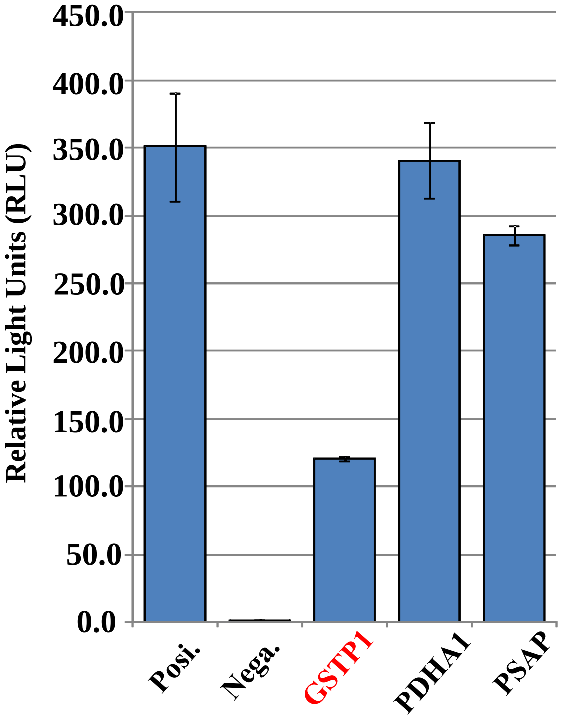
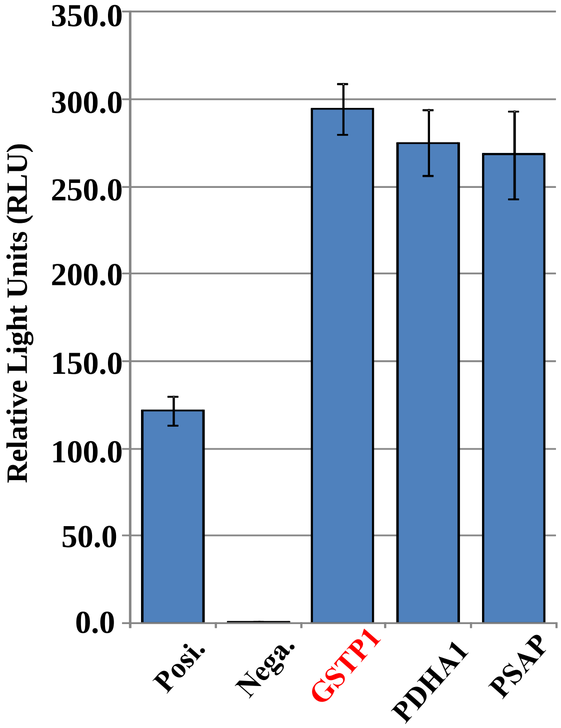
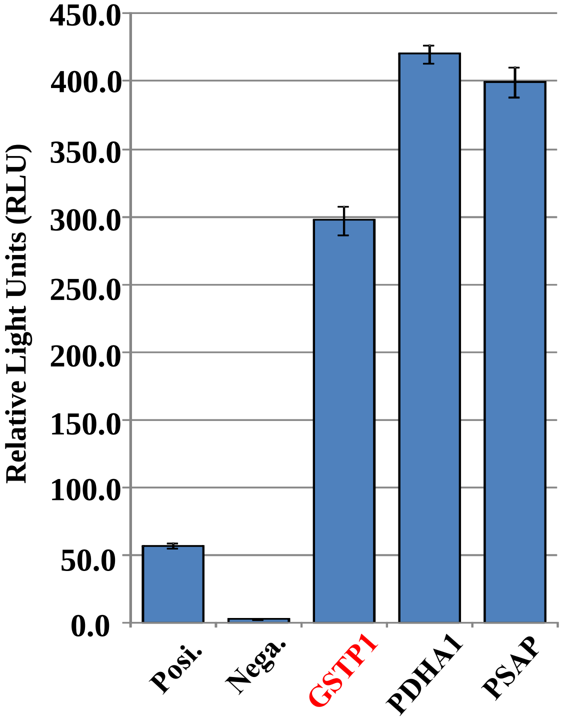
The Promoter Activities of Reporter Constructs



HeLa cells



HepG2 cells



Hep3B cells

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

GSTP1: pGL4-phGSTP1 (RDB# 7477)
PDHA1: pGL4-phPDHA1 (RDB# 7514)
PSAP: pGL4-phPSAP (RDB# 7515)

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.08.28

1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5485

2nd Nucleotide Sequence
  File Name        : RDB7477F.fasta
  Sequence Size    : 721

  Unit Size to Compare = 1
  Pick up Location     = 1
[99.290% / 704 bp]     INT/OPT.Score : <   2786/  2786 >

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

    44’ AGATCTGCAA ATCAACAGAA AGTAGGCAGC AAAGCCAAAG AAAATAGCCT AAGGCACAGC
        ********** ********** ********** ********** ********** **********
    61″ AGATCTGCAA ATCAACAGAA AGTAGGCAGC AAAGCCAAAG AAAATAGCCT AAGGCACAGC

   104’ CACTAAAAGG AACGTGATCA TGTCCTTTGC AGGGACATGG GTGGAGCTGG AAGCCGTTAG
        ********** ********** ********** ********** ********** **********
   121″ CACTAAAAGG AACGTGATCA TGTCCTTTGC AGGGACATGG GTGGAGCTGG AAGCCGTTAG

   164’ CCTCAGCAAA CTCACACAGG AACAGAAAAC CAGCGAGACC GCATGGTCTC ACTTATAAGT
        ********** ********** ********** ********** ********** **********
   181″ CCTCAGCAAA CTCACACAGG AACAGAAAAC CAGCGAGACC GCATGGTCTC ACTTATAAGT

   224’ GGGAGCTGAA CAATGAGAAC ACATGGTCAC ATGGCGGCGA TCAACACACA CTGGTGCCTG
        ********** ********** ********** ********** ********** **********
   241″ GGGAGCTGAA CAATGAGAAC ACATGGTCAC ATGGCGGCGA TCAACACACA CTGGTGCCTG

   284’ TTGAGCGGGG TGCTGGGGAG GGAGAGTACC AGGAAGAATA GCTAAGGGAT ACTGGGCTTA
        ********** ********** ********** ********** ********** **********
   301″ TTGAGCGGGG TGCTGGGGAG GGAGAGTACC AGGAAGAATA GCTAAGGGAT ACTGGGCTTA
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344’ ATACCTGGGT GATGGGATGA TCTGTACAGC AAACCATCAT GGCGCACACA CCTATGTAAC
     ********** ********** ********** ********** ********** **********
361″ ATACCTGGGT GATGGGATGA TCTGTACAGC AAACCATCAT GGCGCACACA CCTATGTAAC

404’ AAACCTGCAC ATCCTCTACA TGTACCCCAG AACTTCAAAT AAAAGTTGGA CGGCCAGGCG
     ********** *****  *** ********** ********** ********** **********
421″ AAACCTGCAC ATCCTGCACA TGTACCCCAG AACTTCAAAT AAAAGTTGGA CGGCCAGGCG

464’ TGGTGGCTCA CGCCTGTAAT CCCAGCACTT TGGGAAGCCG AGGCGTGCAG ATCACCTAAG
     ********** ********** ********** ********** ********** **********
481″ TGGTGGCTCA CGCCTGTAAT CCCAGCACTT TGGGAAGCCG AGGCGTGCAG ATCACCTAAG

524’ GTCAGGAGTT CGAGACCAGC CCGGCCAACA TGGTGAAACC CCGTCTCTAC TAAAAATACA
     ********** ********** ********** ********** ********** **********
541″ GTCAGGAGTT CGAGACCAGC CCGGCCAACA TGGTGAAACC CCGTCTCTAC TAAAAATACA

584’ AAAATCAGCC AGATGTGGCA CGCACCTATA ATTCCACCTA CTCGGGAGGC TGAAGCAGAA
     ********** ********** ********** ********** ********** **********
601″ AAAATCAGCC AGATGTGGCA CGCACCTATA ATTCCACCTA CTCGGGAGGC TGAAGCAGAA

644’ TTGCTTGAAC CCGAGAGGCG GAGGTTGCAG TGAGCCGCCG AGATCGCGCC ACTGCACTCC
     **********  ********* ********** *********  ********** *********
661″ TTGCTTGAAC ACGAGAGGCG GAGGTTGCAG TGAGCCGCCC AGATCGCGCC ACTGCACTCA

704’ AGCCTGGGCC ACAGCGTGAG ACTACGTCAT AAAATAAAAT AAAATAACAC AAAATAAAAT
     *
721″ A
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1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5485

2nd Nucleotide Sequence
  File Name         : RDB7477R.fasta (Complementary)
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  Sequence Size     : 734

  Unit Size to Compare = 1
  Pick up Location     = 1

[95.628% / 732 bp]     INT/OPT.Score : <   2293/  2646 >

    601' GCACGCACCT ATAATTCCAC CTACTCGGGA GGCTGAAGCA GAATTGCTTG AACCCGAGAG
                                                            **  *********
      1"                                                  AAAGGCTG GACCCGAGAG

    661' GCGGAGGTTG CAGTGAGCCG CCGAGATCGC GCCACTGCAC TCCAGCCTGG GCCACAGCGT
         ** ******* *** *** ** ** ******  ****  **** ********** *********
     19" GC-GAGGTTG CAGGGAG-CG CCCAGATCG- GCCAACGCAC TCCAGCCTGG GCCACAGCGG

    721' GAGACTACGT CATAAAATAA AATAA----- AATAACACAA AATAAAATAA AATAAAA---
         ****.***** *** ******  ****      **  * *  * ********** *******
     76" GAGANTACGT CATTAAATAA GATAAGATGA AAGTAAATTA AATAAAATAA AATAAAATAA

    773' TAAAATAAAA TAAAATAAAA TAAAA--TAA AATAAAATAA AA--AAATAA AATAAAATAA
         ********** ********** *****  *** *****.**** **  ****** **********
    136" TAAAATAAAA TAAAATAAAA TAAAATATAA AATAANATAA AATAAAATAA AATAAAATAA

    829' AATAAAATAA AGCAATTTCC TTTCCTCTAA GCGGCCTCCA CCCCTCTCCC CTGCCCTGTG
         ********** *********  ********** ********** ********** **********
    196" AATAAAATAA AGCAATTTCT TTTCCTCTAA GCGGCCTCCA CCCCTCTCCC CTGCCCTGTG

    889' AAGCGGGTGT GCAAGCTCCG GGATCGCAGC GGTCTTAGGG AATTTCCCCC CGCGATGTCC
         ********** ********** ********** ********** ********** **********
    256" AAGCGGGTGT GCAAGCTCCG GGATCGCAGC GGTCTTAGGG AATTTCCCCC CGCGATGTCC

    949' CGGCGCGCCA GTTCGCTGCG CACACTTCGC TGCGGTCCTC TTCCTGCTGT CTGTTTACTC
         ********** ********** ********** ********** ********** **********
    316" CGGCGCGCCA GTTCGCTGCG CACACTTCGC TGCGGTCCTC TTCCTGCTGT CTGTTTACTC

   1009' CCTAGGCCCC GCTGGGGACC TGGGAAAGAG GGAAAGGCTT CCCCGGCCAG CTGCGCGGCG
         ********** ********** ********** ********** ********** **********
    376" CCTAGGCCCC GCTGGGGACC TGGGAAAGAG GGAAAGGCTT CCCCGGCCAG CTGCGCGGCG
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1069' ACTCCGGGGA CTCCAGGGCG CCCCTCTGCG GCCGACGCCC GGGGTGCAGC GGCCGCCGGG
      ********** ********** ********** ********** ********** **********
 436" ACTCCGGGGA CTCCAGGGCG CCCCTCTGCG GCCGACGCCC GGGGTGCAGC GGCCGCCGGG

1129' GCTGGGGCCG GCGGGAGTCC GCGGGACCCT CCAGAAGAGC GGCCGGCGCC GTGACTCAGC
      ********** ********** ********** ********** ********** **********
 496" GCTGGGGCCG GCGGGAGTCC GCGGGACCCT CCAGAAGAGC GGCCGGCGCC GTGACTCAGC

1189' ACTGGGGCGG AGCGGGGCGG GACCACCCTT ATAAGGCTCG GAGGCCGCGA GGCCTTCGCT
      ********** ********** ********** ********** ********** **********
 556" ACTGGGGCGG AGCGGGGCGG GACCACCCTT ATAAGGCTCG GAGGCCGCGA GGCCTTCGCT

1249' GGAGTTTCGC CGCCGCAGTC TTCGCCACCA GTGAGTATCA AGATCTGGCC TCGGCGGCCA
      ********** ********** ********** ********** ********** **********
 616" GGAGTTTCGC CGCCGCAGTC TTCGCCACCA GTGAGTATCA AGATCTGGCC TCGGCGGCCA

1309' AGCTTGGCAA TCCGGTACTG TTGGTAAAGC CACCATGGAA GATGCCAAAA ACATTAAGAA
      ********** ********** ********** ********** ********** *** ******
 676" AGCTTGGCAA TCCGGTACTG TTGGTAAAGC CACCATGGAA GATGCCAAAA ACA-TAAGAA
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