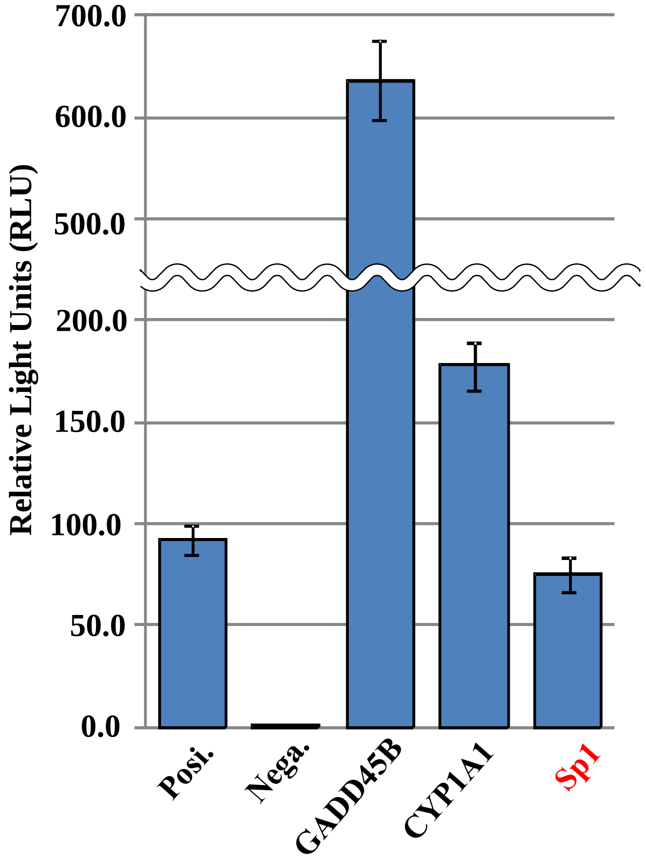
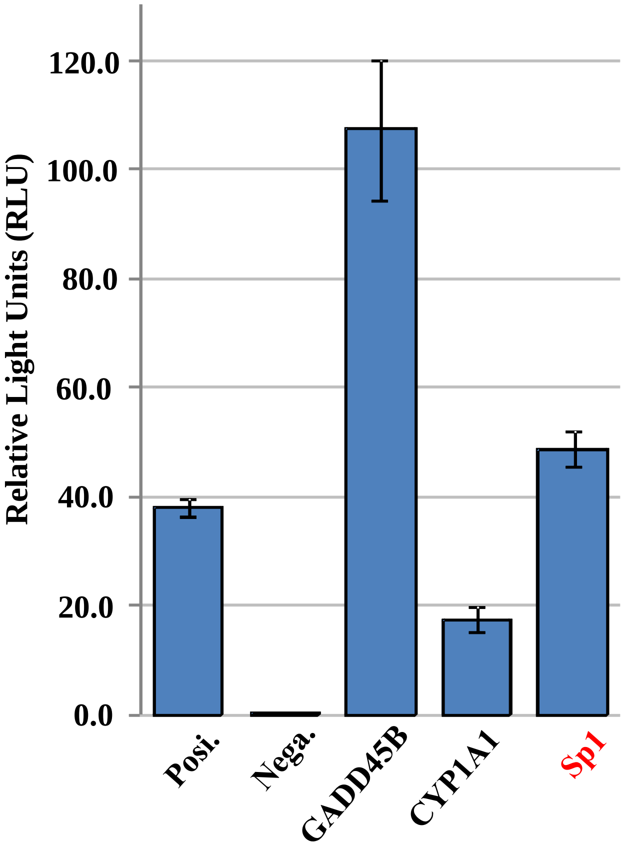
The Promoter Activities of Reporter Constructs

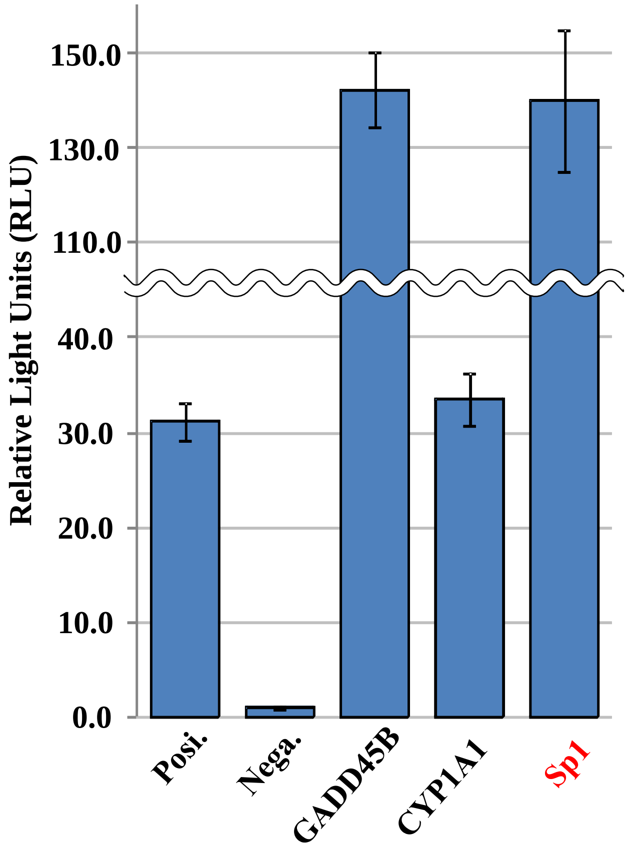
HeLa cells



HepG2 cells



Hep3B cells



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

GADD45B: pGL4-ph GADD45B(RDB# 7529)
CYP1A1: pGL4-ph CYP1A1(RDB# 7541)
Sp1: pGL4-ph Sp1(RDB# 7531)

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.11.05

1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5729

2nd Nucleotide Sequence
  File Name        : RDB7531F.fasta
  Sequence Size    : 774

  Unit Size to Compare = 1
  Pick up Location     = 1



[97.781% / 766 bp]     INT/OPT.Score : <   1252/  2812 >

    1'                GGCCTA ACTGGCCGGT ACCTGAG-CT CGCTAG-CCT CGAGGATGCA
                      ****** ********** ******* ** ****** *** **********
    1" GCCGAACTTT CTCTGGCCTA ACTGGCCGGT ACCTGAGACT CGCTAGACCT CGAGGATGCA

   45' GCAGAGGCCT CAGTTCTTAC CTTCAAAGGG CTTAAAATAG TTTAGGAGAA TTCACATTTT
       ********** ********** ********** ********** ********** **********
   61" GCAGAGGCCT CAGTTCTTAC CTTCAAAGGG CTTAAAATAG TTTAGGAGAA TTCACATTTT

  105' AAAACATAAG AACATATAAG -CAGGTGACA ACATATAAGA TACAAATACT GAAGGACATG
       ********** **********  ********* ********** ********** **********
  121" AAAACATAAG AACATATAAG ACAGGTGACA ACATATAAGA TACAAATACT GAAGGACATG

  164' ACCTCATCGT GTCATTGACA AGCTATTAAG GCCGGCTCCA CCAAAACACG GATAAAGAGG
       ********** ********** ********** ********** ********** **********
  181" ACCTCATCGT GTCATTGACA AGCTATTAAG GCCGGCTCCA CCAAAACACG GATAAAGAGG

  224' AGGCCAGAAA TCCAGGTGCC TGCAGTAAAG TTTCTTAACC TTCGTGATTG CAAAAAGCTG
       ********** ********** ********** ********** ********** **********
  241" AGGCCAGAAA TCCAGGTGCC TGCAGTAAAG TTTCTTAACC TTCGTGATTG CAAAAAGCTG
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284' GAGCTCAGCT ATCTTGCTTT ATGCATAGGC GGTATTTACT ATT-AAGGGG GAAAAAATGG
     ********** ********** ********** ********** *** ****** **********
301" GAGCTCAGCT ATCTTGCTTT ATGCATAGGC GGTATTTACT ATTAAAGGGG GAAAAAATGG

343' AAGTGACTTA TCCGCACTTT AGCCTCAAGG CTTGAAAAGT TAACCAGTCG TTTAAGTGGT
     ********** ********** ********** **********  ********* **********
361" AAGTGACTTA TCCGCACTTT AGCCTCAAGG CTTGAAAAGT CAACCAGTCG TTTAAGTGGT

403' TAGCGCCTTT GTCTGGGGGA ACTTAATAAA ATCGCGTTTT CTGGAGTCTC ACGGAGACTC
     ********** ********** ********** ********** ********** **********
421" TAGCGCCTTT GTCTGGGGGA ACTTAATAAA ATCGCGTTTT CTGGAGTCTC ACGGAGACTC

463' TGCATATTGG TCAGCTCAGT ATTAACTTAT TCGGTGAGTG CTGTCACCAG ATCTCGTCCC
     ********** ********** ********** ********** ********** **********
481" TGCATATTGG TCAGCTCAGT ATTAACTTAT TCGGTGAGTG CTGTCACCAG ATCTCGTCCC

523' GCCTGCATTC CCAGGGCTTG CAGCGACATT GAGGCATCTG CCCGCCTGTC CGACCACCCG
     ********** ********** ********** ********** ********** **********
541" GCCTGCATTC CCAGGGCTTG CAGCGACATT GAGGCATCTG CCCGCCTGTC CGACCACCCG

583' GGAGGGGGGT AAGATTTGAG AGGTACTTTA TAGGGGCAGT TAAATGAAGA CGCAAACAAG
     ********** ********** ********** ********** ********** ******* **
601" GGAGGGGGGT AAGATTTGAG AGGTACTTTA TAGGGGCAGT TAAATGAAGA CGCAAAC-AG

643' TCCTAGTGTT GATGCGGAAC TGCGCGCCGA ATGCCTTGGC TCTGACACCT GTTGAGCTGC
     ********** ********** ********** ***** **** *********  **********
660" TCCTAGTGTT GATGCGGAAC TGCGCGCCGA ATGCC-TGGC TCTGACACC- GTTGAGCTGC

703' AGGACTCCGC TAAAGCGTCC CACCTAATGA CTGTAACAAC GTCCCCTGAG GAGGGCCAAT
     ****** *** * ****** * ***** **** **** ** ** ** ******  ****** ***
718" AGGACT-CGC T-AAGCGT-C CACCT-ATGA CTGT-AC-AC GT-CCCTGA- GAGGGCAAAT

763' ATGGCGACGG TCTCCTCTTG GCATAGCCCT CTTCCCTCCC TCATGATGGG CAGCTCCAGT

770" GCAAA
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1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5729

2nd Nucleotide Sequence
  File Name        : RDB7531R.fasta (Complementary)
  Sequence Size    : 730

  Unit Size to Compare = 1
  Pick up Location     = 1



[95.951% / 741 bp]     INT/OPT.Score : <   1816/  2660 >

    841’ AGGAGGCGGT GCCAGGCCTA CTTCGTCCCC TCATTGGATT GAATAACTGA GGGAGCCGCC
                                      *** **  *   *    ** *      **** ****
      1″                              CCC TCTCTCCCTA TGATGATACT AGGAG-CGCC

    901’ AATTCTCCTC TGCCACTCCA AGTTTCCGCC CTCAGTTAAT TCGGCGTTTA ATTGGCTTTT
            *** *** ** ******  **  * **** ******* ** ****** *** ****** ***
     33″ --ATCT-CTC TG-CACTCC- AG--TTCGCC CTCAGTT-AT TCGGCG-TTA ATTGGC-TTT

    961’ AGTTCACGTC AATATGCGTC CTTTCCTGTC TCTTTTCAGT CTAACTCCAA TCATAACGTT
         ********** ********** ********** ********** ********** **********
     83″ AGTTCACGTC AATATGCGTC CTTTCCTGTC TCTTTTCAGT CTAACTCCAA TCATAACGTT

   1021’ CCTGGCTGCC CGCCTGATTT CTGATTGGTT TTAATCAGCT TCATCCTCTC CTATTCCTGC
         ********** ********** ********** ********** ********** **********
    143″ CCTGGCTGCC CGCCTGATTT CTGATTGGTT TTAATCAGCT TCATCCTCTC CTATTCCTGC

   1081’ CTACTTCTTA CCTCTCCGCC CACTAGGATT TTGCCCAAGC ATATCCCGGA TTCTGGTTGG
         ********** ********** ********** ********** ********** **********
    203″ CTACTTCTTA CCTCTCCGCC CACTAGGATT TTGCCCAAGC ATATCCCGGA TTCTGGTTGG

   1141’ CCGTTGTTCT GTCATTCCTA TCAAAGCTTT GCCTATCCCT ACGTCTCAGG GAGCCCGCCT
         ********** ********** ********** ********** ********** **********
    263″ CCGTTGTTCT GTCATTCCTA TCAAAGCTTT GCCTATCCCT ACGTCTCAGG GAGCCCGCCT
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1201’ GCCGGTTGAC TGGTTTCCTT CCAAGCCAAT CATCTCCAGC TCCCGCCCAT CTTCACTTCC
      ********** ********** ********** ********** ********** **********
 323″ GCCGGTTGAC TGGTTTCCTT CCAAGCCAAT CATCTCCAGC TCCCGCCCAT CTTCACTTCC

1261’ TGCATCCTTC ATTGGCTTTT AACACTGAGA GGGCGGTCTT TTTAGGCGGA CACCAGGCAC
      ********** ********** ********** ********** ********** **********
 383″ TGCATCCTTC ATTGGCTTTT AACACTGAGA GGGCGGTCTT TTTAGGCGGA CACCAGGCAC

1321’ GCAACTTAGT CTCACACGCC TTGGAGAGCA AGCGAGTCTT GCCATTGGAT AATTCCACCG
      ********** ********** ********** ********** ********** **********
 443″ GCAACTTAGT CTCACACGCC TTGGAGAGCA AGCGAGTCTT GCCATTGGAT AATTCCACCG

1381’ TCTTTCTTCT GCAAGTCCCT CCTTT-CCCC CTCCCTCATT GGGCGGGGCA GCAGAGAAGG
      ********** ********** ***** **** ********** ********** **********
 503″ TCTTTCTTCT GCAAGTCCCT CCTTTCCCCC CTCCCTCATT GGGCGGGGCA GCAGAGAAGG

1440’ GGCGGGGCCT AGGTTGGGCT TGTGGCGCGC TGCTCCCTCC TCCTTACCCC CCCCTCCCTG
      ********** ********** ********** ********** ********** **********
 563″ GGCGGGGCCT AGGTTGGGCT TGTGGCGCGC TGCTCCCTCC TCCTTACCCC CCCCTCCCTG

1500’ TCCGGTCCGG GTTCGCTTGC CTCGTCAGCA TCAAGATCTG GCCTCGGCGG CCAAGCTTGG
      ********** ********** ********** ********** ********** **********
 623″ TCCGGTCCGG GTTCGCTTGC CTCGTCAGCA TCAAGATCTG GCCTCGGCGG CCAAGCTTGG

1560’ CAATCCGGTA CTGTTGGTAA AGCCACCATG GAA-GATGCC AAA-AACATT AAGAAGGGCC
      ********** ********** ********** *** ****** *** ****
 683″ CAATCCGGTA CTGTTGGTAA AGCCACCATG GAACGATGCC AAACAACA
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