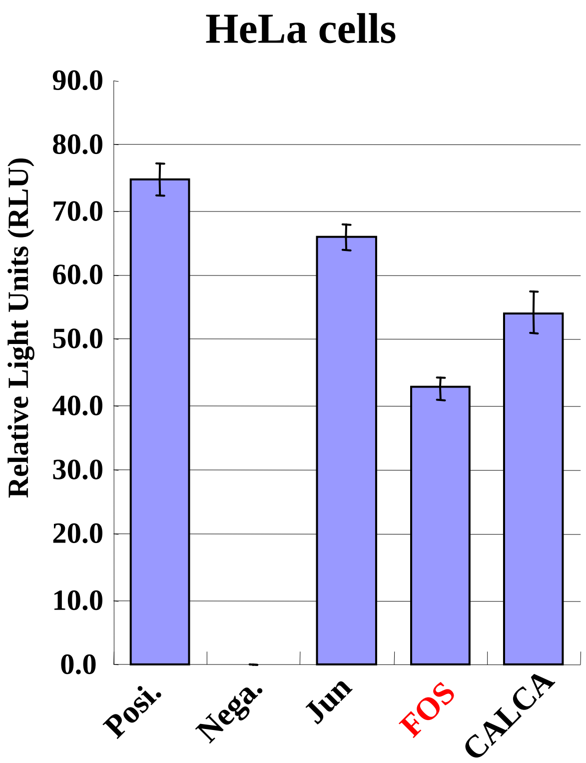
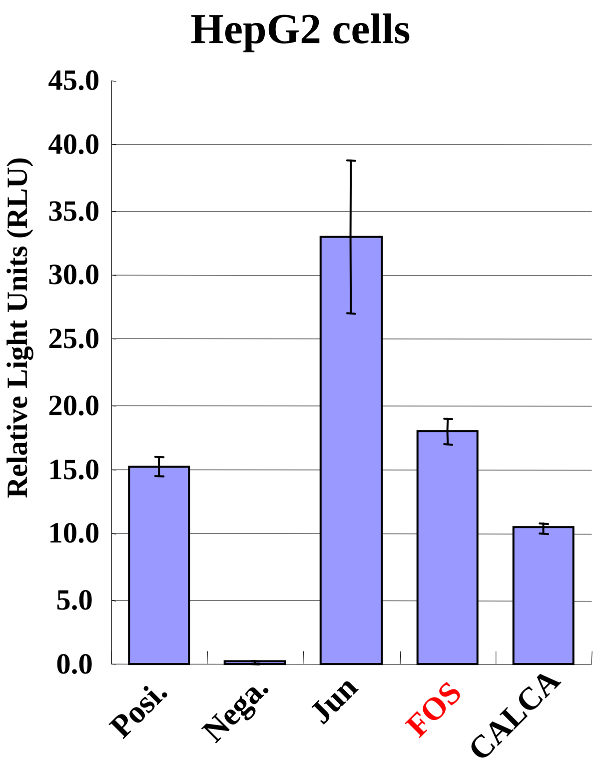
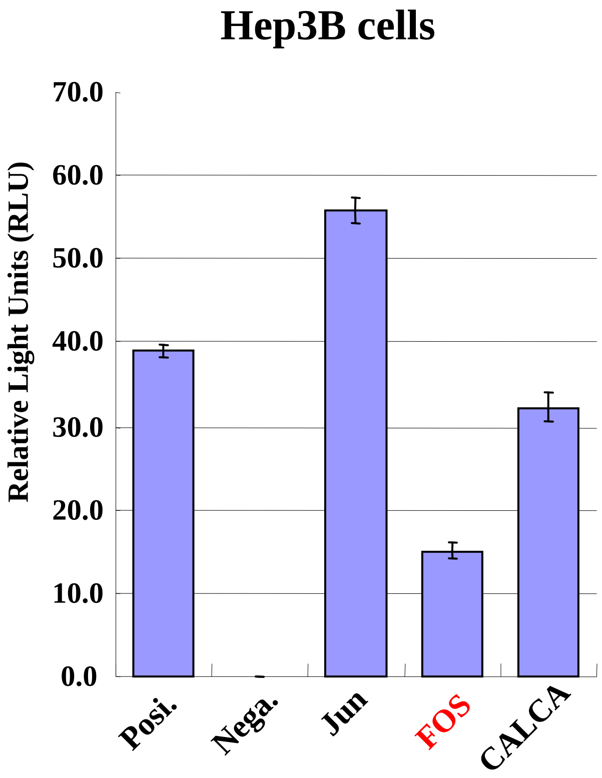
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

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

Jun: pGL4-phJun (RDB#7298)
FOS: pGL4-phFOS(RDB#7292)
CALCA:pGL4-phCALCA (RDB#7291)

2009, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.01.25

1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5528

2nd Nucleotide Sequence
  File Name         : RDB7292F.fasta
  Sequence Size     : 555

  Unit Size to Compare = 1
  Pick up Location     = 1



[97.566% / 534 bp]     INT/OPT.Score : <    246/  1938 >

     1’                                    GGCCTAACT GGCCGGTACC TGAGCTCGCT
                                           ********* *** ****** **********
     1″ GAATAGCTTT GCCGTGCGAA GACTTTCTCT NGGCCTAACT GGCTGGTACC TGAGCTCGCT

    30’ AGCCTCG-AG GATTCCCAGC AGTCGAGGTA TTCNCGCCCA GGCGCAGCTG GACACTGTCC
        ******* ** ********** **********  ** ****** ********** **********
    61″ AGCCTCGTAG GATTCCCAGC AGTCGAGGTA -TC-CGCCCA GGCGCAGCTG GACACTGTCC

    89’ TTCCAGCCCC CGTCCTCCAC CCTCNCAAGT CCGCGCTGGA AAATCACCCG CTGCGGGCTC
        ********** ********** **** ***** ********** ********** **********
   119″ TTCCAGCCCC CGTCCTCCAC CCTC-CAAGT CCGCGCTGGA AAATCACCCG CTGCGGGCTC

   149’ CCGTAAGCAC AGCTTNCCTG GCGGGACCGA ACCAGCCCTC AGCGCAGATT TGAGTTCCCC
        ********** ***** **** ********** ********** ********** **********
   178″ CCGTAAGCAC AGCTT-CCTG GCGGGACCGA ACCAGCCCTC AGCGCAGATT TGAGTTCCCC

   209’ GCAGGANAGC ACACCCCGCC TTGTCATCCC GAACTGACCA CCCTGCCCAC ATAACCANCA
        ****** *** ********** ********** ********** ********** ******* **
   237″ GCAGGA-AGC ACACCCCGCC TTGTCATCCC GAACTGACCA CCCTGCCCAC ATAACCA-CA
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269’ CCTCGCACTC CCTACCCCTG GGGCCCAGCT CAGAACCGGG CAGACACCNC CCTTCAAATG
     ********** ********** ********** ********** ******** * **********
295″ CCTCGCACTC CCTACCCCTG GGGCCCAGCT CAGAACCGGG CAGACACC-C CCTTCAAATG

329’ TCTTCGCACG TAGGTTTTGC ACAGTGTTTA TCTGCTGGTN GTCTCAGGGA TTTGACAGTT
     ********** ********** ********** *********  ********** **********
354″ TCTTCGCACG TAGGTTTTGC ACAGTGTTTA TCTGCTGGT- GTCTCAGGGA TTTGACAGTT

389’ TCCTTAATAT TCCCACACAT GGCCGAGAAA NAATAAATAA ATAAATGCGC TGTCTTCTTT
     ********** ********** **********  ********* ********** **********
413″ TCCTTAATAT TCCCACACAT GGCCGAGAAA -AATAAATAA ATAAATGCGC TGTCTTCTTT

449’ AAAAAAATAA ATAAATAAAG TNACCCAGTA TCGTAAAGTA GGTTATCGTA TTCTCTTATT
     ********** ********** * ******** ********** ********** **********
472″ AAAAAAATAA ATAAATAAAG T-ACCCAGTA TCGTAAAGTA GGTTATCGTA TTCTCTTATT

509’ TTGGATCCTC CANCTTTCTG CTTCCAAACG CAGGAACAGT GCTAGTATTG CTCGAGCCCG
     ********** ** ******* *****
531″ TTGGATCCTC CA-CTTTCTG CTTCCC
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1st Nucleotide Sequence
  File Name          : Reference Seq.gnu
  Sequence Size      : 5528

2nd Nucleotide Sequence
  File Name          : RDB7292R.fasta (Complementary)
  Sequence Size      : 236

  Unit Size to Compare = 1
  Pick up Location     = 1


[95.745% / 235 bp]     INT/OPT.Score : <    507/   816 >
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1081’ CNTGCGAAAT GCTCACGAGA TTAGGACACG CGCCAAGGCG GGGGCAGGGA GCNTGCGA-G
                           ******* ********** ********** * .***** *
   1″                         GGACACG CGCCAAGGCG GGGGCAGGGA GGCTGCGAGG

1140’ CGCTGGGGAC GCAGCCGGGC GGCCG-CAGA AGCGCCCAGG CCCGCNGCGC CACCCCTCTG
      ********** ********** ***** **** ********** ***** **** **********
  38″ CGCTGGGGAC GCAGCCGGGC GGCCGCCAGA AGCGCCCAGG CCCGC-GCGC CACCCCTCTG

1199’ GCGCCACCGT GGTTGAGCCC GTGACGTTTA CACTCANTTC ATAAAACGCT TGTTATAAAA
      ********** ********** ********** ******.*** ********** **********
  97″ GCGCCACCGT GGTTGAGCCC GTGACGTTTA CACTCAATTC ATAAAACGCT TGTTATAAAA

1259’ GCAGTGGCTG CGGCGCC-TC GTACTCCANA CCGCATCTG- CAGCGAGCAT CTGAGAAGCC
      ********** ******* ** ******** * *********  ********** **********
 157″ GCAGTGGCTG CGGCGCCTTC GTACTCCA-A CCGCATCTGC CAGCGAGCAT CTGAGAAGCC

1317’ AAGACTGAG- CCATCAAGAT CTGGCCTCGG CGGCCAAGCT TGGCAATCCG GTACTGTTGG
      *********  ********
 216″ AAGACTGAGC CCATCAAGGA T
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