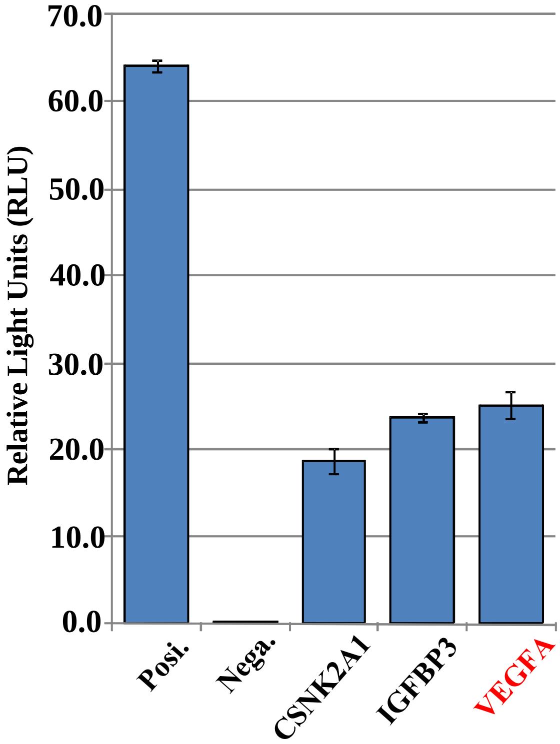
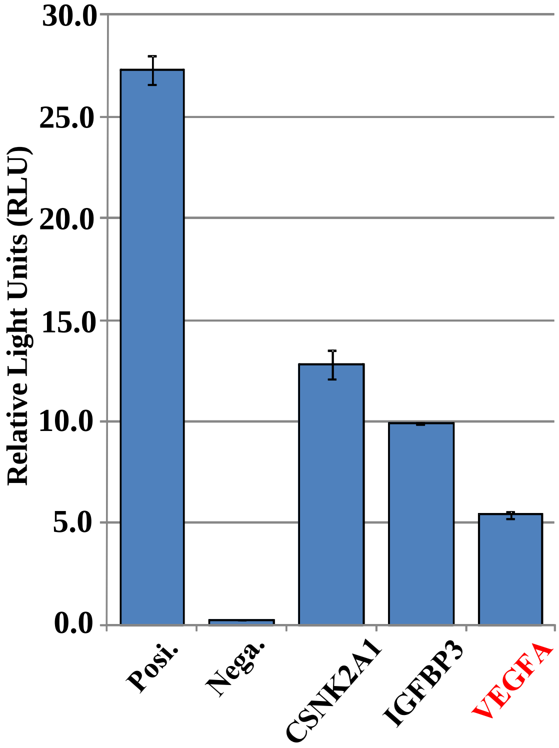
The Promoter Activities of Reporter Constructs

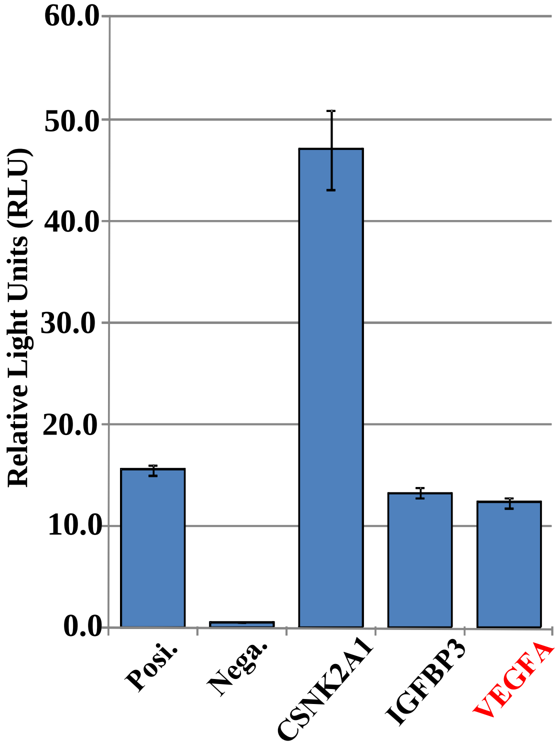
HeLa cells



HepG2 cells



Hep3B cells



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

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

2010, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.01.29

1st Nucleotide Sequence
  File Name         : Reference Seq VEGF---insert
  Sequence Size     : 1305

2nd Nucleotide Sequence
  File Name         : RDB7681F_1.fasta
  Sequence Size     : 793

Unit Size to Compare : 6

Percent Similarity    : 94.5
Percent Identity      : 94.5


     1’ GGCGGGTAGG TTTGAATCAT CACGCAGGCC CTGGCCTCCA CCCGCCCCCA CCAGCCCCCT
        ********** ********** ********** ********** *** ****** **********
    52″ GGCGGGTAGG TTTGAATCAT CACGCAGGCC CTGGCCTCCA CCCACCCCCA CCAGCCCCCT

    61’ GGCCTCAGTT CCCTGGCAAC ATCTGGGGTT GGGGGGGCAG CAGGAACAAG GGCCTCTGTC
        ********** ********** ********** ********** ********** **********
   112″ GGCCTCAGTT CCCTGGCAAC ATCTGGGGTT GGGGGGGCAG CAGGAACAAG GGCCTCTGTC

   121’ TGCCCAGCTG CCTCCCCCTT TGGGTTTTGC CAGACTCCAC AGTGCATACG TGGGCTCCAA
        ********** ********** ********** ********** ********** **********
   172″ TGCCCAGCTG CCTCCCCCTT TGGGTTTTGC CAGACTCCAC AGTGCATACG TGGGCTCCAA

   181’ CAGGTCCTCT TCCCTCCCAG TCACTGACTA ACCCCGGAAC CACACAGCTT CCCGTTCTCA
        ********** ********** ********** ********** ********** **********
   232″ CAGGTCCTCT TCCCTCCCAG TCACTGACTA ACCCCGGAAC CACACAGCTT CCCGTTCTCA

   241’ GCTCCACAAA CTTGGTGCCA AATTCTTCTC CCCTGGGAAG CATCCCTGGA CACTTCCCAA
        ********** ********** ********** ********** ********** **********
   292″ GCTCCACAAA CTTGGTGCCA AATTCTTCTC CCCTGGGAAG CATCCCTGGA CACTTCCCAA
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301’ AGGACCCCAG TCACTCCAGC CTGTTGGCTG CCGCTCACTT TGATGTCTGC AGGCCAGATG
     ********** ********** ********** ********** ********** ****** ***
352″ AGGACCCCAG TCACTCCAGC CTGTTGGCTG CCGCTCACTT TGATGTCTGC AGGCCAAATG

361’ AGGGCTCCAG ATGGCACATT GTCAGAGGGA CACACTGTGG CCCCTGTGCC CAGCCCTGGG
     ********** ********** ********** ********** ********** **********
412″ AGGGCTCCAG ATGGCACATT GTCAGAGGGA CACACTGTGG CCCCTGTGCC CAGCCCTGGG

421’ CTCTCTGTAC ATGAAGCAAC TCCAGTCCCA AATATGTAGC TGTTTGGGAG GTCAGAAATA
     ********** ********** ********** ********** ********** **********
472″ CTCTCTGTAC ATGAAGCAAC TCCAGTCCCA AATATGTAGC TGTTTGGGAG GTCAGAAATA

481’ GGGGGTCCAG GAGCAAACTC CCCCCACCCC CTTTCCAAAG CCCATTCCCT CTTTAGCCAG
     ********** ********** ********** ********** ********** **********
532″ GGGGGTCCAG GAGCAAACTC CCCCCACCCC CTTTCCAAAG CCCATTCCCT CTTTAGCCAG

541’ AGCCGGGGTG TGCAGACGGC AGTCACTAGG GGGCGCTCGG CCACCACAGG GAAGCTGGGT
     ********** ********** ********** ********** ********** **********
592″ AGCCGGGGTG TGCAGACGGC AGTCACTAGG GGGCGCTCGG CCACCACAGG GAAGCTGGGT

601’ GAATGGAGCG AGCAGCGTCT TCGAGAGTGA GGACGTGTGT GTCTGTGTGG GTGAGTGAGT
     ********** ********** ********** ********** ********** **********
652″ GAATGGAGCG AGCAGCGTCT TCGAGAGTGA GGACGTGTGT GTCTGTGTGG GTGAGTGAGT

661’ GTGTGCGTGT --GGGGTTGA GGGCGTTGGA GCGGGGAGAA GGCCAGGGGT CACTCCAGGA
     **********   ****** * ***  *** *  ****** *  *** * *     *    *  *
712″ GTGTGCGTGT TGGGGGTTTA GGGTTTTGAA CCGGGGAAAG GGCAAAGAAA AAAAAAAAAA

719’ TTCCAATAGA TCTGTGTGTC CC
         *    *
772″ AAAAACCCAA AAAAAAAAAA AA
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1st Nucleotide Sequence

File Name : Reference Seq VEGF---insert

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  Sequence Size     : 1305

2nd Nucleotide Sequence
  File Name         : RDB7681R.fasta (Complementary)
  Sequence Size     : 855

Unit Size to Compare : 6

Percent Similarity   : 95.4
Percent Identity     : 95.0


   571’ GGGCGCTCGG CCACCAC-AG GGAAGCTGGG TGAATGGAGC GA--GCAGCG --TCTTCGAG
        *********  *  * ** ** * ******** ****  ***   *   **. *   * *** *
   855″ GGGCGCTCGC CACCAACAAG GAAAGCTGGG TGAAATGAGG AAAGCCANGG TTTTTTCAAA

   626’ AGTGAG-GAC GTG-TGTGT- CTGTGTGGGT GAG----TGA GTGTGTGCGT GTGGGGTTG-
        * ****  ** * * *****  **** *****  **        *****  * *  ********
   795″ AATGAGAAAC GGGTTGTGTC CTGTATGGGT AAGGTAAAAG GTGTGGCCAT TTGGGGTTGA

   678’ AGGGCGTTGG A-GCGGGGAG AA-GGCCA-- GGGGTC-ACT CCAG-GATTC CAAT-AGATC
        **** ***** * *******. ** *****   ****** *** ****  **** ***. *****
   735″ AGGGGGTTGG AGGCGGGGAN AAGGGCCAGG GGGGTCAACT CCAGAAATTC CAANAAGATC

   731’ TGT-GTGTCC CTCTCCCCAC CCGTCCCTGT CCGGCTCTCC GCCTTCCCCT GCCCCCTTCA
         ** * **** ********** ********** ********** *********  **********
   675″ GGTGGGGTCC CTCTCCCCAC CCGTCCCTGT CCGGCTCTCC GCCTTCCCCG GCCCCCTTCA

   790’ ATATTCCTAG CAAAGAGGGA ACGGCTCTCA GGCCCT-GTC CGCACGTAAC CTCACTTTCC
        ********** ********** ********** ****** *** ********** *********
   615″ ATATTCCTAG CAAAGAGGGA ACGGCTCTCA GGCCCTGGTC CGCACGTAAC CTCACTTTCG

   849’ TGCTCCCTCC TCGCCAATGC CCCGCGGGCG CGTGTCTCT- GGACAGAGTT TCC-GGGGGC
        ********** ********** ********** *********  ********** *** ******
   555″ TGCTCCCTCC TCGCCAATGC CCCGCGGGCG CGTGTCTCTG GGACAGAGTT TCCGGGGGGC

   907’ GGATGGGTAA TTTTCAGGCT GTGAACCTTG GTGGGGGTCG AGCTTCCCCT TCATTGCGGC
        ********** ********** ********** ********** ********** **********
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 495″ GGATGGGTAA TTTTCAGGCT GTGAACCTTG GTGGGGGTCG AGCTTCCCCT TCATTGCGGC

 967’ GGGCTGCGGG CCAGGCTTCA CTGAGCGTCC GCAGAGCCCG GGCCCGAGCC GCGTGTGGAA
      ********** ********** *** ****** ********** ********** *********
 435″ GGGCTGCGGG CCAGGCTTCA CTGGGCGTCC GCAGAGCCCG GGCCCGAGCC GCGTGTGGAG

1027’ GGGCTGAGGC TCGCCTGTCC CCGCCCCCCG GGGCGGGCCG GGGGCGGGGT CCCGGCGGGG
      ********** ********** ********** ********** ********** **********
 375″ GGGCTGAGGC TCGCCTGTCC CCGCCCCCCG GGGCGGGCCG GGGGCGGGGT CCCGGCGGGG

1087’ CGGAGCCATG CGCCCCCCCC TTTTTTTTTT AAAAGTCGGC TGGTAGCGGG GAGGATCGCG
      ********** ********** ********** ********** ********** **********
 315″ CGGAGCCATG CGCCCCCCCC TTTTTTTTTT AAAAGTCGGC TGGTAGCGGG GAGGATCGCG

1147’ GAGGCTTGGG GCAGCCGGGT AGCTCGGAGG TCGTGGCGCT GGGGGCTAGC ACCAGCGCTC
      ********** ********** ********** ********** ********** **********
 255″ GAGGCTTGGG GCAGCCGGGT AGCTCGGAGG TCGTGGCGCT GGGGGCTAGC ACCAGCGCTC

1207’ TGTCGGGAGG CGCAGCGGTT AGGTGGACCG GTCAGCGGAC TCACCGGCCA GGGCGCTCGG
      ********** ********** ********** ********** ********** **********
 195″ TGTCGGGAGG CGCAGCGGTT AGGTGGACCG GTCAGCGGAC TCACCGGCCA GGGCGCTCGG

1267’ TGCTGGAATT TGATATTCAT TGATCCGGGT TTTATCCCT
      ********** ********** ********** *********
 135″ TGCTGGAATT TGATATTCAT TGATCCGGGT TTTATCCCT
```