** ********** *********  ********** **********
297″ GTTAGGTCAC CAGACTTCTC TGAGCCCCAG TTTCCCCAG- CAGTGTATAC GGGCTATGTG

339' GGGAGTATTC AGGAGACAGA CAACTCACTC NGTCAAATCC TCCCCTTCCT GGCCAACAAA
     ********** ********** **********  ********* ********** **********
356″ GGGAGTATTC AGGAGACAGA CAACTCACTC -GTCAAATCC TCCCCTTCCT GGCCAACAAA

399' GCTGCTGCAA CCACAGGGAT TNTCTTCTGT TCAGGTGAGT GTAGGGTGTA GGGAGATTGG
     ********** ********** * ******** ********** *** **  **  *********
415″ GCTGCTGCAA CCACAGGGAT T-TCTTCTGT TCAGGTGAGT GTAAGGCATA AGGAGATTGG

459' TTCAATGTCC AANTTCTTCT GTTTCCCTGG AGATCAGGTT GCCCTTTTTT GGTAGTCTCT
     ********** ** ******* ********** ********** ********** **********
474″ TTCAATGTCC AA-TTCTTCT GTTTCCCTGG AGATCAGGTT GCCCTTTTTT GGTAGTCTCT

519' CCANATTCCC TCCTTCCCGG AAGCATGTGA CAATCAACAA CTTTGTATAC TTAANGTTCA
     ***. * **   ********* ********** ********** ********** **** *****
533″ CCAATTCCCT CCCTTCCCGG AAGCATGTGA CAATCAACAA CTTTGTATAC TTAA-GTTCA

579' GTGGACCTCA ATTTCCTCAT CTGTGAAATA AACGGGACTG AAAAANTCAT TCTGGCCTCA
     ********** ********** ********** *********
592″ GTGGACCTCA ATTTCCTCAT CTGTGAAATA AACGGGACTT
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1st Nucleotide Sequence
  File Name          : Reference Seq.GNU
  Sequence Size      : 5469

2nd Nucleotide Sequence
  File Name          : RDB7302R.fasta (Complementary)
  Sequence Size      : 612

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

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[97.101% / 621 bp]     INT/OPT.Score : <    393/  2229 >

  721’ ATATTNGTGG GGCTTTTCTG GAAATTGCAG AGAGGTGCAT CG-TTTTTAT -AATTTATNG
                         *** ********** ********** ** *******  *******.
    1″                   CTG GAAATTGCAG AGAGGTGCAT CGTTTTTTAT AAATTTATGA

  779’ AATTTTTATG TATTAATGTC ATCCTCCTGA TCTTTTCAGC TGCATTGGGN TAAATCCTTG
       * ******** ********** ********** ********** *********  **********
   44″ ATTTTTTATG TATTAATGTC ATCCTCCTGA TCTTTTCAGC TGCATTGGG- TAAATCCTTG

  839’ CCTGCCAGAG TGGGTCAGCG GTGAGCCAGA AAGGGGGCTC NATTCTAACA GTGCTGTGTC
       ********** ********** ********** **********  ********* **********
  103″ CCTGCCAGAG TGGGTCAGCG GTGAGCCAGA AAGGGGGCTC -ATTCTAACA GTGCTGTGTC

  899’ CTCCTGGAGA GTGCCAACTC ATTCTCCAAG TNAAAAAAAG CCAGATTTGT GGCTCACTTC
       ********** ********** ********** * ******** ********** **********
  162″ CTCCTGGAGA GTGCCAACTC ATTCTCCAAG T-AAAAAAAG CCAGATTTGT GGCTCACTTC

  959’ GTGGGGAAAT GTGTCCAGCG CANCCAACGC AGGCGAGGGA CTGGGGGAGG AGGGAAGTGC
       ********** ********** ** ******* ********** ********** **********
  221″ GTGGGGAAAT GTGTCCAGCG CA-CCAACGC AGGCGAGGGA CTGGGGGAGG AGGGAAGTGC

 1019’ CCTCCTGCAG CACNGCGAGG TTCCGGGACC GGCTGGCCTG CTGGAACTCG GCCAGGCTCA
       ********** *** ****** ********** ********** ********** **********
  280″ CCTCCTGCAG CAC-GCGAGG TTCCGGGACC GGCTGGCCTG CTGGAACTCG GCCAGGCTCA

 1079’ GCTGNGCTCG GCGCTGGGCA GCCAGGAGCC TGGGCCCCGG GGAGGGCGGT CCCGGNGCGG
       **** ***** ********** ********** ********** ********** ***** ****
  339″ GCTG-GCTCG GCGCTGGGCA GCCAGGAGCC TGGGCCCCGG GGAGGGCGGT CCCGG-GCGG

 1139’ CGCGGTGGGC CGAGCGCGGG TCCCGCCTCC TTGAGGCGGG CCCGGGNCGG GGCGGTTGTA
       ********** ********** ********** ********** ****** *** **********
  397″ CGCGGTGGGC CGAGCGCGGG TCCCGCCTCC TTGAGGCGGG CCCGGG-CGG GGCGGTTGTA

 1199’ -TATCAGGGC CGCGCTGAGC TGCGCCAGCT GAGGTGTGNA GCAGCTGCCG AAGTCAGTTC
        ********* ********** ********** ******** * ********** **********
  456″ CTATCAGGGC CGCGCTGAGC TGCGCCAGCT GAGGTGTG-A GCAGCTGCCG AAGTCAGTTC
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1258’ CTTGTGGAGC CATCAAGATC TGGCCTCGGC GGCCAAGCTT GGCA-ATCCG GTACTGTTGG
      ********** ********** ********** ********** **** ***** **********
 515″ CTTGTGGAGC CATCAAGATC TGGCCTCGGC GGCCAAGCTT GGCACATCCG GTACTGTTGG

1317’ TAAAGCCACC ATGGAA-GAT GCCAAA-AAC ATTAAGAAGG GCCCAGCGCC ATTCTACCCA
      ********** ****** *** ****** *** ********
 575″ TAAAGCCACC ATGGAACGAT GCCAAACAAC ATTAAGAA
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