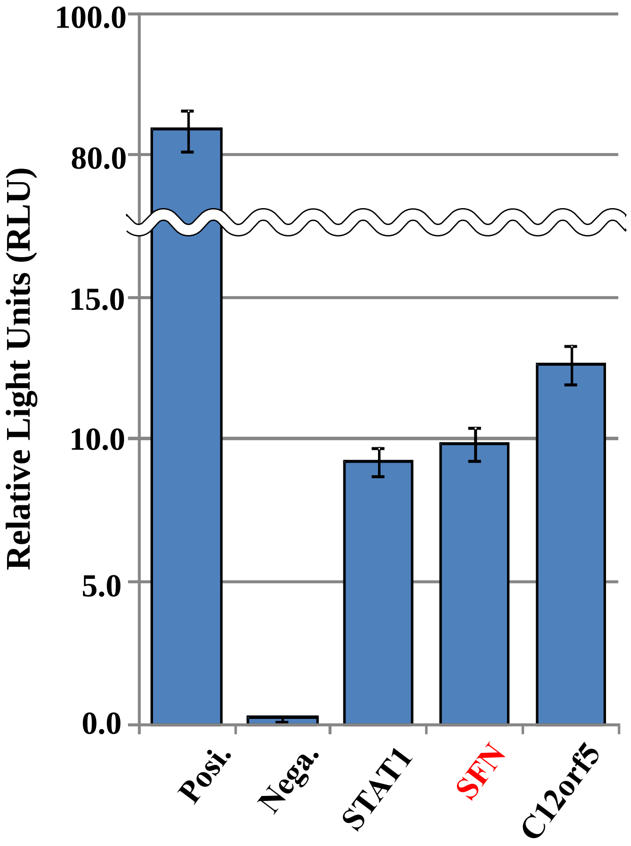
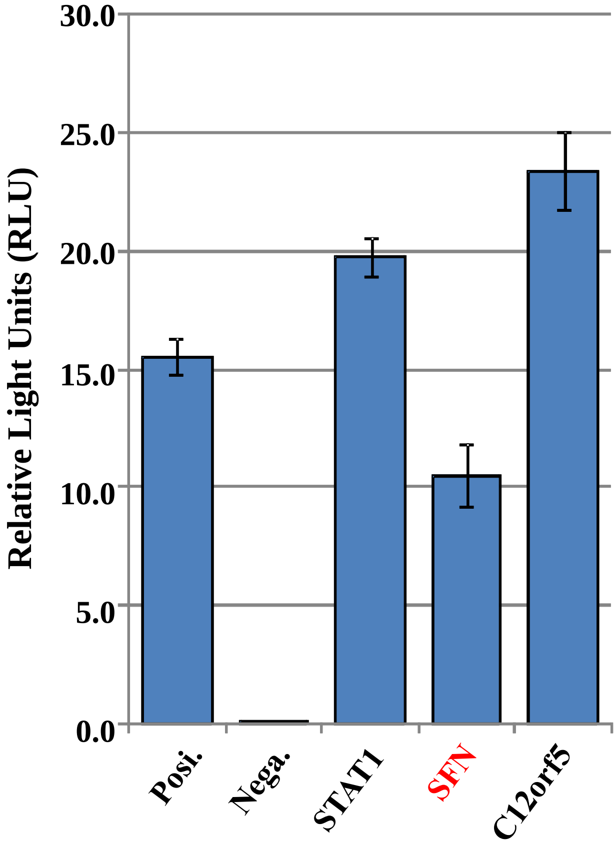
The Promoter Activities of Reporter Constructs

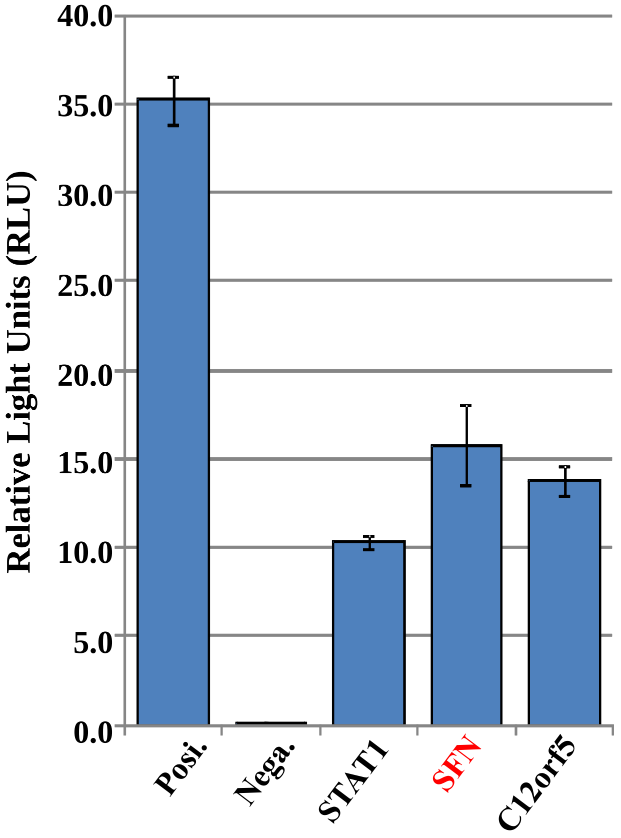
HeLa cells



HepG2 cells



Hep3B cells



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

STAT1: pGL4-phSTAT1 (RDB# 7405)
SFN: pGL4-phSFN (RDB# 7408)
C12orf5: pGL4-phC12orf5 (RDB# 7414)

2010, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.06.24

1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5594

2nd Nucleotide Sequence
  File Name        : RDB7408F.fasta
  Sequence Size    : 400

  Unit Size to Compare = 1
  Pick up Location     = 1



[99.250% / 400 bp]     INT/OPT.Score : <   1232/  1552 >

      1' GGCCTAACTG GCCGGTACCT GAGCTCGCTA GCCTCGAGGA TAGCCCAGGA GTTTGAGACC
                                                    ********* **********
     76"                                             AGCCCAGGA GTTTGAGACC

     61' TGCCTGGGCA ATGTAGTGAG ATCTGCTCTC TATTTAAAAA AAAAAAAAAG GAAAGAACAA
         ********** ********** ********** ********** ********** **********
     95" TGCCTGGGCA ATGTAGTGAG ATCTGCTCTC TATTTAAAAA AAAAAAAAAG GAAAGAACAA

    121' GTAAACTTCT GAGAAACAGG CTGGGGGAGG CATCACGTAG CTGGAATTGC TGCCCCATAA
         ********** ********** ********** ********** ********** **********
    155" GTAAACTTCT GAGAAACAGG CTGGGGGAGG CATCACGTAG CTGGAATTGC TGCCCCATAA

    181' AACAGAATGG TATGTGTCAC TGCCACCTCC CTTTCTCAGT CCTCTCTCTC CCCAGGTTGC
         ********** ********** ********** ********** ********** **********
    215" AACAGAATGG TATGTGTCAC TGCCACCTCC CTTTCTCAGT CCTCTCTCTC CCCAGGTTGC

    241' TAGCGTCCCC CCTGGGGGAT CAAACTGGAC TGCTTCCCAG CCTCAGACAG AGAGCAGTCT
         ********** ********** ********** ********** ********** **********
    275" TAGCGTCCCC CCTGGGGGAT CAAACTGGAC TGCTTCCCAG CCTCAGACAG AGAGCAGTCT
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    301’ GAGTCAGGCA GGAAAGTGGG ACAGCCGGGG AGCTGGACCC CACCCTCT-G TGAGCCCCGC
         ********** ********** ********** ********** ******** * **********
    335″ GAGTCAGGCA GGAAAGTGGG ACAGCCGGGG AGCTGGACCC CACCCTCTGG TGAGCCCCGC

    360’ T-GGTACCTG ATGGCATGTG GCTTGGAGAG GGCAGGTGAC CTGGCGTGGA GGGCCAGAGG
         * ******** ********** ********** ********** ********** **********
    395″ TGGGTACCTG ATGGCATGTG GCTTGGAGAG GGCAGGTGAC CTGGCGTGGA GGGCCAGAGG

    419’ GTAAATCCTC -AAACAAGTG GCAACAGGCC ACCAACTTGA AAGGGAAAAT TGTGTAGTGA
         **********  ********* *
    455″ GTAAATCCTC AAAACAAGTG G




1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5594

2nd Nucleotide Sequence
  File Name         : RDB7408R.fasta (Complementary)
  Sequence Size     : 400

  Unit Size to Compare = 1
  Pick up Location     = 1



[98.500% / 400 bp]     INT/OPT.Score : <   1380/  1557 >

    961’ CCTGGCAGGA TTAGGAACCC CATCCTCCTG AACCTTTATG GGCTCTGTCG AGGCTGAAGC
                                             ****** ** ***** * **********
     87″                                     TTTATG GGTTCTGTTG AGGCTGAAGC

   1021’ AGCCAGGGGC TAAAGCCGTC CTTAGCCCC- TGGAAGGGCA CTGTGAAAGT GGATCTGATT
         ********.  ********** *********  ********** ********** **** *****
    113″ AGCCAGGGNT TAAAGCCGTC CTTAGCCCCT TGGAAGGGCA CTGTGAAAGT GGATGTGATT
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1080’ TGAGAAGCCG TTTCCTGATG TGGGCAGCCA TGTGATGCCA GCCCCGAACA AGAGGGGGCA
      ********** ********** ********** ********** ********** **********
 173″ TGAGAAGCCG TTTCCTGATG TGGGCAGCCA TGTGATGCCA GCCCCGAACA AGAGGGGGCA

1140’ GCCTGGAGCC TGGAAAGGTG CCAGTGCAGG TGGGGCCCAC GCCCAGATTT CTCCTGCTGA
      ********** ********** ********** ********** ********** **********
 233″ GCCTGGAGCC TGGAAAGGTG CCAGTGCAGG TGGGGCCCAC GCCCAGATTT CTCCTGCTGA

1200’ CTGTTCTGAT GATTCACCCC CACATCCCAG CCTTTTTACC TTTACTGCAG AGCCGGAAAG
      ********** ********** ********** ********** ********** **********
 293″ CTGTTCTGAT GATTCACCCC CACATCCCAG CCTTTTTACC TTTACTGCAG AGCCGGAAAG

1260’ GGTGTGGGGA AGAGAGGAGA GGGAGGCAGG TCTTGGGCCC TGGTCCCGCC CCCTGCTCCT
      ********** ********** ********** ********** ********** **********
 353″ GGTGTGGGGA AGAGAGGAGA GGGAGGCAGG TCTTGGGCCC TGGTCCCGCC CCCTGCTCCT

1320’ CCCCACCCTT CTCTGGGCCT GGCCACCCAG CCAAAAGGCA GGCCAAGAGC AGGAGAGACA
      ********** ********** ********** ********** ********** **********
 413″ CCCCACCCTT CTCTGGGCCT GGCCACCCAG CCAAAAGGCA GGCCAAGAGC AGGAGAGACA

1380’ CAGAGTCCGG CATTATCAAG ATCTGGCCTC GGCGGCCAAG CTTGGCAATC CGGTACTGTT
      ********** ****
 473″ CAGAGTCCGG CATT
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