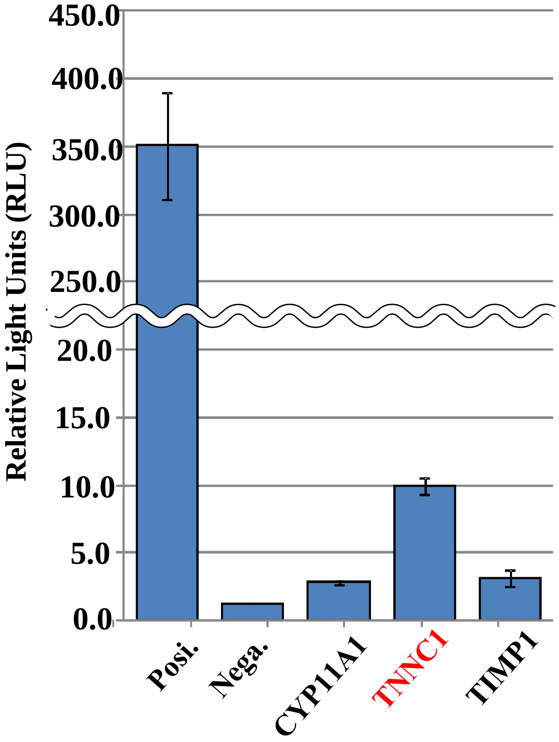
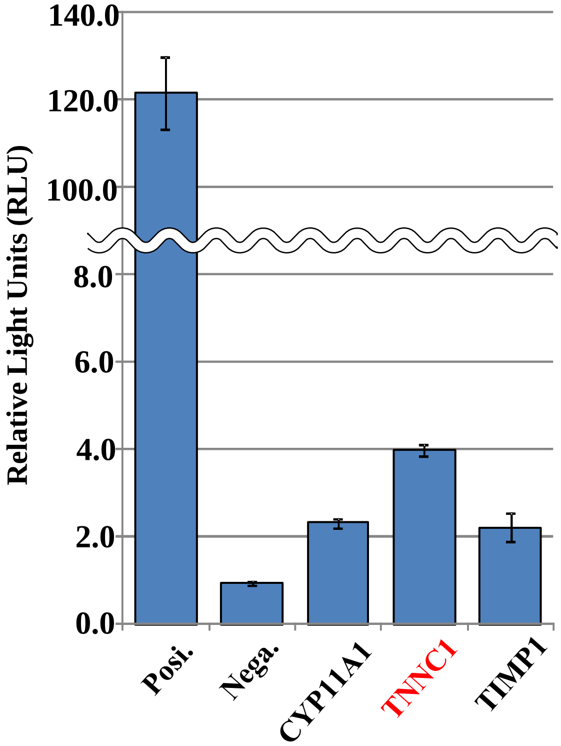
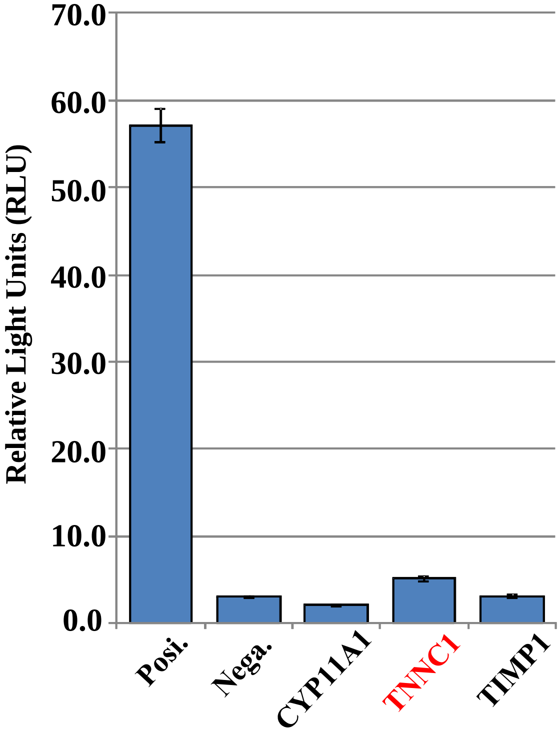
The Promoter Activities of Reporter Constructs



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     : 5638

2nd Nucleotide Sequence
  File Name         : RDB7517F.fasta
  Sequence Size     : 684

  Unit Size to Compare = 1
  Pick up Location     = 1
[91.743% / 545 bp]     INT/OPT.Score : <    353/  1723 >

     1’               GGCCTAA CTGGCCGGTA CCTGAGCTCG CTAGCCTCGA GGAT-TGGTG
                      ******* ********** ********** ********** **** *****
     1″ GAACATTGTC TCTGGCCTAA CTGGCCGGTA CCTGAGCTCG CTAGCCTCGA GGATGTGGTG

    47’ ACAGCTCTGG GCATCGCCCN CTGGGT-CCT CGGGAAGAGG GGACAGAAGG TCCCGAGTCT
        ********** ****   **. ****** *** ********** ********** **********
    61″ ACAGCTCTGG GCATGCGCCC CTGGGTGCCT CGGGAAGAGG GGACAGAAGG TCCCGAGTCT

   106’ CCCAGGCCAC ANCGAAGCAA GTCACTGCTC TTCCTGGCCT CAGTTTACTC CTCCTGATAA
        ********** * ******** ********** ********** ********** **********
   121″ CCCAGGCCAC A-CGAAGCAA GTCACTGCTC TTCCTGGCCT CAGTTTACTC CTCCTGATAA

   166’ AGNGAGGCCA TAATAGTGCC TCACCTGGCT GTTGGGCTCT TTCTCTTTAG GGCNAAGGCA
        ** ******* ********** ********** ********** ********** *** ******
   180″ AG-GAGGCCA TAATAGTGCC TCACCTGGCT GTTGGGCTCT TTCTCTTTAG GGC-AAGGCA

   226’ GGTTGGAGGG GAAAATAGGA CCTGTGCTTA CCGCCGGAGC AGGGNCGAGA GTGATTCTGG
        ********** ********** ********** ********** **** ***** **********
   238″ GGTTGGAGGG GAAAATAGGA CCTGTGCTTA CCGCCGGAGC AGGG-CGAGA GTGATTCTGG

   286’ GCCAGTTCTG AACCTCTCTG AGATTCGGAG ATCTCNTTGT CAGTGGGGCT TCTGGACAAC
        ********** ********** ********** ***** **** ********** **********
   297″ GCCAGTTCTG AACCTCTCTG AGATTCGGAG ATCTC-TTGT CAGTGGGGCT TCTGGACAAC
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346' TGAGTGGGTT GATTGATGCG CGGCCCNAGC ACGCAG--TA GTGCTCGAGG CAGGGAGCGT
     ******** * ********** ****** *** **** *   * ********** **********
356" TGAGTGGGCT GATTGATGCG CGGCCC-AGC ACGCGGCCCA GTGCTCGAGG CAGGGAGCGT

404' GTTTATCAAG AGGGATAAAN CTTGATACGA ACTCTGTACG AAGGAAGGTG TAGGTGGATG
     ********** *********  ********** ********** ********** **********
415" GTTTATCAAG AGGGATAAA- CTTGATACGA ACTCTGTACG AAGGAAGGTG TAGGTGGATG

464' GA-GGGGT-G TGNTG---CT GCCACTG--- -AGCACAAGA ACCCCAC--G GGGT--GGCC
     ** ***** * **.**   **  ** * *       ** ** *  **** *  * ****  * **
474" GAGGGGGTGG TGGTGTTCCT CCCCCCGAAC CCCCAAAAAA CCCCCCCGGG GGGTGGGCCC

511' TG-CCAAA-G TTCAAANACG AGGGAGACAG GTTGATCTGG ACCCAGGAAC TACAGTGCTG
     ** ***** * ******.*
534" TGCCCAAAGG TTCAAAAAAC CAAAGGGGAA AACCAGGGTT CCCCCCCCCC ACCCCCAAAA

569' AATCCTANAA CCGGGGAAAG ATGAGACCTA GAAGAGGGAG GTGGTAACCT AATTGGAGNG

594" AAACCCACAC ATCCCCTCCC ATTCCCTAAA ACCCCACGGG AACCCCCCCC ACCACCCCCC

629' GTGAGGAGGG AAAGAGCCTG CCACAGATGG GGCATCTATA GGGGTGCTGN TTGAATAACT

654" CAAAAAACGG AAAAGCTCAC TNNNCCNCNA T




1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5638

2nd Nucleotide Sequence
  File Name        : RDB7517R.fasta (Complementary)
  Sequence Size    : 700

  Unit Size to Compare = 1
  Pick up Location     = 1
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[97.737% / 707 bp]     INT/OPT.Score : <    505/  2612 >

  781’ CACCCTGTCC TAAGGTGGGT CAGTCACTTC CTCCTTCACC AGTTCCACAG NCATCTTACT
                                        ********* **********  *********
    1″                                 TTCCTTCACC AGTTCCACAG -CATCTTACT

  841’ ATGAGCTTGG CATTCGAGGC TTCTCTTGGC AGGGCCCTGC ANCTCCTAGC CTCTCCTTGC
       ********** ********** ********** ********** * ******** **********
   30″ ATGAGCTTGG CATTCGAGGC TTCTCTTGGC AGGGCCCTGC A-CTCCTAGC CTCTCCTTGC

  901’ ACATTGCACC CCCATTCCAG AGAGGTTTAG TTNAAAGGCG GGGGTTACCA AGTCAGTCAG
       ********** ********** * ******** ** ******* ********** **********
   89″ ACATTGCACC CCCATTCCAG AAAGGTTTAG TT-AAAGGCG GGGGTTACCA AGTCAGTCAG

  961’ ATCTTGGGCA AGTCACCACT CCTNCCAGAG CCTCAGTTTC CTTATCTGGA AAGTGGAGGT
       ********** ********** *** ****** ********** ********** **********
  148″ ATCTTGGGCA AGTCACCACT CCT-CCAGAG CCTCAGTTTC CTTATCTGGA AAGTGGAGGT

 1021’ CATGGCAACC CGCCNAACCT GGTTGGATGG GAGCCTGAGC TGTTGTGTTG CACCTTGCCT
       ********** **** ***** ********** ********** ********** **********
  207″ CATGGCAACC CGCC-AACCT GGTTGGATGG GAGCCTGAGC TGTTGTGTTG CACCTTGCCT

 1081’ GGGGCNCCAC GACTTTGTAG CTCCTGTCCT GCACTGGGCT TATGTTTTCA TTCATTNCCA
       ***** **** ********** ********** ********** ********** ****** ***
  266″ GGGGC-CCAC GACTTTGTAG CTCCTGTCCT GCACTGGGCT TATGTTTTCA TTCATT-CCA

 1141’ GAAACCTTTT CAGAGAGTCC CTTTGGGGAG TGTGGGGGAC AGGAGGGNAA AGAAACCTGG
       ********** ********** ********** ********** ******* ** **********
  324″ GAAACCTTTT CAGAGAGTCC CTTTGGGGAG TGTGGGGGAC AGGAGGG-AA AGAAACCTGG

 1201’ TCCTTGTAGC CGTTCGTCTG CTCCCTGCCC TGGGCAGANG GACGTGGGGA CTCAGGCCAG
       ********** ********** ********** ******** * *** ****** **********
  383″ TCCTTGTAGC CGTTCGTCTG CTCCCTGCCC TGGGCAGA-G GACATGGGGA CTCAGGCCAG

 1261’ CCTGAGATCA CTGGGACCAG AGGAGGGGCN TGGAGGATAC TACACGCAGG GGTGGGCTGG
       ********** ********** *********  ********** ********** **********
  442″ CCTGAGATCA CTGGGACCAG AGGAGGGGC- TGGAGGATAC TACACGCAGG GGTGGGCTGG

 1321’ GCTGGGCTGG GCTGGGCCAG NGAATGCAGC GGGGCAGGGC TATTTAAGTC AAGGGCCGGC
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      ********** **********  ********* ********** ********** **********
 501″ GCTGGGCTGG GCTGGGCCAG -GAATGCAGC GGGGCAGGGC TATTTAAGTC AAGGGCCGGC

1381' TGGCAACCCC ANGCAAGCTG TCCTGTGAGC CGCCAGCATG GATGACATCT ACAAGGCATC
      ********** * ******** ********** ********** ********** **********
 560″ TGGCAACCCC A-GCAAGCTG TCCTGTGAGC CGCCAGCATG GATGACATCT ACAAGGCATC

1441' AAGATCTGGC CTCGGCGGCC AAGCTTGGCA ATCCGGTACT GTTGGTAAAG CCACCATGGA
      ********** ********** ********** ********** ********** **********
 619″ AAGATCTGGC CTCGGCGGCC AAGCTTGGCA ATCCGGTACT GTTGGTAAAG CCACCATGGA

1501' AGATGCCAAA AACATTAAGA AGGGCCCAGC GCCATTCTAC CCACTCGAAG ACGGGACCGC
      **********  ***** *
 679″ AGATGCCAAA CACATTCACG AA
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