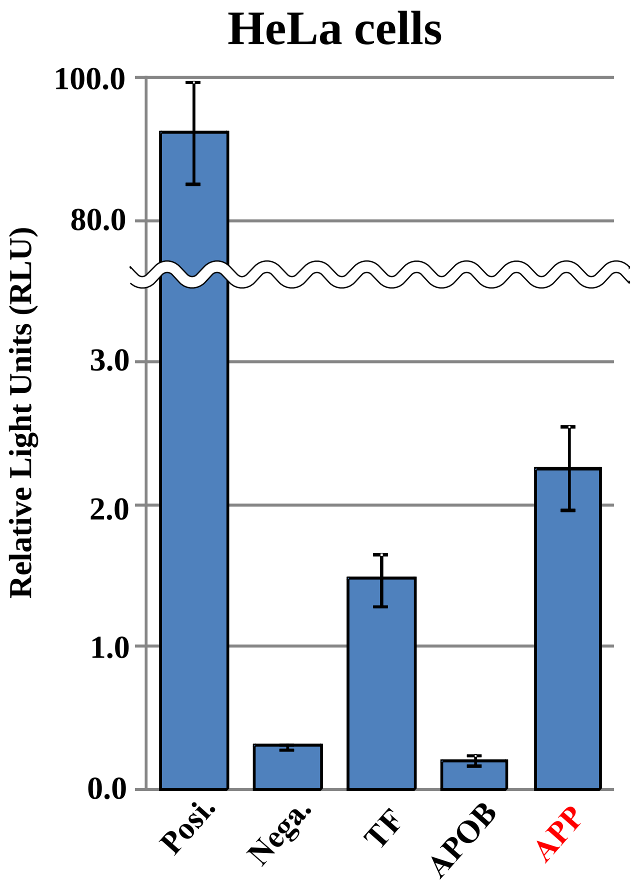
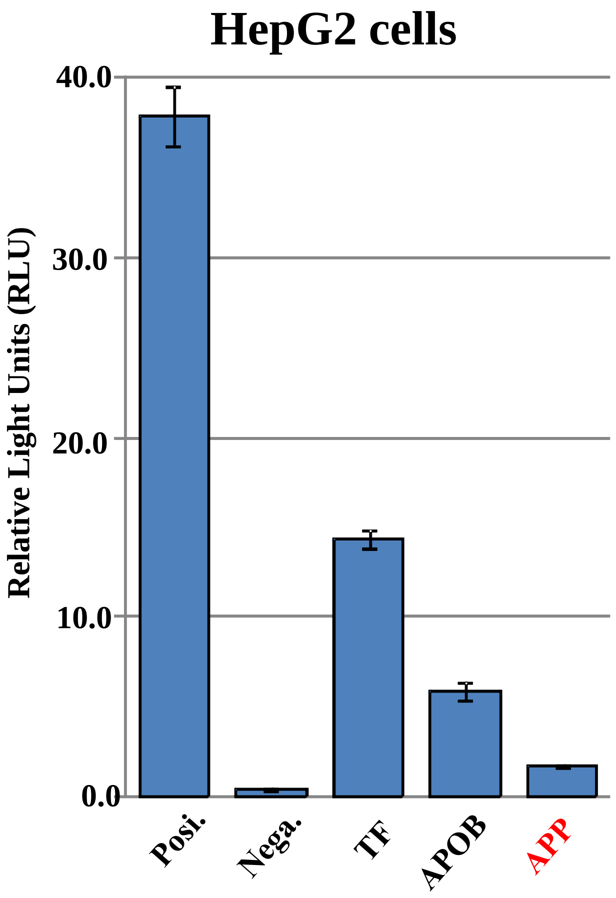
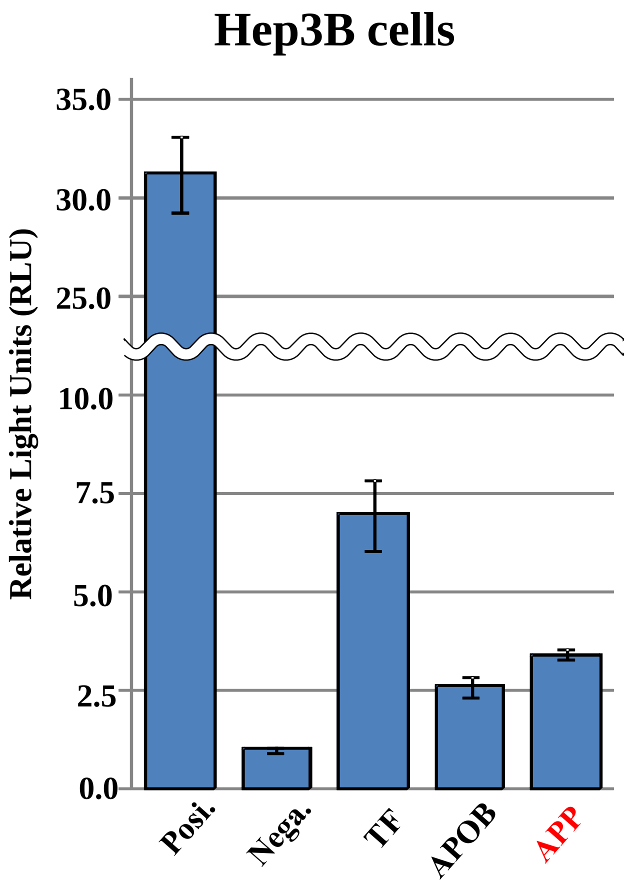
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

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

TF: pGL4-phTF (RDB# 7540)
APOB : pGL4-ph APOB (RDB# 7527)
APP : pGL4-ph APP(RDB# 7692)

2010, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.01.21

1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5714

2nd Nucleotide Sequence
  File Name        : RDB7692F.fasta
  Sequence Size    : 561

  Unit Size to Compare = 1
  Pick up Location     = 1



[98.117% / 531 bp]     INT/OPT.Score : <    600/  1994 >

      1'                                  GGCCTAACT GG-CCGGTAC CTGAGCTCGC
                                          ********* ** ******* **********
      1″ TAGAATGCTG TGCGGTGCCG AACTGTACTC TGGCCTAACT GGTCCGGTAC CTGAGCTCGC

     29' TAG-CCTCGA GGATCCTAGT GCGGGAAAAG ACACACAAGA CAACATTTAG GGGAGCTGGT
         *** ****** ********** ********** ********** ********** **********
     61″ TAGACCTCGA GGATCCTAGT GCGGGAAAAG ACACACAAGA CAACATTTAG GGGAGCTGGT

     88' ACAGAAATGA CTTCCCAGGA AGGAAGTCTG TACCCCGCTG GCTGAGCCAT CCTT-CCCGG
         ********** ********** ********** ********** ********** **** *****
    121″ ACAGAAATGA CTTCCCAGGA AGGAAGTCTG TACCCCGCTG GCTGAGCCAT CCTTCCCCGG

    147' GCCTAGGCAC CCTTGTCAGC GCAATGAGCA AGGGAGAGAA GGCAGGCTGC AGTGCAGCCC
         ********** ********** ********** ********** ********** **********
    181″ GCCTAGGCAC CCTTGTCAGC GCAATGAGCA AGGGAGAGAA GGCAGGCTGC AGTGCAGCCC

    207' TCAGAAGGGC CAGAGCACTC CCTGGCTTCA GTCCTTCGCT CCAAGCCCTG TGTGGAGT-G
         ********** ********** ********** ********** ********** ******** *
    241″ TCAGAAGGGC CAGAGCACTC CCTGGCTTCA GTCCTTCGCT CCAAGCCCTG TGTGGAGTCG
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266’ GGCTGTGGCT TGGTAACTAA ATGCTACTTC AGG-TCAAGA GCAGGGGATA TATCTGGGCA
     ********** ********** ********** *** ****** **********  *********
301″ GGCTGTGGCT TGGTAACTAA ATGCTACTTC AGGCTCAAGA GCAGGGGATA CATCTGGGCA

325’ GTTCTAGAGC ATTCTAAACT ATCTGGACAC TAACTGGACA GTGGACGGTT TGTGTTTAAT
     ********** ********** ********** ********** ********** **********
361″ GTTCTAGAGC ATTCTAAACT ATCTGGACAC TAACTGGACA GTGGACGGTT TGTGTTTAAT

385’ CCAGGAGAAA GTGGCATGGC AGAAGGTTCA TTTCTATAAT TCAGGACAGA CACAATGAAG
     ********** ********** ********** ********** ********** **********
421″ CCAGGAGAAA GTGGCATGGC AGAAGGTTCA TTTCTATAAT TCAGGACAGA CACAATGAAG

445’ AA-CAAGGGC AGCGTTTGAG GTCAGAAGTC CTCATTTACG GGGGTCGAAT ACGAATGATC
     ** ******* ********** ********** ********** ********** **********
481″ AACCAAGGGC AGCGTTTGAG GTCAGAAGTC CTCATTTACG GGGGTCGAAT ACGAATGATC

504’ TCTCCTAATT TTTCCTTCTT CCCCAACTCA GATGGATGTT ACATCCCTGC TTAACAACAA
     ********** ***  * *** **
541″ TCTCCTAATT TTT-TTCCTT CC




1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5714

2nd Nucleotide Sequence
  File Name        : RDB7692R.fasta (Complementary)
  Sequence Size    : 569

  Unit Size to Compare = 1
  Pick up Location     = 1


[98.759% / 564 bp]     INT/OPT.Score : <   1516/  2167 >
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1021’ CTTTTCTAGA GCCTCAGCGT CCTAGGACTC ACCTTTCCCT GATCCTGCAC CGTCCCTCTC
                       **** *.******** ********** ********** **********
   1″         CC TTTCAGGCGT CNTAGGACTC ACCTTTCCCT GATCCTGCAC CGTCCCTCTC

1081’ CTGGCCCCAG ACTCTCCCTC CCACTGTTCA CGAAGCCCAG GT-GGGCCGT CGGCCGGGGA
      ********** ********** ********** ********** ** ******* **********
  53″ CTGGCCCCAG ACTCTCCCTC CCACTGTTCA CGAAGCCCAG GTGGGGCCGT CGGCCGGGGA

1140’ GCGGAGGGGG CGCGTGGGGT GCAGGCGGCG CCAAGGGCGC GTGCACCTGT GGGCGCGGGG
      ********** ********** ********** **********  ********* **********
 113″ GCGGAGGGGG CGCGTGGGGT GCAGGCGGCG CCAAGGGCGC -TGCACCTGT GGGCGCGGGG

1200’ CGCGAGGGCC CCTCCCGGCG C-GAGCGGGC GCAGTTCCCC GGCGGCGCCG CTAGGGGTCT
      ********** ********** * ******** ********** ********** **********
 172″ CGCGAGGGCC CCTCCCGGCG CGGAGCGGGC GCAGTTCCCC GGCGGCGCCG CTAGGGGTCT

1259’ CTCTCGGGTG CCGAGCGGGG TGGGCCGGAT CAGCTGACTC GCCTGGCTCT GAGCCCCGCC
      ********** ********** ********** ********** ********** **********
 232″ CTCTCGGGTG CCGAGCGGGG TGGGCCGGAT CAGCTGACTC GCCTGGCTCT GAGCCCCGCC

1319’ GCCGCGCTCG GGCTCCGTCA GTTTCCTCGG CAGCGGTAGG CGAGAGCACG CGGAGGAGCG
      ********** ********** ********** ********** ********** **********
 292″ GCCGCGCTCG GGCTCCGTCA GTTTCCTCGG CAGCGGTAGG CGAGAGCACG CGGAGGAGCG

1379’ TGCGCGGGGG CCCCGGGAGA CGGCGGCGGT GGCGGCGCGG GCAGAGCAAG GACGCGGCGG
      ********** ********** ********** ********** ********** **********
 352″ TGCGCGGGGG CCCCGGGAGA CGGCGGCGGT GGCGGCGCGG GCAGAGCAAG GACGCGGCGG

1439’ ATCCCACTCG CACAGCAGCG CACTCGGTGC CCCGCGCAGG GTCGCGATGC TGCCCGGTTT
      ********** ********** ********** ********** ********** **********
 412″ ATCCCACTCG CACAGCAGCG CACTCGGTGC CCCGCGCAGG GTCGCGATGC TGCCCGGTTT

1499’ GGCACTGCTC CTGCTATCAA GATCTGGCCT CGGCGGCCAA GCTTGGCAAT CCGGTACTGT
      ********** ********** ********** ********** ** ******* **********
 472″ GGCACTGCTC CTGCTATCAA GATCTGGCCT CGGCGGCCAA GC-TGGCAAT CCGGTACTGT

1559’ TGGTAAAGCC ACCATGGAAG ATGCCAAAAA CATTAAGAAG GGCCCAGCGC CATTCTACCC
      **** ***** ********** ******** * **********
 531″ TGGT-AAGCC ACCATGGAAG ATGCCAAACA CATTAAGAAG
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