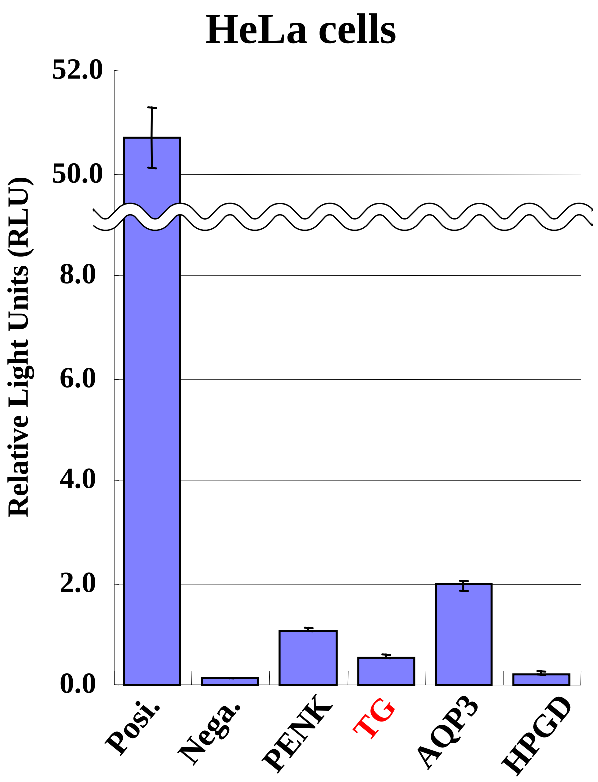
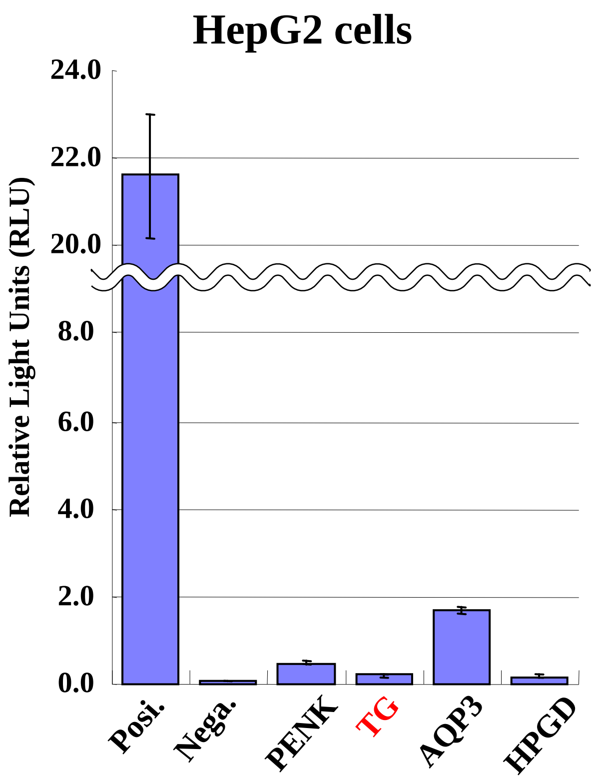
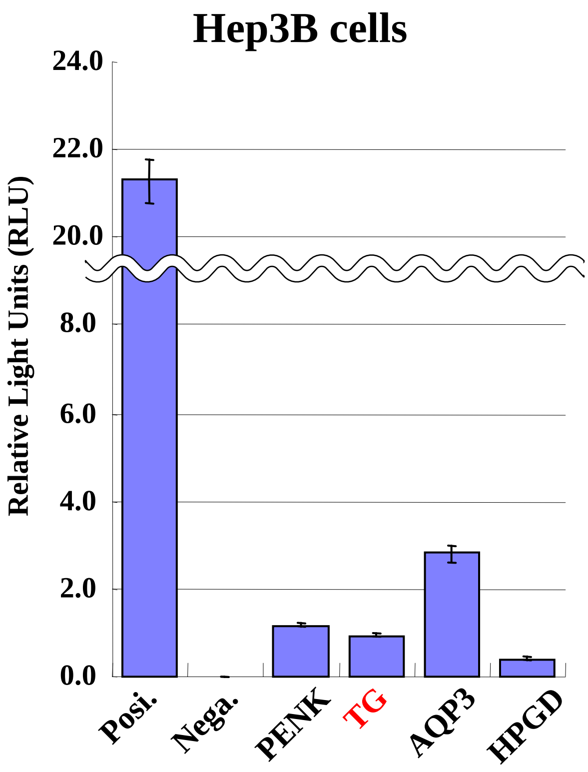
The Promoter Activities of Reporter Constructs


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 : 2009.06.25

1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5429

2nd Nucleotide Sequence
  File Name        : RDB7304F.fasta
  Sequence Size    : 498

  Unit Size to Compare = 1
  Pick up Location     = 1



[98.152% / 487 bp]     INT/OPT.Score : <    282/  1804 >

      1'                    GG CCTAACTGG- CCGGTACCTG AGCTCGCTAG CCTCGAGGAT
                            ** *********  ********** ********** **********
      1" TGCCAGAACA TTTACTCTGG CCTAACTGGT CCGGTACCTG AGCTCGCTAG CCTCGAGGAT

     42' GATTCTCACA GGTCCCTCCA TCTCTCCTCA GGTGCCAGGC NTCAGCAACC TGCCCTCATT
         ********** ********** ********** **********  ********* **********
     61" GATTCTCACA GGTCCCTCCA TCTCTCCTCA GGTGCCAGGC -TCAGCAACC TGCCCTCATT

    102' ACCTGCCAGT TCCTGACCCT ATCTGTCACT ANGCTCCTTA CCTGGCTGGA TTGGTCTTCT
         ********** ********** ********** * ******** ********** **********
    120" ACCTGCCAGT TCCTGACCCT ATCTGTCACT A-GCTCCTTA CCTGGCTGGA TTGGTCTTCT

    162' GAATACTTGC CATTCCCTGG CANTGATGCT TTTGCAAAAT AAGAAAATCA ATAATAATAA
         ********** ********** ** ******* ********** ********** **********
    179" GAATACTTGC CATTCCCTGG CA-TGATGCT TTTGCAAAAT AAGAAAATCA ATAATAATAA

    222' TAATAACTGC TAGNTGTCTA ATAAGCATGT GCTCTTCAAT GTCTATTCTC TTACAACTAC
         ********** *** ****** ********** ********** ********** **********
    238" TAATAACTGC TAG-TGTCTA ATAAGCATGT GCTCTTCAAT GTCTATTCTC TTACAACTAC
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    282' CTTANACAAA TAGGGACATA TTATTATTCT CCTTTTAACT TTGCTTTCCA GAGAANGGAG
         **** ***** ********** ********** ********** ********** ***** ****
    297″ CTTA-ACAAA TAGGGACATA TTATTATTCT CCTTTTAACT TTGCTTTCCA GAGAA-GGAG

    342' GCTGGGGCTC AGGGAGATGA GGTGAGTTTT TCCAGGTCTC ACAGGANACA GGACTGAAGG
         ********** ********** ********** ********** ****** *** **********
    355″ GCTGGGGCTC AGGGAGATGA GGTGAGTTTT TCCAGGTCTC ACAGGA-ACA GGACTGAAGG

    402' AAGGAAGCCA TGTTTGCCAG GAGAAACCAA ATGGACANTA CAGGCTTTCT GTGGAATACA
         ********** ********** ********** ******* ** ********** **********
    414″ AAGGAAGCCA TGTTTGCCAG GAGAAACCAA ATGGACA-TA CAGGCTTTCT GTGGAATACA

    462' CAGTTCCTGC TATCTTTTGG TTGACAAANG TCTGAGGTCC TAGGAAAGAG AGGAAAGTAA
         ********** ********** *****
    473″ CAGTTCCTGC TATCTTTTGG TTGACC





1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5429

2nd Nucleotide Sequence
  File Name        : RDB7304R.fasta (Complementary)
  Sequence Size    : 444

  Unit Size to Compare = 1
  Pick up Location     = 1



[97.561% / 451 bp]     INT/OPT.Score : <    428/  1638 >

    841' AAGGAGNGAA GGAGAAGGAG AAAGGGTAGG GTGGGGAAGG AAAGAACAAA GGATTGCNTT
                                ********* ********** ********** ******* **
      1″                        AAGGGTAGG GTGGGGAAGG AAAGAACAAA GGATTGC-TT
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 901’ TTCCCTCACT GTGGGCTTGA GCCTGTTCCC TCCAAAGATA CAGAGCTTNT GGTCTTTACC
      ********** ********** ********** ********** ******** * **********
  39″ TTCCCTCACT GTGGGCTTGA GCCTGTTCCC TCCAAAGATA CAGAGCTT-T GGTCTTTACC

 961’ CATAAAAAAG GATTTTGAAG TCACCCCACC CCGTTCTGTN TCCCCCACAG TTTAGACAAG
      ********** ********** ********** *********  ********** **********
  98″ CATAAAAAAG GATTTTGAAG TCACCCCACC CCGTTCTGT- TCCCCCACAG TTTAGACAAG

1021’ ATCCTCATGC TCCACTGGCC ACACGAGTGC NCCTCAGGAG GAGTAGACAC AGGTGGAGGG
      ********** ********** **********  ********* ********** **********
 157″ ATCCTCATGC TCCACTGGCC ACACGAGTGC -CCTCAGGAG GAGTAGACAC AGGTGGAGGG

1081’ AGCTCCTTTT GACCAGCAGA GNAAAACAGG ATGGGGCACT GCCTCACTGA GGACCTGGGG
      ********** ********** * ******** ********** ********** **********
 216″ AGCTCCTTTT GACCAGCAGA G-AAAACAGG ATGGGGCACT GCCTCACTGA GGACCTGGGG

1141’ GTGGGAAGGA AANGTGCCAA CGGCAGCTCT ATAAAAGCTC CCTGGCCAGG GG-ACCTAGG
      ********** ** ******* ********** ********** ********** ** *******
 275″ GTGGGAAGGA AA-GTGCCAA CGGCAGCTCT ATAAAAGCTC CCTGGCCAGG GGAACCTAGG

1200’ GCAANGCAGT GGTTTCTCCT CCTTCCTCCA TCAAGATCTG GCCTCGGCGG CCAAGCTTGG
      **** ***** ********** ********** ********** ********** **********
 334″ GCAA-GCAGT GGTTTCTCCT CCTTCCTCCA TCAAGATCTG GCCTCGGCGG CCAAGCTTGG

1260’ C-AATCCGGT ACTGTTGGTA AAGCCACCAT GGAAGATGCC AAA-AACATT AAGAAGGGCC
      * ******** ********** ********** **** ***** *** ****** **
 393″ CAAATCCGGT ACTGTTGGTA AAGCCACCAT GGAACATGCC AAACAACATT AA
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