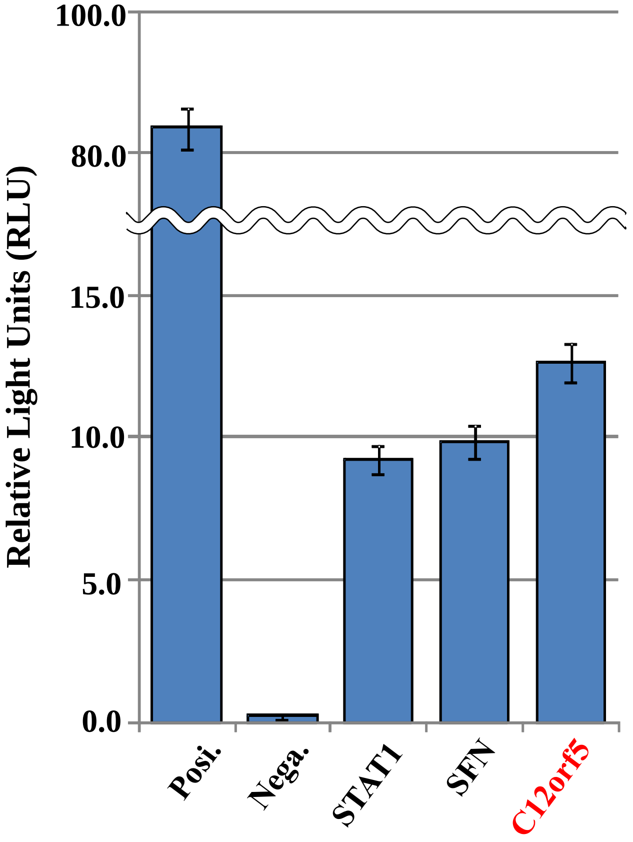
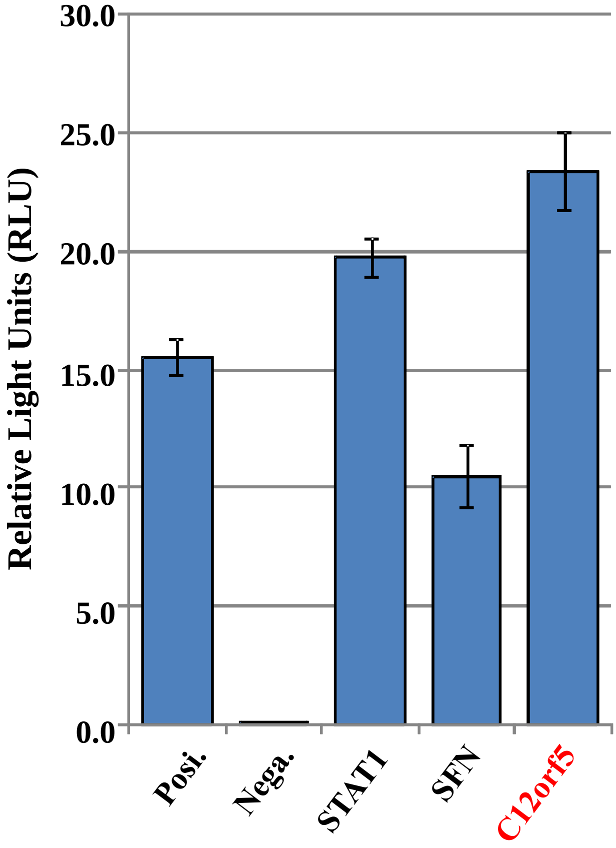
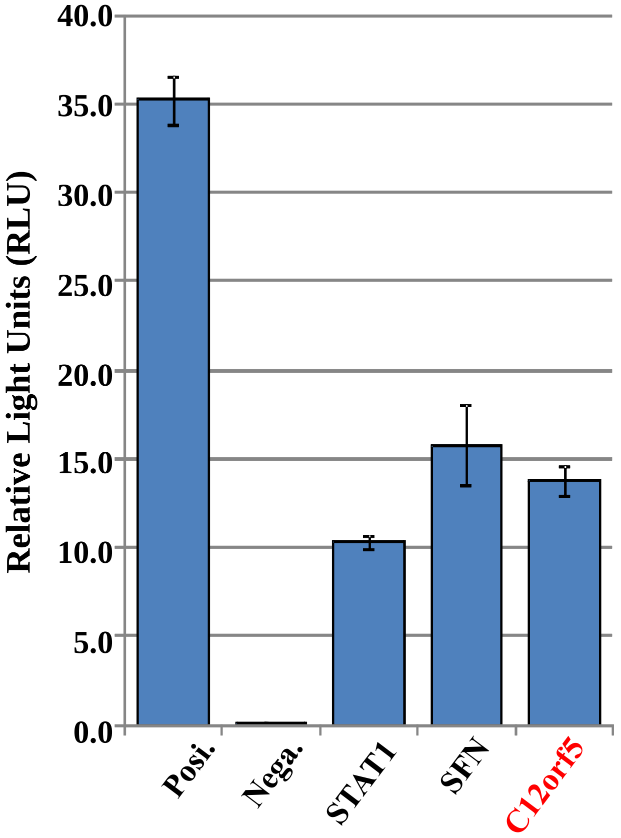
The Promoter Activities of Reporter Constructs


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 : 2009.06.26

1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5577

2nd Nucleotide Sequence
  File Name        : RDB7414F.fasta
  Sequence Size    : 400

  Unit Size to Compare = 1
  Pick up Location     = 1



[98.000% / 400 bp]     INT/OPT.Score : <    878/  1520 >

      1' GGCCTAACTG GCCGGTACCT GAGCTCGCTA GCCTCGAGGA TAGAGTGCAG CAGGTAATCG
                                                      ********* **********
     60″                                              AGAGTGCAG CAGGTAATCG

     61' AAAAAGGTTG TGGCCGGGCG CGGTGGCTCA CGCCTGTAAT CCCACCACTT TGGGAGGTCG
         ********** ********** ********** ********** ********** **********
     79″ AAAAAGGTTG TGGCCGGGCG CGGTGGCTCA CGCCTGTAAT CCCACCACTT TGGGAGGTCG

    121' AGGCGGGCGG ATCACGAGGT CAGGAGATCG AGACCATCCT GGCTAACACG GTGAAACCCT
         ********** ********** ********** ********** ********** **********
    139″ AGGCGGGCGG ATCACGAGGT CAGGAGATCG AGACCATCCT GGCTAACACG GTGAAACCCT

    181' GTCTCTACTA AAAATACAAA AAATTAGCCG GGCGTGGTGG CAGGCGCCTG TAGTCCCAGC
         ********** ********** ********** ********** ********** **********
    199″ GTCTCTACTA AAAATACAAA AAATTAGCCG GGCGTGGTGG CAGGCGCCTG TAGTCCCAGC

    241' TACTCGGGAG GCTGAGCC-- -AGAATGGCG TGAACCCGGG AGGCGGAGCT TGCAGTGAGC
         ********** ********    ********* ********** ********** **********
    259″ TACTCGGGAG GCTGAGCCAG GAGAATGGCG TGAACCCGGG AGGCGGAGCT TGCAGTGAGC
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   298' CGAGATCACA CCACTGCACT CCAGCCTGGG TGACAGAGCC AGACTCCATC TCAAAA----
        ********** ********** ********** ********** ********** ******
   319″ CGAGATCACA CCACTGCACT CCAGCCTGGG TGACAGAGCC AGACTCCATC TCAAAATAAA

   354' -AAATAAATA AATAAATAAA AAAGAGAAGG TTGCTTTAGG AGGAAGTTAA GTTTAAAAGT
         ********* ********** ********** ********** ********** **********
   379″ TAAATAAATA AATAAATAAA AAAGAGAAGG TTGCTTTAGG AGGAAGTTAA GTTTAAAAGT

   413' AAAAAGCAAA GAATTGAACA TACTGACATA TTGATTCTTT GAAAAGAAAT TTAGAACTCA
        ********** ********** *
   439″ AAAAAGCAAA GAATTGAACA T




1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5577

2nd Nucleotide Sequence
  File Name         : RDB7414R.fasta (Complementary)
  Sequence Size     : 400

  Unit Size to Compare = 1
  Pick up Location     = 1



[99.750% / 400 bp]     INT/OPT.Score : <   1594/  1594 >

   961' GGACTAACAG ACCTCATAGA ACACAGTCTG TTGGTCGCTG TACACCCGTG AGGGGTTCAT
                         **** ********** ********** ********** **** *****
    85″                  TAGA ACACAGTCTG TTGGTCGCTG TACACCCGTG AGGGATTCAT

  1021' CACAGTGGCC AGCTATAAGA CGAACGGTTG CATTCCAGCC TCAATCGCAA CAACCACAAA
        ********** ********** ********** ********** ********** **********
   129″ CACAGTGGCC AGCTATAAGA CGAACGGTTG CATTCCAGCC TCAATCGCAA CAACCACAAA
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1081’ TCAGTGCGCC GGCTTCCTTA TCTGCCCCGA ACGCAGGCTG CCGGCTATCG AGGGAAGGAA
      ********** ********** ********** ********** ********** **********
 189″ TCAGTGCGCC GGCTTCCTTA TCTGCCCCGA ACGCAGGCTG CCGGCTATCG AGGGAAGGAA

1141’ TCCTACCGCG GACTCCGCGG GCGGGGCCTC CCGCACCTGC CGCGCGCCAA TCACAGGCCG
      ********** ********** ********** ********** ********** **********
 249″ TCCTACCGCG GACTCCGCGG GCGGGGCCTC CCGCACCTGC CGCGCGCCAA TCACAGGCCG

1201’ GCGCGCAGGG GCGCAAGCGC CGCAGCCCTG GGCGGGGCCC CCGTGGCTCC CTCGTCTCCC
      ********** ********** ********** ********** ********** **********
 309″ GCGCGCAGGG GCGCAAGCGC CGCAGCCCTG GGCGGGGCCC CCGTGGCTCC CTCGTCTCCC

1261’ CCGCCCCGTC GGCCTCGCCC GGCCCTGAGT GGCCTTCGGG GATGACGTGC GAGGCCGCCT
      ********** ********** ********** ********** ********** **********
 369″ CCGCCCCGTC GGCCTCGCCC GGCCCTGAGT GGCCTTCGGG GATGACGTGC GAGGCCGCCT

1321’ CGGCCTATGG CGGCGGAGCC GGCCGGCTGC TTGGCGGAAG TGGTGTGGGG GAGGTAATCA
      ********** ********** ********** ********** ********** ******
 429″ CGGCCTATGG CGGCGGAGCC GGCCGGCTGC TTGGCGGAAG TGGTGTGGGG GAGGTA
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