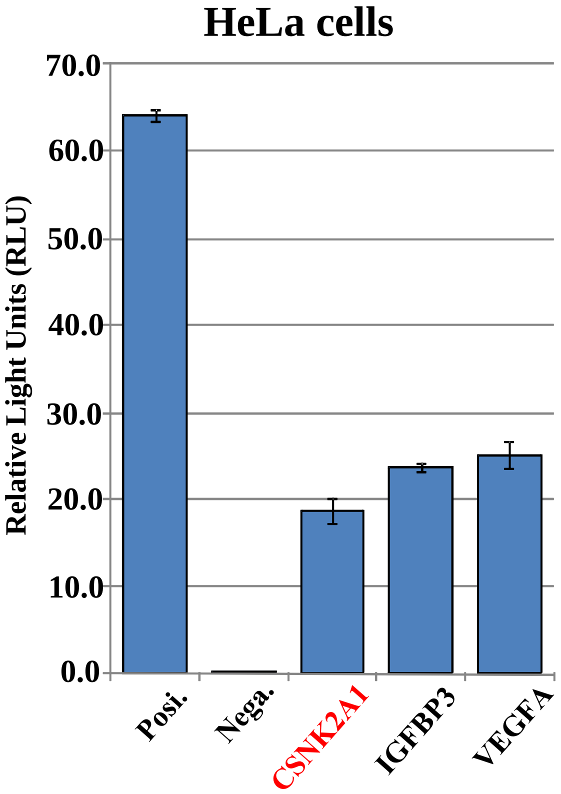
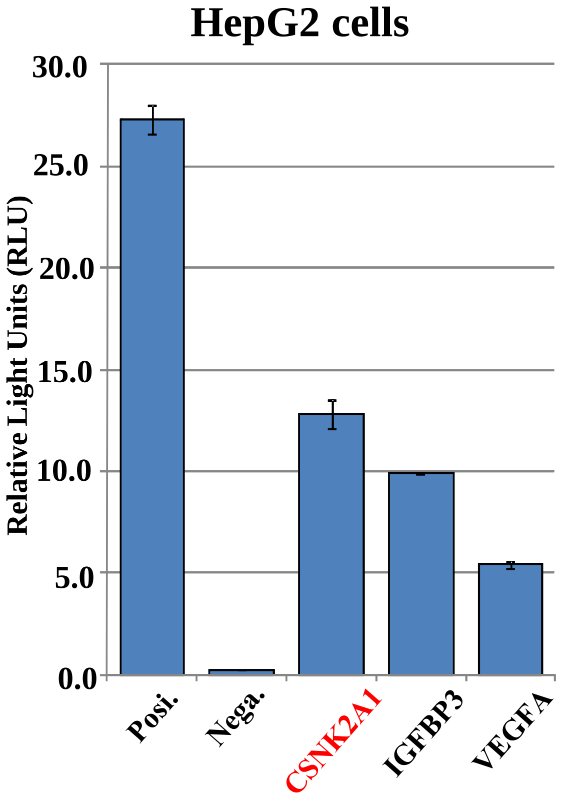
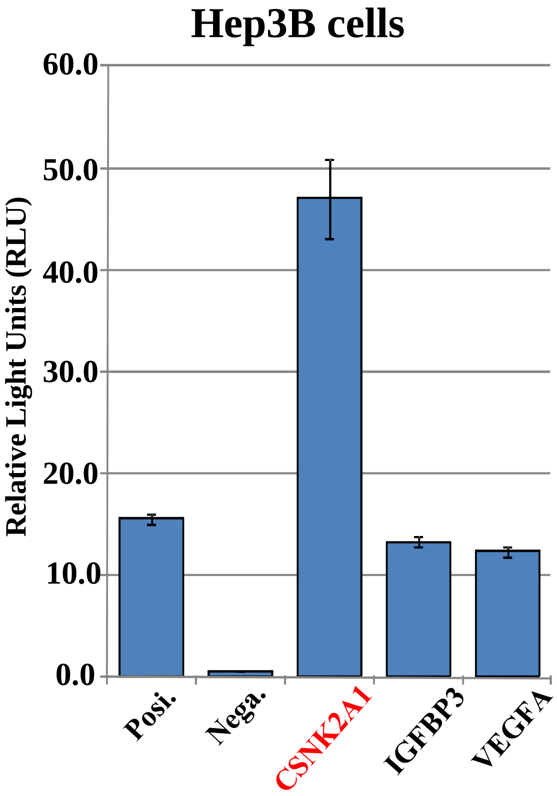
The Promoter Activities of Reporter Constructs







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

CSNK2A1: pGL4-phCSNK2A1 (RDB# 7483)
IGFBP3: pGL4-phIGFBP3 (RDB# 7568)
VEGFA: pGL4-phVEGFA (RDB# 7681)

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[ GENETYX : Nucleotide Sequence Homology Data ]
Date : 2009.08.17

1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5672

2nd Nucleotide Sequence
  File Name        : RDB7483F.fasta
  Sequence Size    : 671

  Unit Size to Compare = 1
  Pick up Location     = 1

[97.744% / 665 bp]     INT/OPT.Score : <    375/  2440 >

      1'                     GG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGAT-
                             ** ********** ********** ********** *********
      1″ GTGCCAGAAC ATGTCTCTGG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATG

     42' ACCAGCCCTA ACCCCACATG GGGAAGAGGT GNCCTCTTTG GGAGCAGAGG TGCTAGTCAG
         ********** ********** ********** * ******** ********** **********
     61″ ACCAGCCCTA ACCCCACATG GGGAAGAGGT G-CCTCTTTG GGAGCAGAGG TGCTAGTCAG

    102' CTGACAAACT GTGAAGGCAG GGNCTGTGGA GGGTGGAGAG GCCCATTCCT GAGACAACCA
         ********** ********** ** ******* ********** ********** **********
    120″ CTGACAAACT GTGAAGGCAG GG-CTGTGGA GGGTGGAGAG GCCCATTCCT GAGACAACCA

    162' GCTATTCTGA GACNAGTTAG GGATAATGGT TGGTACTGAA AGAACCTGGC CTCCTCACCC
         ********** *** ****** ********** ********** ********** **********
    179″ GCTATTCTGA GAC-AGTTAG GGATAATGGT TGGTACTGAA AGAACCTGGC CTCCTCACCC

    222' TCGTNTCCAG TGCTCACACC TCTGTCCCAC CAGAGGTGAG ACTAATACTT GAACTNCCTT
         **** ***** ********** ********** ********** ********** ***** ****
    238″ TCGT-TCCAG TGCTCACACC TCTGTCCCAC CAGAGGTGAG ACTAATACTT GAACT-CCTT

    282' TCAGCAACTC TTAGACGCTT CAGCTTTTAT CAGGGCCTGC AAAGGANGAG GTTGATCATC
         ********** ********** ********** ********** ****** *** **********
    296″ TCAGCAACTC TTAGACGCTT CAGCTTTTAT CAGGGCCTGC AAAGGA-GAG GTTGATCATC
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342' AGATGGAGCC CTGTCCACTG GGGGCTCCCA GTCTGATNGG AGGAGACAGA CTGAGGTCCT
     ********** ********** ********** ******* ** ********** **********
355″ AGATGGAGCC CTGTCCACTG GGGGCTCCCA GTCTGAT-GG AGGAGACAGA CTGAGGTCCT

402' CAGGTTACTG ACTGATAGTG TCTGGGTTNG GAGGGAGTTA AACAGAGAGG AGACCCCTAG
     ********** ********** ******** * ********** ********** **********
414″ CAGGTTACTG ACTGATAGTG TCTGGGTT-G GAGGGAGTTA AACAGAGAGG AGACCCCTAG

462' AGGAAAGGAT CCCTGAATTN AGTTCAATCG GCATACAGAA ATTATCCAGT CCATGAGGTG
     ********** *********  ********** ********** ********** **********
473″ AGGAAAGGAT CCCTGAATT- AGTTCAATCG GCATACAGAA ATTATCCAGT CCATGAGGTG

522' ACAGTAAGAG NAAGTAACTG CCAGTGTAAA GGGAGGGAGG CAACACAGCT AAGTTCCAGG
     **********  ********* ********** ********** * ******** **********
532″ ACAGTAAGAG -AAGTAACTG CCAGTGTAAA GGGAGGGAGG CCACACAGCT AAGTTCCAGG

582' ANATTGTTTG CAGTCTTGTG GGTGGAATCT TCCGGAATTT GAGAAGAGAG TGNGCAGAAT
     * ******** ********** ********** ********** ********** ** *******
591″ A-ATTGTTTG CAGTCTTGTG GGTGGAATCT TCCGGAATTT GAGAAGAGAG TG-GCAGAAT

642' AGGAGGCTGG AAAGGAGGGT TTGGCCAAAT TATGGAGGAC TCTNGAATGT CAAGTGAAGA
     ********** ********** * *
649″ AGGAGGCTGG AAAGGAGGGT TGG




1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5672

2nd Nucleotide Sequence
  File Name        : RDB7483R.fasta (Complementary)
  Sequence Size    : 697

  Unit Size to Compare = 1
  Pick up Location     = 1
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[96.897% / 709 bp]     INT/OPT.Score : <    372/  2567 >

  841’ GAGGCAGATA GAAG-GAAAA AAAAACACTG TATTTTGGAC GCACAGCTCN TTGGCAGGAC
         *******. ****  **** ********** ******* ** *********  * ***** **
    1″   GGCAGATN GAAGAAAAAA AAAAACACTG TATTTTGAAC GCACAGCTC- TGGGCAGAAC

  900’ TCCTGTAGGA GGAAGGAATT GGGCCTTGGT CTCTTGAGAG NCTAGTATCC TCACTTCTCA
       ********** *********  ** ******* **********  ********* **********
   58″ TCCTGTAGGA GGAAGGAATG GGCCCTTGGT CTCTTGAGAG -CTAGTATCC TCACTTCTCA

  960’ GACTCCTGCG CCATGCCCTT CCTAGGGTCC ANACTTTCAT TCACTTCTTC CGAACTCCAA
       ********** ********** ********** * ******** ********** **********
  117″ GACTCCTGCG CCATGCCCTT CCTAGGGTCC A-ACTTTCAT TCACTTCTTC CGAACTCCAA

 1020’ GTTTGAATAG AAAGTGTTGC TGNAAACCCT AATTTAAAAC GAGGGGTCAG AGCAAAAGAG
       ********** ********** ** ******* ********** ********** **********
  176″ GTTTGAATAG AAAGTGTTGC TG-AAACCCT AATTTAAAAC GAGGGGTCAG AGCAAAAGAG

 1080’ ACTTCAGCTC CCANGAATGC TTGGCTCTAC AGCTCTGCAG GTCGCGCATG GTTCTTTTCA
       ********** *** ****** ********** ********** ********** **********
  235″ ACTTCAGCTC CCA-GAATGC TTGGCTCTAC AGCTCTGCAG GTCGCGCATG GTTCTTTTCA

 1140’ AGAANAGGGG GGCCAGCTGG GTGAAGTGTG GGAAACCTGG GTACCGCCAT CTTAANCTTG
       **** ***** ********** ********** ********** ********** ***** ****
  294″ AGAA-AGGGG GGCCAGCTGG GTGAAGTGTG GGAAACCTGG GTACCGCCAT CTTAA-CTTG

 1200’ GGTCAAACCA ACTGTTCACC TAATGGGAGG TTCGTGTTCT CTCTGTNTGT CACTTGTTAA
       ********** ********** ********** ********** ****** *** **********
  352″ GGTCAAACCA ACTGTTCACC TAATGGGAGG TTCGTGTTCT CTCTGT-TGT CACTTGTTAA

 1260’ CACTATTGAA ATAAAATGCG CTTAACTATT GCAAGTCNTC CTTATTCTGC TTTGCGTTGG
       ********** ********** ********** ******* ** ********** **********
  411″ CACTATTGAA ATAAAATGCG CTTAACTATT GCAAGTC-TC CTTATTCTGC TTTGCGTTGG

 1320’ GGATTCCTTC CATTTTGCAC CCTAGGCCNA GAACTGAATC CCTAAGGTTA CAATAGGACA
       ********** ********** ******** * ********** ********** **********
  470″ GGATTCCTTC CATTTTGCAC CCTAGGCC-A GAACTGAATC CCTAAGGTTA CAATAGGACA
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1380' TCCCAGCATG GCCGCATTCN AGAGAGATTC CTCTGGGGGC GGAGTCGGAA GCTGTCTCGC
      ********** *********  ********** ********** ********** **********
 529″ TCCCAGCATG GCCGCATTC- AGAGAGATTC CTCTGGGGGC GGAGTCGGAA GCTGTCTCGC

1440' CCCGCCTCCT NGGTAGGAGG GGGTTTCCGC TTATCAAGAT CTGGCCTCGG CGGCCAAGCT
      **********  ********* ********** ********** ********** **********
 588″ CCCGCCTCCT -GGTAGGAGG GGGTTTCCGC TTATCAAGAT CTGGCCTCGG CGGCCAAGCT

1500' TGGCAATCCG GTACTGTTGG TAAAGCCACC ATGGAAGATG CCAAA-AACA TTAAGAAGGG
      ********** ********** ********** ****** *** ***** **** *
 647″ TGGCAATCCG GTACTGTTGG TAAAGCCACC ATGGAACATG CCAAACAACA T
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