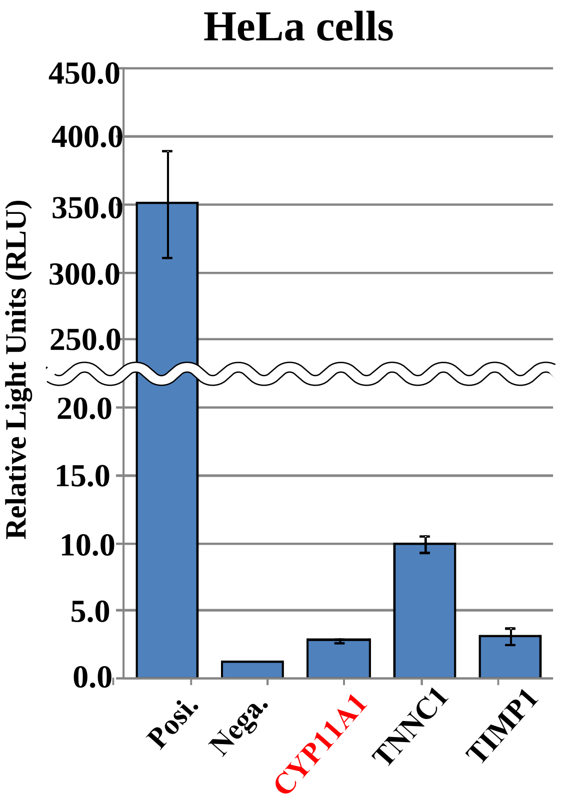
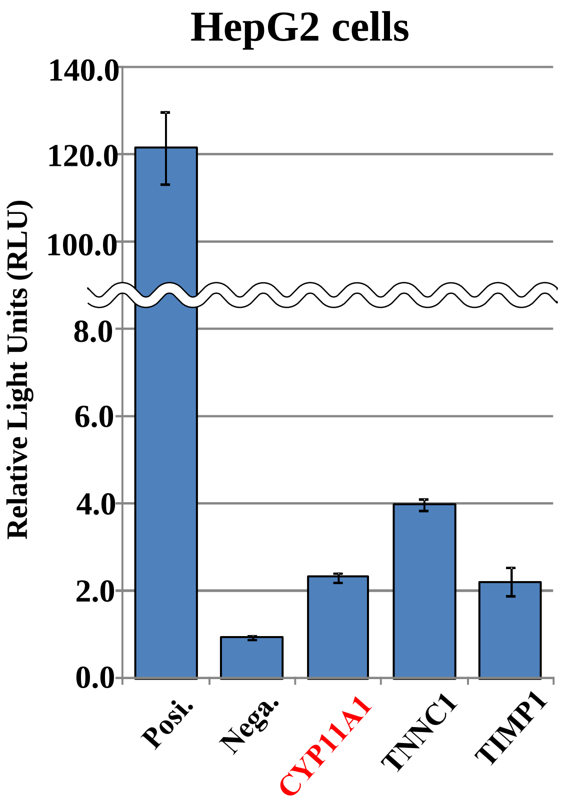
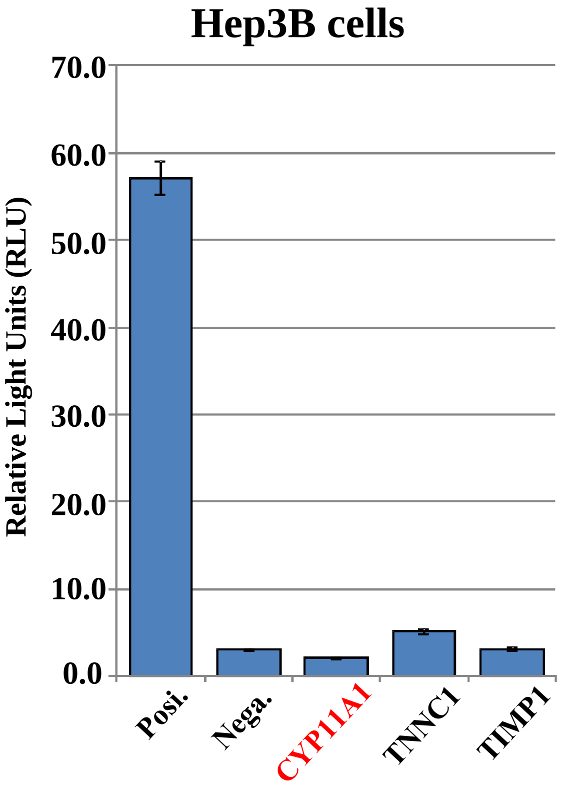
# The Promoter Activities of Reporter Constructs







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

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

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.07.13

1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5460

2nd Nucleotide Sequence
  File Name        : RDB7460F.fasta
  Sequence Size    : 502

  Unit Size to Compare = 1
  Pick up Location     = 1



[98.167% / 491 bp]     INT/OPT.Score : <   1899/  1910 >

     1’            GGCCTAACT GGCCGGTACC TGAGCTCGCT AGCCTCGAGG ATTGCAATTC
                   ********* ********** ********** ********** **********
     1″ ACATTGTCTC TGGCCTAACT GGCCGGTACC TGAGCTCGCT AGCCTCGAGG ATTGCAATTC

    50’ AATGGCTTTT AGTGTATCAG AGAGTTGTTC AATAATTACC ACAATATACT TTAGAATATT
        ********** ********** ********** ********** ********** **********
    61″ AATGGCTTTT AGTGTATCAG AGAGTTGTTC AATAATTACC ACAATATACT TTAGAATATT

   110’ TTCATTTTCA TCATCCTAAG AATCCCTACA CACTTTATGT CCCATCCTCT AATTCCTCTA
        ********** ********** ********** ********** ********** **********
   121″ TTCATTTTCA TCATCCTAAG AATCCCTACA CACTTTATGT CCCATCCTCT AATTCCTCTA

   170’ TCCCCCTAGC TCTAAGCAAC CACCAGTCTA TTTTCTGTCT CTTAGATGTG TGTTTTAAAT
        ********** ********** ********** ********** ********** **********
   181″ TCCCCCTAGC TCTAAGCAAC CACCAGTCTA TTTTCTGTCT CTTAGATGTG TGTTTTAAAT

   230’ GCCTTATTTG CCAGAAAATA AGATTTTGGG GAAAAAAAGC AAGAAGTTGT ACCTTCCAAT
        ********** ********** ********** ********** ********** **********
   241″ GCCTTATTTG CCAGAAAATA AGATTTTGGG GAAAAAAAGC AAGAAGTTGT ACCTTCCAAT
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    290’ GATAAGTATA AGGTATAGTG TAGATTGCTG TCATGAAATG CTCTACATGG CACATGTATG
         ********** ********** ********** ********** ********** **********
    301″ GATAAGTATA AGGTATAGTG TAGATTGCTG TCATGAAATG CTCTACATGG CACATGTATG

    350’ TTTTCTGACC TACACATTTT TACCAAGTGG GCTGTAATTT TGTTGAAATG ACTTGAAAAC
         ********** ********** ********** ********** ********** **********
    361″ TTTTCTGACC TACACATTTT TACCAAGTGG GCTGTAATTT TGTTGAAATG ACTTGAAAAC

    410’ TCTACAGGTG ACTGACCCTT GTTGTTTGGG AAAGTGGTAG GTGCAGGGTG ATGGGGGG--
         ********** ********** ********** ********** ********** ********
    421″ TCTACAGGTG ACTGACCCTT GTTGTTTGGG AAAGTGGTAG GTGCAGGGTG ATGGGGGGTG

    468’ TGGGTGTGGG GGCTGACCTG GGCTGGAAGG ATGGGTCTGG GGATATGATA TGATGGGAGG
         ********** ** .*. . . **
    481″ TGGGTGTGGG GGGNGNGNGN GG




1st Nucleotide Sequence
  File Name          : Reference Seq.gnu
  Sequence Size      : 5460

2nd Nucleotide Sequence
  File Name          : RDB7460.fasta (Complementary)
  Sequence Size      : 815

  Unit Size to Compare = 1
  Pick up Location     = 1
[98.403% / 814 bp]     INT/OPT.Score : <   2876/  3081 >

    541’ GCTCTGAGGG G-AAAGCAGC ACAGA-TCAA GTGTGTGG-A CAGGG-AAGA -GCTGACA-T
             ****** * *****.** ***** ***  ******** * ***** ****  ******* *
      1″     TGAGGG GAAAAGCNGC ACAGATTCAG GTGTGTGGAA CAGGGAAAGA GGCTGACATT

    595’ CCTGAG-TTC CATGGCAA-C CAGATTTGCC AAGG-TCTTA GAGTGTGTCC AGAGTGGAGC
         ****** *** ******** * ********** **** ***** ********** **********
     57″ CCTGAGTTTC CATGGCAACC CAGATTTGCC AAGGTTCTTA GAGTGTGTCC AGAGTGGAGC
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 652’ CTGACCACAG ACCTCAGCTC AAGGGACCCA GAGCCCCTCT GAGTCAGCTG TACTGAATTA
      ********** ********** ********** ********** ********** **********
 117″ CTGACCACAG ACCTCAGCTC AAGGGACCCA GAGCCCCTCT GAGTCAGCTG TACTGAATTA

 712’ CAGCCCCAAA TCTGGGTCAA CTGGGGAGAG ACGACGAGGA TTAGGGTTCC AAGGTGAAAC
      ********** ********** ********** ********** ********** **********
 177″ CAGCCCCAAA TCTGGGTCAA CTGGGGAGAG ACGACGAGGA TTAGGGTTCC AAGGTGAAAC

 772’ TGTGCCATTG CGCTCCAGCC TGGGCAACAA GAATGAAACT CTCTTAAAAT AAAATAAAAT
      ********** ********** ********** ********** ********** **********
 237″ TGTGCCATTG CGCTCCAGCC TGGGCAACAA GAATGAAACT CTCTTAAAAT AAAATAAAAT

 832’ AAAATAAAAT AAAATAAAAT AAAATAGCCT AAGGATGCAT TTCTCAGAAC TTATCCCTGT
      ********** ********** ********** ********** ********** **********
 297″ AAAATAAAAT AAAATAAAAT AAAATAGCCT AAGGATGCAT TTCTCAGAAC TTATCCCTGT

 892’ TGTTCAATGA TGTGTGTCTA TACAGTGGGG CCATAACTAA GACGTATGTT GCCCAAGCTG
      ********** ********** ********** ********** ********** **********
 357″ TGTTCAATGA TGTGTGTCTA TACAGTGGGG CCATAACTAA GACGTATGTT GCCCAAGCTG

 952’ GCAAGATAGC TCTGACCTTC TCTTGGGCCC CTCATTTCCC CCAAACACAG GTTGTCTGCA
      ********** ********** ********** ********** ********** **********
 417″ GCAAGATAGC TCTGACCTTC TCTTGGGCCC CTCATTTCCC CCAAACACAG GTTGTCTGCA

1012’ GTCTTGACCA ATGGCTGCCA GGGCATGGAC TCCGCTGCAG GGGCCAGTGG GAGGCCCCAG
      ********** ********** ********** ********** ********** **********
 477″ GTCTTGACCA ATGGCTGCCA GGGCATGGAC TCCGCTGCAG GGGCCAGTGG GAGGCCCCAG

1072’ CTCAGGCAAA AGCACAGGCA GATATTTCAG GAGTCTGCTA GGGCTGGCAC TGAGGGCAGA
      ********** ********** ********** ********** ********** **********
 537″ CTCAGGCAAA AGCACAGGCA GATATTTCAG GAGTCTGCTA GGGCTGGCAC TGAGGGCAGA

1132’ GACAGAGGGG TCTCCCTGTC CTTTGGAGAA CCTCACGCTG CAGAAATTCC AGACTGAACC
      ********** ********** ********** ********** ********** **********
 597″ GACAGAGGGG TCTCCCTGTC CTTTGGAGAA CCTCACGCTG CAGAAATTCC AGACTGAACC

1192’ TTCATACCGA GTAGGGGAGG AGCTGTCTGC GGGTTTGAGC CTGCAGCAGG AGGAAGGACG
      ********** ********** ********** ********** ********** **********
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 657″ TTCATACCGA GTAGGGGAGG AGCTGTCTGC GGGTTTGAGC CTGCAGCAGG AGGAAGGACG

1252' TGAACATTAT CAAGATCTGG CCTCGGCGGC CAAGCTTGGC AATCCGGTAC TGTTGGTAAA
      ********** ********** ********** ********** ********** **********
 717″ TGAACATTAT CAAGATCTGG CCTCGGCGGC CAAGCTTGGC AATCCGGTAC TGTTGGTAAA

1312' GCCACCATGG AAGATGCCAA AAACATTAA- GAAGGGCCCA GCGCCATTCT ACCCACTCGA
      ********** ********** *********  **** ***
 777″ GCCACCATGG AAGATGCCAA AAACATTAAT GAAGAGCCA
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