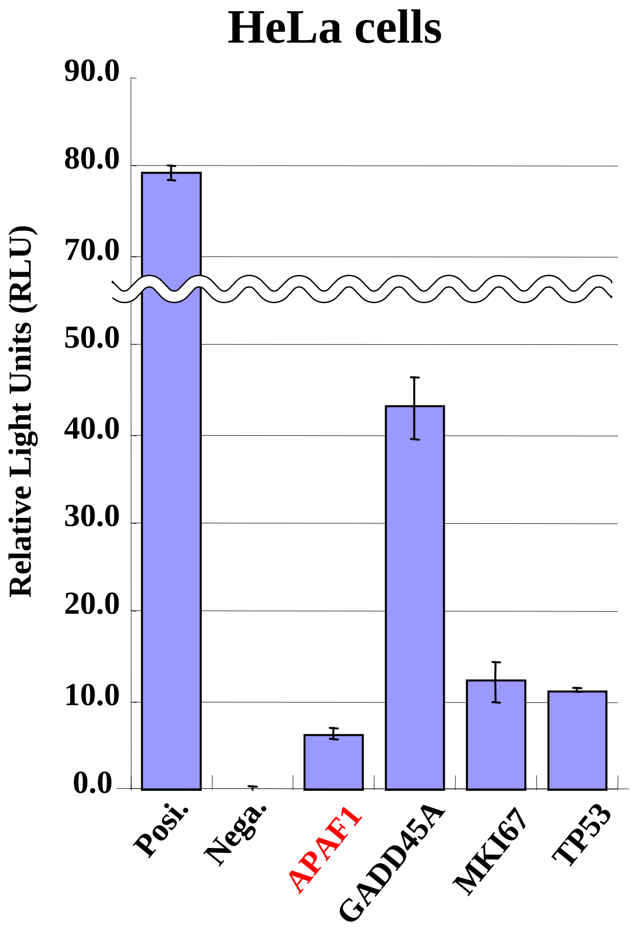
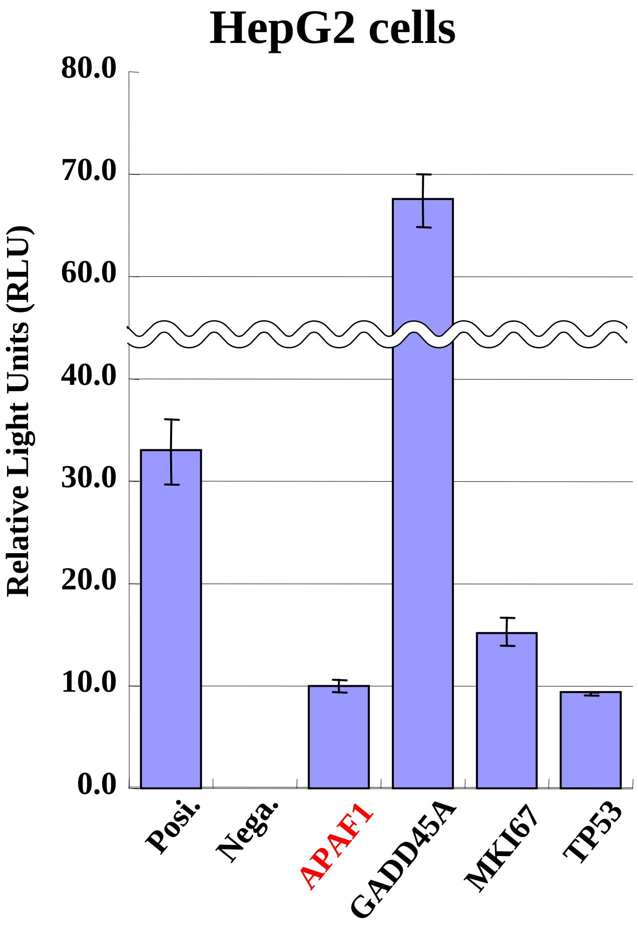
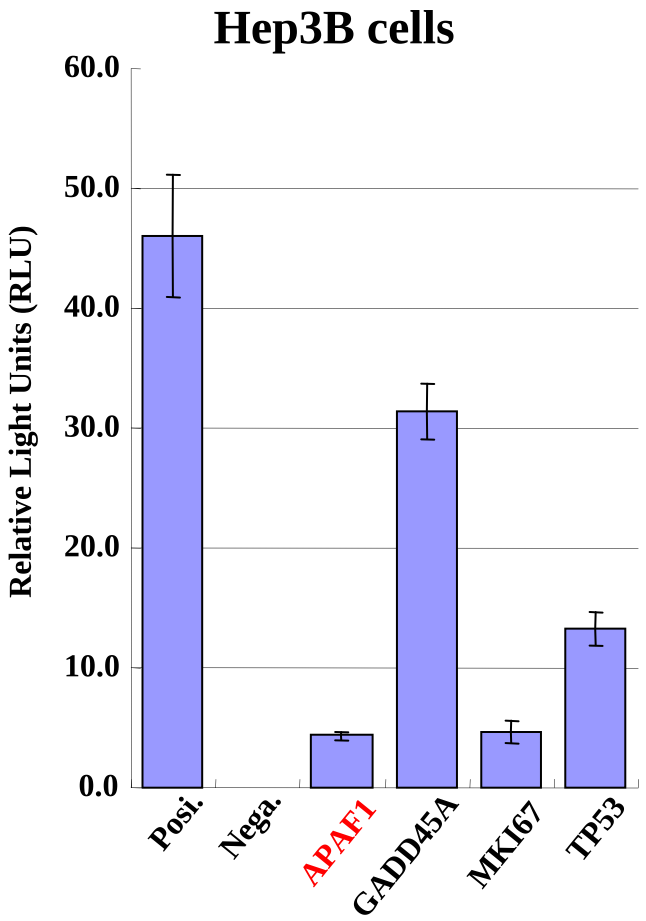
The Promoter Activities of Reporter Constructs







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

APAF1: pGL4-phAPAF1 (RDB# 7316)
GADD45A: pGL4-phGADD45A (RDB# 7320)
MKI67: pGL4-phMKI67 (RDB# 7323)
TP53: pGL4-phTP53 (RDB#7330)

2009, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.03.01

1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5394

2nd Nucleotide Sequence
  File Name        : RDB7316F.fasta
  Sequence Size    : 614

  Unit Size to Compare = 1
  Pick up Location     = 1



[99.328% / 595 bp]     INT/OPT.Score : <   1932/  2316 >

      1'                     G GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT
                             * ********** ********** ********** **********
      1″ GTGCCAGAAC ATTGTCTCTG GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT

     42' -CGGACAGGA AGTAACGGTT TAT-AACAAC GTGAACGCTT CTGACGTGT- AGCGGGAGCT
          ********* ********** *** ****** ********** *********  **********
     61″ GCGGACAGGA AGTAACGGTT TATGAACAAC GTGAACGCTT CTGACGTGTG AGCGGGAGCT

     99' TCAGAAAGCG -TGGCCGAAT CTGCAGCTCT TAACAAATGG CTCGTTCCCA AACCTTAGCC
         **********  ********* ********** ********** ********** **********
    121″ TCAGAAAGCG TTGGCCGAAT CTGCAGCTCT TAACAAATGG CTCGTTCCCA AACCTTAGCC

    158' TCAACTCCTT CTGAGCGATA GGGGCATGCT ACCAGCACGG GGGGAAATGA GATACAAGAA
         ********** ********** ********** ********** ********** **********
    181″ TCAACTCCTT CTGAGCGATA GGGGCATGCT ACCAGCACGG GGGGAAATGA GATACAAGAA

    218' ACGCCCGAAA GGGAAAAACA AGGCTGGGCT GTTTCCTTCC TTTGGGGTCA AGACAGAGGC
         ********** ********** ********** ********** ********** **********
    241″ ACGCCCGAAA GGGAAAAACA AGGCTGGGCT GTTTCCTTCC TTTGGGGTCA AGACAGAGGC
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278’ ACAGAAGGCC CAGGTCTGGG AGGTTGGATC ACCTCCGGCT GGATGTTGAG CCGGGTGGGA
     ********** ********** ********** ********** ********** **********
301″ ACAGAAGGCC CAGGTCTGGG AGGTTGGATC ACCTCCGGCT GGATGTTGAG CCGGGTGGGA

338’ GCCCAAACAG CAGGGGGCCC ACAGGAGGCC GGCCCAGGCA GCCTCGCGTC CACTTACCAG
     ********** ********** ********** ********** ********** **********
361″ GCCCAAACAG CAGGGGGCCC ACAGGAGGCC GGCCCAGGCA GCCTCGCGTC CACTTACCAG

398’ GCCAGGCCCA GGCACGTCCC CAGCGACAGC AGGCTCAGGC ACGTTCGGGG GTCTGCCCAG
     ********** ********** ********** ********** ********** **********
421″ GCCAGGCCCA GGCACGTCCC CAGCGACAGC AGGCTCAGGC ACGTTCGGGG GTCTGCCCAG

458’ CCCCCGCCTC CGCTGCTCCG GGCCACGGGG GTCTTCCCGC CCTCGCTCCG CTTCCCGGGC
     ********** ********** ********** ********** ********** **********
481″ CCCCCGCCTC CGCTGCTCCG GGCCACGGGG GTCTTCCCGC CCTCGCTCCG CTTCCCGGGC

518’ TCCGCAGCAG GGGCTCCCTT GGGCCCCGAC TTCTTCCGGC TCTTCACCTC AGACATGTCT
     ********** ********** ********** ********** ********** **********
541″ TCCGCAGCAG GGGCTCCCTT GGGCCCCGAC TTCTTCCGGC TCTTCACCTC AGACATGTCT

578’ GGAGACCCTA GGACGACAAG CCCAGGGCAG CTTCTTCACC AGGGGGAGCA GGACGTGGCC
     ********** ****
601″ GGAGACCCTA GGAC
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1st Nucleotide Sequence
  File Name          : Reference Seq.gnu
  Sequence Size      : 5394

2nd Nucleotide Sequence
  File Name          : RDB7316R.fasta (Complementary)
  Sequence Size      : 621

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

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[98.637% / 587 bp]     INT/OPT.Score : <   1920/  2248 >

 661' GGGCGGTGAC CGCGCCCCCT CACAGACTTG GCACCGCCCA GAG--CCCAG CCCC-TTCCC
                                            **** ***  ***** **** *****
   1″   CCCCCCCT TCAACAAGAA CTTTGGGGCA CCCGGCCCCA GAGCCCCCAG CCCCTTTCCC

 718' TCT-CCCCGG CATCCTCGTT GCTTCACTGA GTCTTTCAGC TGCCAGCTCC ATAGTTCCCC
      *** ****** ********** ********** ********** ********** **********
  59″ TCTCCCCCGG CATCCTCGTT GCTTCACTGA GTCTTTCAGC TGCCAGCTCC ATAGTTCCCC

 777' TAGGAGAGGT GGGCGGCGAC CTCAACCCAC AGCGCCTTCC ACTGCGATAT TGCTCCAAAT
      ********** ********** ********** ********** ********** **********
 119″ TAGGAGAGGT GGGCGGCGAC CTCAACCCAC AGCGCCTTCC ACTGCGATAT TGCTCCAAAT

 837' CCGAGGAAAT TCAAACTCCC GGGCGCGCGC AGGCCGACGG GACCCGAGGA GGAGGGGCAG
      ********** ********** ********** ********** ********** **********
 179″ CCGAGGAAAT TCAAACTCCC GGGCGCGCGC AGGCCGACGG GACCCGAGGA GGAGGGGCAG

 897' GACGAAGGGG TCGCGCGCGC CACGTCGGGC GCGCCGCCGC TGCCCGAGTC CGGCATTGGT
      ********** ********** ********** ********** ********** **********
 239″ GACGAAGGGG TCGCGCGCGC CACGTCGGGC GCGCCGCCGC TGCCCGAGTC CGGCATTGGT

 957' GGGAACGCGG CGCGTCCCTG AGGCTTAGCC ACGCCCCGTC CGCGGGGTAG GCGGGCACTT
      ********** ********** ********** ********** ********** **********
 299″ GGGAACGCGG CGCGTCCCTG AGGCTTAGCC ACGCCCCGTC CGCGGGGTAG GCGGGCACTT

1017' CTACGCGCGC GGGCATGAGC CGTGGCAGGA GTGCGCGGCG GCAGCGGTGG CCGCCCCTTG
      ********** ********** ********** ********** ********** **********
 359″ CTACGCGCGC GGGCATGAGC CGTGGCAGGA GTGCGCGGCG GCAGCGGTGG CCGCCCCTTG

1077' GGGCTTGGGG TGTGTTTATT TGCATAAGCG GGCGCGCGCC GTCCGGGCTG GGTGGATCCG
      ********** ********** ********** ********** ********** **********
 419″ GGGCTTGGGG TGTGTTTATT TGCATAAGCG GGCGCGCGCC GTCCGGGCTG GGTGGATCCG

1137' GCGGGATTTG ACTGCTCCGC TGTCCAGAGG CGGAGAAGAA GAGGTAGCGA GTGGACGATC
      ********** ********** ********** ********** ********** **********
 479″ GCGGGATTTG ACTGCTCCGC TGTCCAGAGG CGGAGAAGAA GAGGTAGCGA GTGGACGATC

1197' AAG-ATCTGG CCTCGGCGGC CAAGCTTGGC A-ATCCGGTA CTGTTGGTAA AGCCACCATG
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      *** ****** ********** ********** * ******** ********** **********
 539″ AAGAATCTGG CCTCGGCGGC CAAGCTTGGC ACATCCGGTA CTGTTGGTAA AGCCACCATG

1255' GAAGATGCCA AAAACATTAA GAAGGGCCCA GCGCCATTCT ACCCACTCGA AGACGGGACC
      *** ****** ** ******* ***
 599″ GAACATGCCA AACACATTAA GAA
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