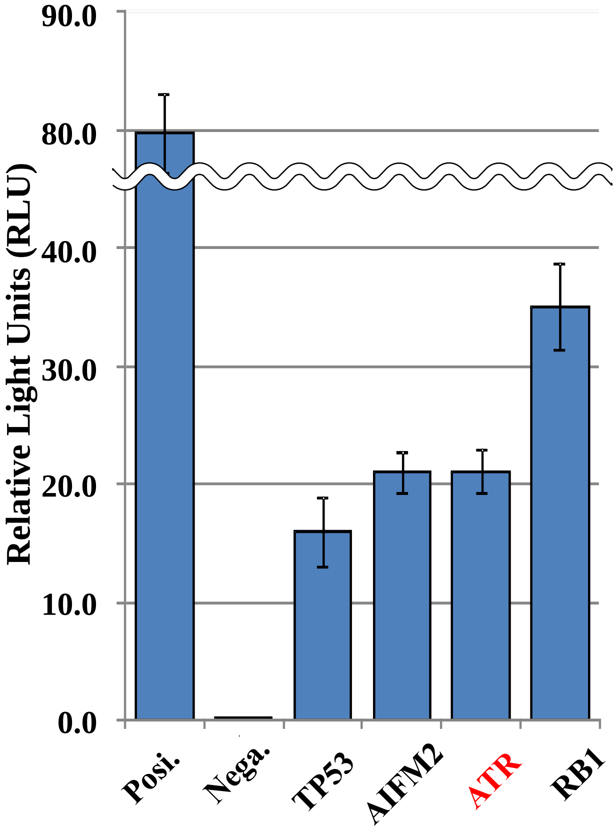
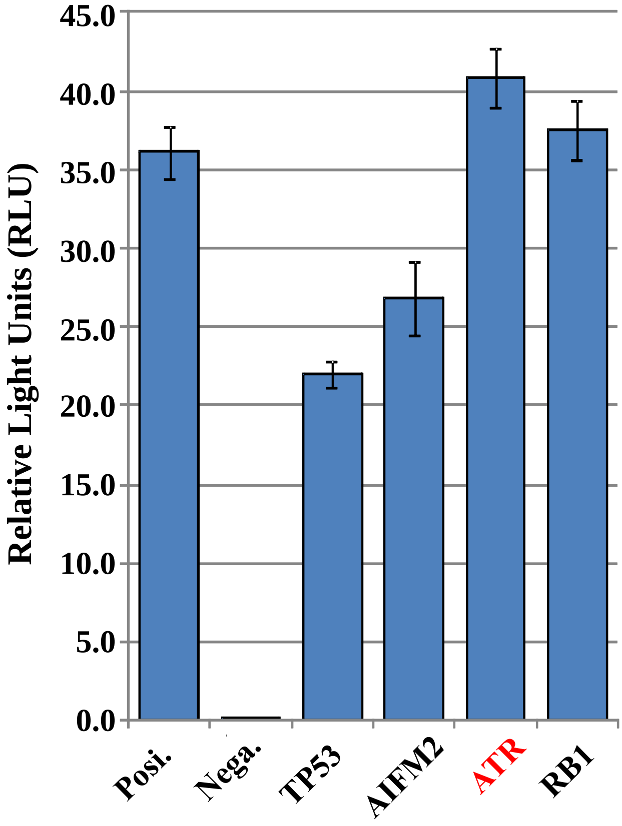
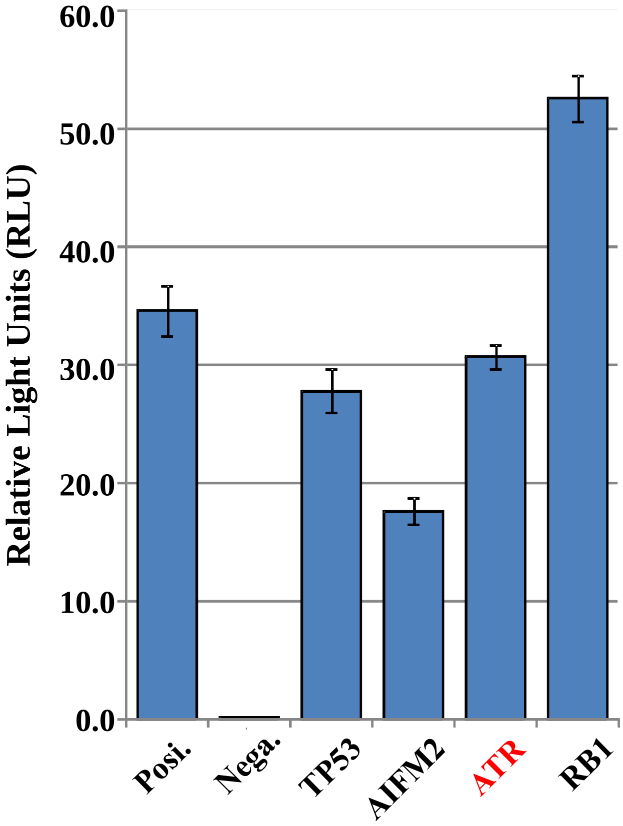
# The Promoter Activities of Reporter Constructs



HeLa cells



HepG2 cells



Hep3B cells

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

**TP53: pGL4-phTP53 (RDB# 7330)**
**AIFM2: pGL4-phAIFM2 (RDB# 7332)**
**ATR: pGL4-phATR (RDB# 7334)**
**RB1: pGL4-phRB1 (RDB#7345)**

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    : 5389

2nd Nucleotide Sequence
  File Name        : RDB7334F.fasta
  Sequence Size    : 677

  Unit Size to Compare = 1
  Pick up Location     = 1



[98.643% / 663 bp]     INT/OPT.Score : <   1028/  2556 >

     1'                 GGCCTA AC--TGGCCG GTACCTGAGC TCGCTAGCCT CGAGGATGCT
                        ****** **  ** *** ********** ********** **********
     1" AGAACATTTA CTCTGGCCTA ACTGTGTCCG GTACCTGAGC TCGCTAGCCT CGAGGATGCT

    45' GAGGCAGGAG GATCAATTGA GCCCAGGCTG AGGTGAGAGG ATCGCTTGAG CCTGGGAGAT
        ********** ********** ********** ********** ********** **********
    61" GAGGCAGGAG GATCAATTGA GCCCAGGCTG AGGTGAGAGG ATCGCTTGAG CCTGGGAGAT

   105' TGAGGCTGCA GTGAGCTATG ATTGCAACAT TCATTGCACT AGAACCTGAA CAACAGAGTA
        ********** ********** ********** ********** ********** **********
   121" TGAGGCTGCA GTGAGCTATG ATTGCAACAT TCATTGCACT AGAACCTGAA CAACAGAGTA

   165' AGACAATGTA TCTAACAAAA AAAAGAGGGT GAGACAGAAT GTGTATATAT GTTAGTCTAT
        ********** ********** ********** ********** ********** **********
   181" AGACAATGTA TCTAACAAAA AAAAGAGGGT GAGACAGAAT GTGTATATAT GTTAGTCTAT

   225' ATGAGGCTCT TTGGTGTTAA TTTGGCAAAC ACCTG-AAGG AAAAAGGGCA ATGACAGAGT
        ********** ********** ********** ***** **** ********** **********
   241" ATGAGGCTCT TTGGTGTTAA TTTGGCAAAC ACCTGAAAGG AAAAAGGGCA ATGACAGAGT
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284' GGTGTTCAAG GCAGAGAGTA CAGCAAATGC AAAGTTCTTG AGGCAAGAGC ATATTTGGCT
     ********** ********** ********** ********** ********** **********
301″ GGTGTTCAAG GCAGAGAGTA CAGCAAATGC AAAGTTCTTG AGGCAAGAGC ATATTTGGCT

344' GTCATTCCAT CACTTTTTTC TTTAAGATAC TGTATCGGTT AACTATCCTC ATGTACCAAA
     ********** ********** ********** ********** ********** **********
361″ GTCATTCCAT CACTTTTTTC TTTAAGATAC TGTATCGGTT AACTATCCTC ATGTACCAAA

404' GAACAAATGT AAACATACTG CATGACTTTG AGTGATTAAC TACATAACTT TGACATGTC-
     ********** ********** ********** ********** ********** *********
421″ GAACAAATGT AAACATACTG CATGACTTTG AGTGATTAAC TACATAACTT TGACATGTCA

463' AACAATCTCT TATGGTGGTC ATCTTTCCAA TAAATTGAGT TGAGCTAGAA AATGTGTATT
     ********** ********** ********** ********** ********** **********
481″ AACAATCTCT TATGGTGGTC ATCTTTCCAA TAAATTGAGT TGAGCTAGAA AATGTGTATT

523' GCCAAAATCC ATTGATTTAC TTTAAAAATT AAATCACAGG TTGCGGATGC CCGTAATGGT
     ********** ********** ********** ********** ********** **********
541″ GCCAAAATCC ATTGATTTAC TTTAAAAATT AAATCACAGG TTGCGGATGC CCGTAATGGT

583' GGCATTTCCA CACACAGTAC TGTTGCTGAT TTGATGAGAC ACAAATATAT TCCAACCCCA
     ********** ********** ********** ***** **** ********** **********
601″ GGCATTTCCA CACACAGTAC TGTTGCTGAT TTGATAAGAC ACAAATATAT TCCAACCCCA

643' TTTTCAAATA TTAAAAGTTG GTAGGGTCCT CAACGAAACC TAACAGTGAC TTCAAGTTGA
      **** **** * *****
661″ -TTTCCAATA TAAAAAGG




1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5389

2nd Nucleotide Sequence
  File Name        : RDB7334R.fasta (Complementary)
  Sequence Size    : 695
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Unit Size to Compare = 1
Pick up Location     = 1



[96.692% / 665 bp]     INT/OPT.Score : <   1266/  2426 >

    601’ ACTGTTGCTG ATTTGATGAG ACACAAATAT ATT-CCAA-- CCCCA-TTTT CAAATA-TTA
                                ** *** ** *** ****   ***** **** ****** ***
      1″  CTGATTTGG AAGGAGAACA CCAAAAAAAT ATTCCCAACC CCCCATTTTT CAAATATTTA

    656’ AAAGTTGGTA GGGTCCTCAA CGAAACCTAA CAGTGACTTC AAGTTGAAAA AAAATGCTTA
         ***** ** * ********** ******** * *** ****** **** ***** **** *** *
     60″ AAAGTGGGGA GGGTCCTCAA CGAAACCTTA CAGGGACTTC AAGTGGAAAA AAAAAGCTAA

    716’ AAAGGAAAAA AACAGGGAGA GCCCACCTTT TGGCCTGTAT CTCTCAGAAA GA-GGGACAA
         ***** **** ********** ********** ***** **** ********** ** *******
    120″ AAAGGGAAAA AACAGGGAGA GCCCACCTTT TGGCCGGTAT CTCTCAGAAA GAGGGGACAA

    775’ GAGCGGTGGG AACGTGAGGA ACTTTTAAAA TGTGAGAGCG TTACTC-TGG GGAAACCTGG
         ********** ********** ********** ********** ****** *** **********
    180″ GAGCGGTGGG AACGTGAGGA ACTTTTAAAA TGTGAGAGCG TTACTCTTGG GGAAACCTGG

    834’ AGTTTACTCT TGGCCTTTAC TCGCTGGACT GTCATAGTTC TCACA-TTTG TGAAGCGAGT
         ********** ********** ********** ********** ***** **** **********
    240″ AGTTTACTCT TGGCCTTTAC TCGCTGGACT GTCATAGTTC TCACATTTTG TGAAGCGAGT

    893’ CTGGGCTGGC GGCCCTCAAG CCCTATCCTC CCCCGATGCG GAAGTCTTGC -TTCTCTGTG
         ********** ********** ********** ********** **********  *********
    300″ CTGGGCTGGC GGCCCTCAAG CCCTATCCTC CCCCGATGCG GAAGTCTTGC TTTCTCTGTG

    952’ CCTCCCAGGC TTGAGAACAG CAGAGTCTGG CCGCTCAAAA CGAAAGCTTC ACGAACGTCG
         ********** ********** ********** ********** ********** **********
    360″ CCTCCCAGGC TTGAGAACAG CAGAGTCTGG CCGCTCAAAA CGAAAGCTTC ACGAACGTCG

   1012’ CTCGCTCGGT GCTGAGAAAG AAGCCTGACG CGACCCGGGA AACTTGACCG ACGCACGCCC
         ********** ********** ********** ********** ********** **********
    420″ CTCGCTCGGT GCTGAGAAAG AAGCCTGACG CGACCCGGGA AACTTGACCG ACGCACGCCC
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1072' GCCCGCTTGC CCCGCCCCCT AACGGCTTCC CGGCTTCCCC CGGGTCCTAT GCAGAAAAGA
      ********** ********** ********** ********** ********** **********
 480″ GCCCGCTTGC CCCGCCCCCT AACGGCTTCC CGGCTTCCCC CGGGTCCTAT GCAGAAAAGA

1132' CGCTGGGCCT GGCAAGCGGG GCCAGTAGCG GCTTCCGGGA GGAGTTTTGG CCTCCACATC
      ********** ********** ********** ********** ********** **********
 540″ CGCTGGGCCT GGCAAGCGGG GCCAGTAGCG GCTTCCGGGA GGAGTTTTGG CCTCCACATC

1192' AAGATCTGGC CTCGGCGGCC AAGCTTGGCA ATCCGGTACT GTTGGTAAAG CCACCATGGA
      ********** ********** ********** ********** ********** **********
 600″ AAGATCTGGC CTCGGCGGCC AAGCTTGGCA ATCCGGTACT GTTGGTAAAG CCACCATGGA

1252' AGA-TGCCAA AAACA-TTAA GAAGGGCCCA GCGCCATTCT ACCCACTCGA AGACGGGACC
      *** ****** ***** **** ******
 660″ AGATTGCCAA AAACATTTAA GAAGGGGACC ATGTCG
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