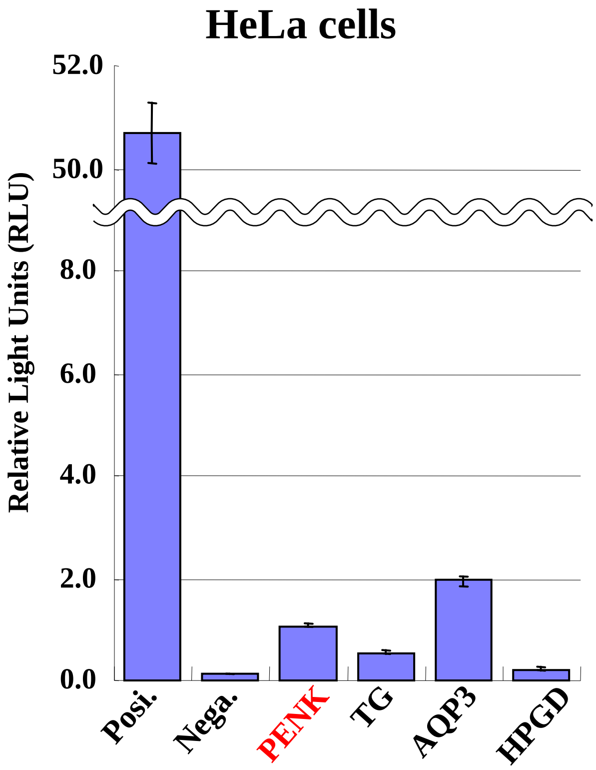
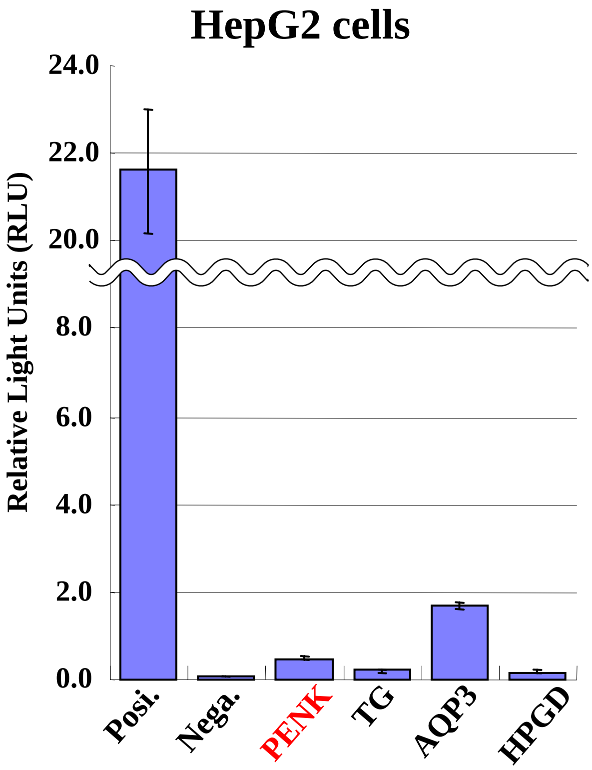
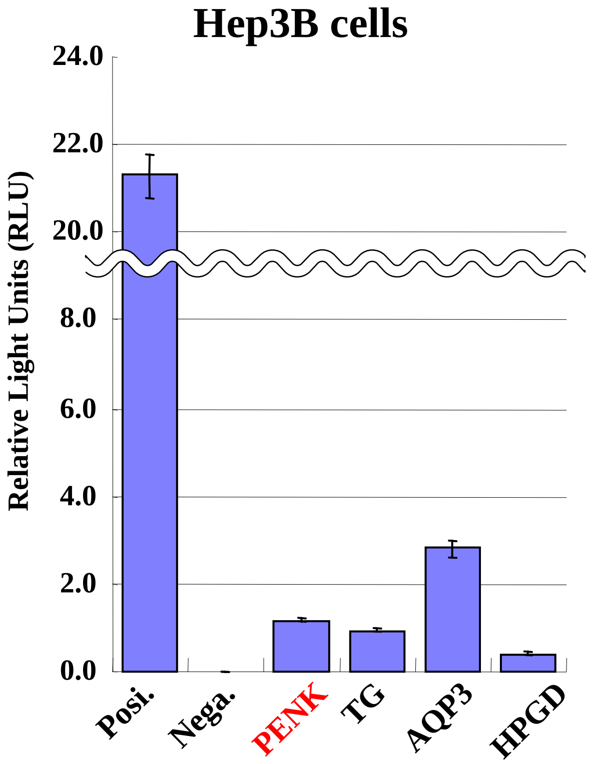
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

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

PENK: pGL4-phPENK (RDB#7293)
TG: pGL4-phTG(RDB#7304)
AQP3:pGL4-phAQP3 (RDB#7311)
HPGD: pGL4-phHPGD (RDB#7457)

2009, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.06.23

1st Nucleotide Sequence
  File Name         : Reference Seq.GNU
  Sequence Size     : 5524

2nd Nucleotide Sequence
  File Name         : RDB7293F.fasta
  Sequence Size     : 678

  Unit Size to Compare = 1
  Pick up Location     = 1



[85.959% / 584 bp]     INT/OPT.Score : <    459/  1548 >

    1’                       GGCCTAACTG GCCGGTACCT GAGCTCGCTA GCCTCG-AGG
                             ********** ********** ********** ****** ***
    1″ GTTGCCAGAA CATTGTCTCT GGCCTAACTG GCCGGTACCT GAGCTCGCTA GCCTCGTAGG

   40’ AT-TTAATT- GAGCGCCTAA ACTGCG-CAC CTTG-ACGCT GTT--AGATG CTGCANGTAA
       ** ******  ********** ****** *** **** ***** ***   **** *****.****
   61″ ATGTTAATTA GAGCGCCTAA ACTGCGACAC CTTGCACGCT GTTGACGATG CTGCATGTAA

   94’ GGAACTCGGA GTCAAGTGTG GGGGACAGGT TGGTCAATAA ATGACGNACA TTCCGGACGG
       ********** ********** ********** ********** ***** .*** **********
  121″ GGAACTCGGA GTCAAGTGTG GGGGACAGGT TGGTCAATAA ATGACTGACA TTCCGGACGG

  154’ CTGTGCTTGG TGCCCACGGG GACCCGCGAG GGGGCCCNAG GGAGGAGGCG GGAAAGGGGC
       ********** ********** ********** ******* ** ********** **********
  181″ CTGTGCTTGG TGCCCACGGG GACCCGCGAG GGGGCCC-AG GGAGGAGGCG GGAAAGGGGC

  214’ AGGTTCACCG GCCCGCTGGG TCTCCAGCNA CATTCCA-GA A-GTCTAA-G CCAGTCCATC
       * ******** ********** ******** * ******* ** * ****** * **********
  240″ ATGTTCACCG GCCCGCTGGG TCTCCAGC-A CATTCCACGA ATGTCTAACG CCAGTCCATC
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271’ TATCCTTCCA AACGCCCCCA CCNTCGCTTC CCTCCCTGGA GCCCGCATCC CACGGTGCAA
     ********** *** ****** **.  ***** ********** ** ******* **********
299″ TATCCTTCCA AACTCCCCCA CCTCAGCTTC CCTCCCTGGA GCTCGCATCC CACGGTGCAA

331’ TTT-CAGTGA -CTTTNATGC -GGAG-AAAC TTG-ATCC-T A-TCTCA--- -CTCTCCCCA
     *** ******  ** *.****  **** **** *** **** * * *****      *** *** *
359″ TTTACAGTGA GCTCTTATGC TGGAGCAAAC TTGAATCCTT ATTCTCACCT CCTCCCCCAA

380’ AAC-TTCCTA A-CT-GCCNT T-GGGTTT-G TCA--CCTGG CCGTGTG-GG GAGCCACCGA
     * * ****** * ** ***.* * ****** * ***  * *** ******* ** **********
419″ ACCTTTCCTA ACCTGGCCAT TGGGGTTTGG TCACCCTTGG CCGTGTGNGG GAGCCACCGA

432’ GCGCCCCCTG TGGCNCCCCA CCCGAGCTCG GCGGGGGGAG CGGCGCGCGG GTGCTGGGGG
     ********** *** . **** ********** ********** * *****  * *** * ****
479″ GCGCCCCCTG TGG-ATCCCA CCCGAGCTCG GCGGGGGGAG CTGCGCGATG GTGATCGGGG

492’ A-CCGANCCC CTCCCGCGAA GGCGTCGGCG CGGGGCTGGC GT-AGGGCCT GCGTCAGCNT
     * * **.*** ***** ** *  *  ***  *    **  * * **  ****** * * * * . 
538″ ATCTGACCCC CTCCC-CG-A CGAATCGCTG TCAGGTCGTC GTGGGGGCCT GGGGCCGATA

550’ GCAGCCCGCC GGCGATTGGG GCGCGCGCGC CTCCTTCGGT TTGGGGCTAN ATTATAAAGT
       **
596″ AGAGGGGCCA ACTTGCCCGN TCCGAAATCG TATTCGAAAA GCCCACCCGT CTCTGGGGGC

610’ GGCTCCAGCA GCCGTTAAGC CCCGGGACGG CGAGGCAGGC GCTCAGAGCC CCGCAGCCTG

656″ AGGAGTTAGC GTGGNGCTGA CCT
```

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1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5524

2nd Nucleotide Sequence
  File Name        : RDB7293R.fasta (Complementary)
  Sequence Size    : 724
```

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Unit Size to Compare = 1
Pick up Location     = 1



[97.083% / 720 bp]     INT/OPT.Score : <   1821/  2674 >

 661' CGCAGCCTGG CCCGTGACCC CGCAGAGACG CTGAGGACCG CGACGGTGA- -GGCCCTA-C
                                               **    ******   * ***** *
   1″                                     CCCCGCG AACCGGTGAN GGCCCCTACC

 718' GTCC--GCCA GCACACCC-- GGGCCCGC-T TCTCCCCGAC GCCCG-CCCT CCTCACACTT
      ****   *** *****.**   **.** ** * * ******** ***** **** **********
  28″ GTCCGGCCCA GCACANCCAG GGNCCGGCTT TTTCCCCGAC GCCCGCCCCT CCTCACACTT

 772' GCCTTCTTCT CTTCCCTCTA GAGTCGTGTC TGAACCCGGC TTTTCC-AAT TGGCCTGCTC
      ********** ********** ********** ********** ****** *** **********
  88″ GCCTTCTTCT CTTCCCTCTA GAGTCGTGTC TGAACCCGGC TTTTCCNAAT TGGCCTGCTC

 831' CATCCGAACA GCGTCAACGT GAGTGAATTT GCCCGAAGCT TGTCTTTGCT GAGCGGGTTT
      ********** ********** ********** ********** ********** **********
 148″ CATCCGAACA GCGTCAACGT GAGTGAATTT GCCCGAAGCT TGTCTTTGCT GAGCGGGTTT

 891' GGGGACGTCT GCCCGCCCTC TTTCCCTTCA CATTTCATTG CATGGGTTCC CCAACAGCGT
      ********** ********** ********** ********** ********** **********
 208″ GGGGACGTCT GCCCGCCCTC TTTCCCTTCA CATTTCATTG CATGGGTTCC CCAACAGCGT

 951' TCCCTGGTTC TTCTTTGTGA CCCCAGTCAA TGTCCTGCCT CCCCCGGCTC CCGCTCTCTC
      ********** ********** ********** ********** ********** **********
 268″ TCCCTGGTTC TTCTTTGTGA CCCCAGTCAA TGTCCTGCCT CCCCCGGCTC CCGCTCTCTC

1011' GCCCCTGGTC TGCGGCGTTC TCTCCGGAAT CTTGCCCTGG GCCGCGGACG CCCAGGAAAA
      ********** ********** ********** ********** ********** **********
 328″ GCCCCTGGTC TGCGGCGTTC TCTCCGGAAT CTTGCCCTGG GCCGCGGACG CCCAGGAAAA

1071' GAGCCGGGTG CCCCAGGCAG CCTCGCGTTG GGGGCGACCG CGCCATCCCG GGAACCGCGA
      ********** ********** ********** ********** ********** **********
 388″ GAGCCGGGTG CCCCAGGCAG CCTCGCGTTG GGGGCGACCG CGCCATCCCG GGAACCGCGA
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1131’ GGCGATCTGA GTCGCCTCCA CGTCTACCTA AAAGCTGTCG GCCGGGAGGG CGGGGCCCCA
      ********** **********  ********* ********** ********** **********
 448″ GGCGATCTGA GTCGCCTCCA GGTCTACCTA AAAGCTGTCG GCCGGGAGGG CGGGGCCCCA

1191’ GAAAGGAGCA TTCCTGCGGG CTTTTGCTCG ACGATCCCCT GCTGAGGCTG TCGCGGCGAG
      ********** ********** ********** ********** ********** **********
 508″ GAAAGGAGCA TTCCTGCGGG CTTTTGCTCG ACGATCCCCT GCTGAGGCTG TCGCGGCGAG

1251’ GGTCCTGCCG AGGGACCCCG TTCTGCGCCC AGGCAGGCTC GAAGCACGCG TCCCTCTCTC
      ********** ***** **** ********** ********** ********** **********
 568″ GGTCCTGCCG AGGGA-CCCG TTCTGCGCCC AGGCAGGCTC GAAGCACGCG TCCCTCTCTC

1311’ CTCGCAGTCC ATGATCAAGA TCTGGCCTCG GCGGCCAAGC TTGGCAATCC GGTACTGTTG
      ********** ********** ********** ********** ********** **********
 627″ CTCGCAGTCC ATGATCAAGA TCTGGCCTCG GCGGCCAAGC TTGGCAATCC GGTACTGTTG

1371’ GTAAAGCCAC CATGGAAGAT GCCAAAAACA TTAAGAAGGG CCCAGCGCCA TTCTACCCAC
      ********** ********** ********** ********
 687″ GTAAAGCCAC CATGGAAGAT GCCAAAAACA TTAAGAAG
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