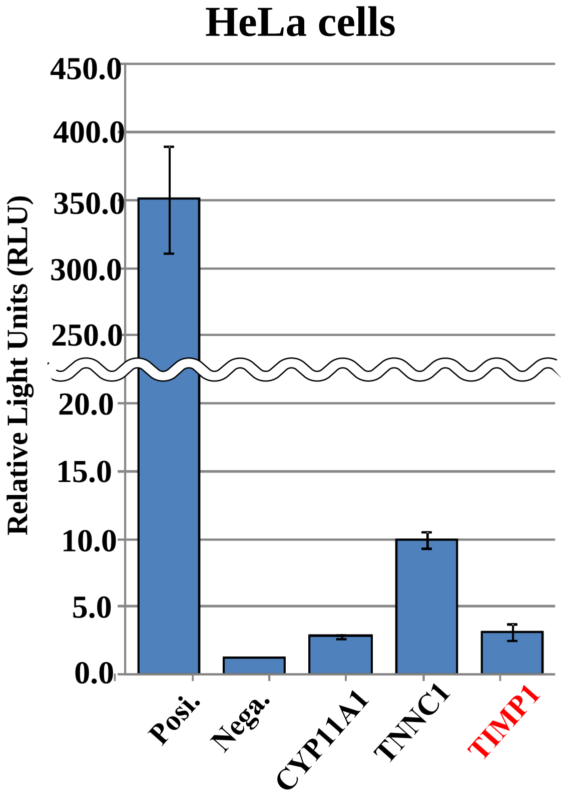
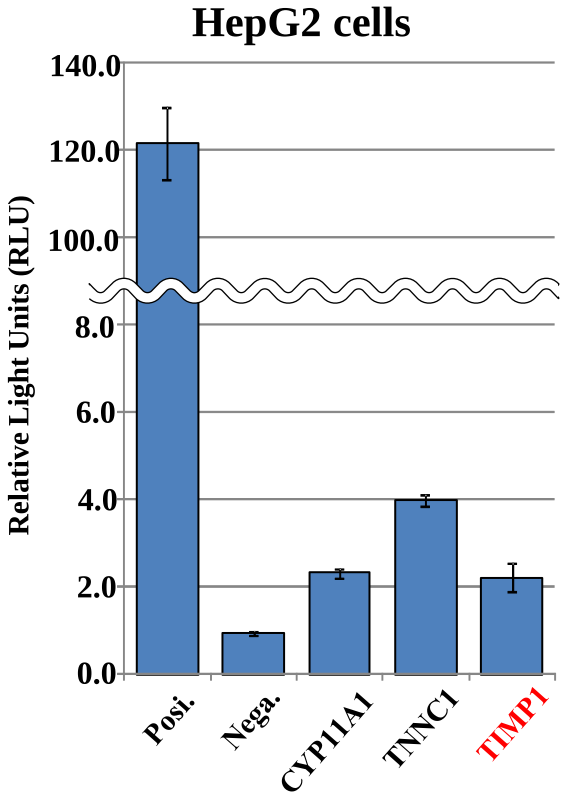
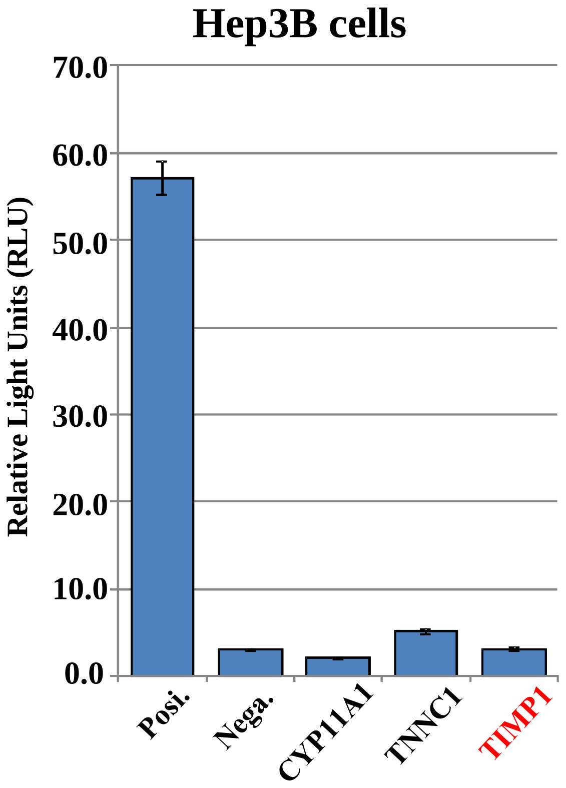
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

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

CYP11A1: pGL4-phCYP11A1 (RDB# 7460)
TNNC1: pGL4-phTNNC1 (RDB# 7517)
TIMP1: pGL4-phTIMP1 (RDB# 7516)

2010, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.09.30
1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5594

2nd Nucleotide Sequence
  File Name         : RDB7516F.fasta
  Sequence Size     : 707

  Unit Size to Compare = 1
  Pick up Location     = 1
[97.869% / 704 bp]     INT/OPT.Score : <    288/  2589 >

    1'                    GGC CTAACTGGCC GGTACCTGAG CTCGCTAGCC TCGAGGATGG
                          *** ********** ********** ********** **********
    1″ GTGCACGAAC TTTCTCTGGC CTAACTGGCC GGTACCTGAG CTCGCTAGCC TCGAGGATGG

   44' GCTTTTAGTG TCCCCATCAA CCAAATAGTN GTACATTGTA CCCATTAGGC AATTTCTCAT
       ********** ********** *********  ********** ********** **********
   61″ GCTTTTAGTG TCCCCATCAA CCAAATAGT- GTACATTGTA CCCATTAGGC AATTTCTCAT

  104' CCCTCACATT CCTCCCACCC NAGAATAGTG CTGGATACGC AGTAAGCACT CCATAAGGGC
       ********** **********  ********* ********** ********** **********
  120″ CCCTCACATT CCTCCCACCC -AGAATAGTG CTGGATACGC AGTAAGCACT CCATAAGGGC

  164' TGCTGGTAGT TNTTTGTTGT GTTCTTGTTA TTGGGCTATC ATCCCTGAGT TAATCAAACT
       ********** * ******** ********** ********** ********** **********
  179″ TGCTGGTAGT T-TTTGTTGT GTTCTTGTTA TTGGGCTATC ATCCCTGAGT TAATCAAACT

  224' TANATTAGCA AGGGAGTATG GTGAGTGAAT GAGATAATTT ATACAAACAC TTTNAGCACA
       ** ******* ********** ********** ********** ********** *** ******
  238″ TA-ATTAGCA AGGGAGTATG GTGAGTGAAT GAGATAATTT ATACAAACAC TTT-AGCACA

  284' TAGTACACAG AAAGTGCTCA ATAAGTGGCT GCCATCATCA CTACNAATTA TTATTATTGA
       ********** ********** ********** ********** **** ***** **********
  296″ TAGTACACAG AAAGTGCTCA ATAAGTGGCT GCCATCATCA CTAC-AATTA TTATTATTGA
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344' TCTATCCTCC TCGAATTAAG GATGTTAATC AGAACNCCCA GGGAAGGTTC CTGCATTGTC
     ********** ********** ********** ***** **** ********** **********
355″ TCTATCCTCC TCGAATTAAG GATGTTAATC AGAAC-CCCA GGGAAGGTTC CTGCATTGTC

404' AGAAAGCTGG TGGGCAAGGA TTGCCCNCAC CCCACCCCCC ACCAGGGGTA CAGGTCCATG
     ********** ********** ****** *** ********** ********** **********
414″ AGAAAGCTGG TGGGCAAGGA TTGCCC-CAC CCCACCCCCC ACCAGGGGTA CAGGTCCATG

464' GGGAGGGGGC AGGGCAGNGA TGGGGTGGGG ATTAGTTTTC TACTGACCCA CTCACTTGCT
     ********** ******* ** ********** ********** ********** **********
473″ GGGAGGGGGC AGGGCAG-GA TGGGGTGGGG ATTAGTTTTC TACTGACCCA CTCACTTGCT

524' TCTTTCACNC ATCATTCATG GCCACCCCCT TCCCAATGCT CATTCATTCA CCCGCACCAN
     ******** * ********** ********** ********** ********** *********
532″ TCTTTCAC-C ATCATTCATG GCCACCCCCT TCCCAATGCT CATTCATTCA CCCGCACCA-

584' TTCCCTGCTT GCTAGGACGG TGCCACTCCT GAGTTACAAC CCTGGTGCCA NGGTAGCCTC
     ********** ********** ********** ********** **********  *********
590″ TTCCCTGCTT GCTAGGACGG TGCCACTCCT GAGTTACAAC CCTGGTGCCA -GGTAGCCTC

644' TGTTTGAATC CCGGCCATGC CCTGTGATCT TAGGAAAATT CNTACAGTTC CTCTACGCCC
     *********  ********** ********** ********** * ******** * ********
649″ TGTTTGAAT- CCGGCCATGC CCTGTGATCT TAGGAAAATT C-TACAGTTC CNCTACGCCC

704' CATATTTCCT CATCCGTAAA ACGGGAATAA GANACCGGTA CCCATCTCAG AGATTTGTTG
     *
707″ C
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1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5594

2nd Nucleotide Sequence
  File Name        : RDB7516R.fasta (Complementary)
  Sequence Size    : 821
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  Unit Size to Compare = 1
  Pick up Location     = 1
[96.655% / 837 bp]     INT/OPT.Score : <    530/  2996 >

 601' CGGTGCCACT CCTGAGTTAC AACCCTGGTG CCANGGTAGC CTCTGTTTGA ATCCCGGCCA
                                                   ***   ***** ****
   1"                                              TTTTG ATCCC-GCCA

 661' TGCCCTGTGA TCTTAGGAAA ATTCNTACAG TTCCTCTACG CCCCATATTT CCTCATCCGT
      ******* ** ** ** **** **** ***** *** ***.**  ********* **********
  15" TGCCCTG-GA TC-TA-GAAA ATTC-TACAG TTCTTCTNCG -CCCATATTT CCTCATCCGT

 721' AAAACGGGAA TAAGANACCG GTACCCATCT CAGAGATTTG TTGTGAGCTT TGAGTGAGAT
      ***** **** * ***. *** ********** ********** **********  *********
  70" AAAAC-GGAA TTAGAACCCG GTACCCATCT CAGAGATTTG TTGTGAGCTT GGAGTGAGAT

 781' AAACTANTGC TGAGTGCCTG GTATACAGTA GGTGCTGTAT AAATGCCGGC TATTTGCNCT
      ****** *** ********** ********** ********** ********** ******* **
 129" AAACTA-TGC TGAGTGCCTG GTATACAGTA GGTGCTGTAT AAATGCCGGC TATTTGC-CT

 841' GTGTTATTTG AGACCCTGGC TTTGGCTCCT GGCCACCTGA GTTCCAGTNC TCAGTTCTGC
      ********** ********** ********** ********** ******** * **********
 187" GTGTTATTTG AGACCCTGGC TTTGGCTCCT GGCCACCTGA GTTCCAGT-C TCAGTTCTGC

 901' CATGTATTGA CTCTGTGATC CTGGGTAAGT CACTTAACCN ACTCCGTGCC TCAGTTTCCC
      ********** ********** ********** *********  ********** **********
 246" CATGTATTGA CTCTGTGATC CTGGGTAAGT CACTTAACC- ACTCCGTGCC TCAGTTTCCC

 961' CATTTTGTAT TCCTCCCCTT TCACCTGCCT NTATCTCCCT CCACTGCTGC TACTTAATTT
      ********** ********** **********  ********* ********** **********
 305" CATTTTGTAT TCCTCCCCTT TCACCTGCCT -TATCTCCCT CCACTGCTGC TACTTAATTT

1021' GTTTCCTCTC TGCCACCCCT CNACCAGCAT GTCAGACATA CAAAACAAGG GATTTTTGTG
      ********** ********** * ******** ********** ********** **********
 364" GTTTCCTCTC TGCCACCCCT C-ACCAGCAT GTCAGACATA CAAAACAAGG GATTTTTGTG

1081' TGCTTGGCAC ACNAGTAGAT GCACAATAAA TGTTGAAGGG CTGAACTAAT TTGGGTTTGA
      ********** ** ******* ********** ********** ********** **********
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 423″ TGCTTGGCAC AC-AGTAGAT GCACAATAAA TGTTGAAGGG CTGAACTAAT TTGGGTTTGA

1141' GTCNATAGGG AGCTTGGGGG ATGTGGGTGA TTGGATAGAT TCTGGAGACT TTAGNGGGAC
      *** ****** ********** ********** ********** ********** **** *****
 482″ GTC-ATAGGG AGCTTGGGGG ATGTGGGTGA TTGGATAGAT TCTGGAGACT TTAG-GGGAC

1201' TGGGCCGGGG GAAATGCGGC CTCTAAGCTC TCCGCTGAGG CGGCTNTGGA AGGAATAGTG
      ********** ********** ********** ********** ***** **** **********
 540″ TGGGCCGGGG GAAATGCGGC CTCTAAGCTC TCCGCTGAGG CGGCT-TGGA AGGAATAGTG

1261' ACTGACGTGG AGGTGGGGGA GGTGGCTGGC CCGGGCNGAG GCCCAGGGAG AGGGAGAGGA
      ********** ********** ********** ****** *** ********** **********
 599″ ACTGACGTGG AGGTGGGGGA GGTGGCTGGC CCGGGC-GAG GCCCAGGGAG AGGGAGAGGA

1321' GGCGGGTGGG AGAGGAGGAG GGTGTATNCT CCTTTCGTCG GCCCGCCCCT TGGCTTCTGC
      ********** ********** ******* ** ********** ********** **********
 658″ GGCGGGTGGG AGAGGAGGAG GGTGTAT-CT CCTTTCGTCG GCCCGCCCCT TGGCTTCTGC

1381' ACTGATGGTG GGTATCAAGA TCTGGCCTCG GCGGCCAAGC TTGGCAATCC GGTACTGTTG
      ********** ********** ********** ********** ********** **********
 717″ ACTGATGGTG GGTATCAAGA TCTGGCCTCG GCGGCCAAGC TTGGCAATCC GGTACTGTTG

1441' GTAAAGCCAC CATGGAAGAT GCCAAAAACA TTAAGAAGGG CCCAGCGCCA TTCTACCCAC
      ********** ********** ********** *********  **
 777″ GTAAAGCCAC CATGGAAGAT GCCAAAAACA TTAAGAAGGA CCACT
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