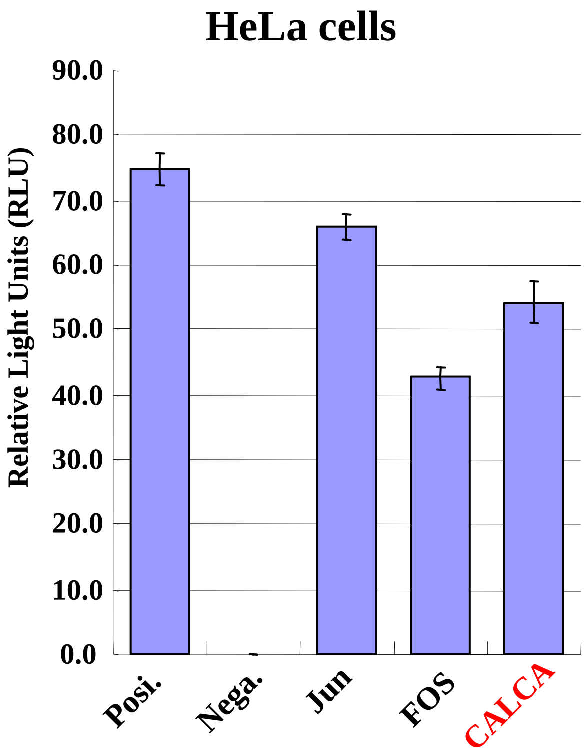
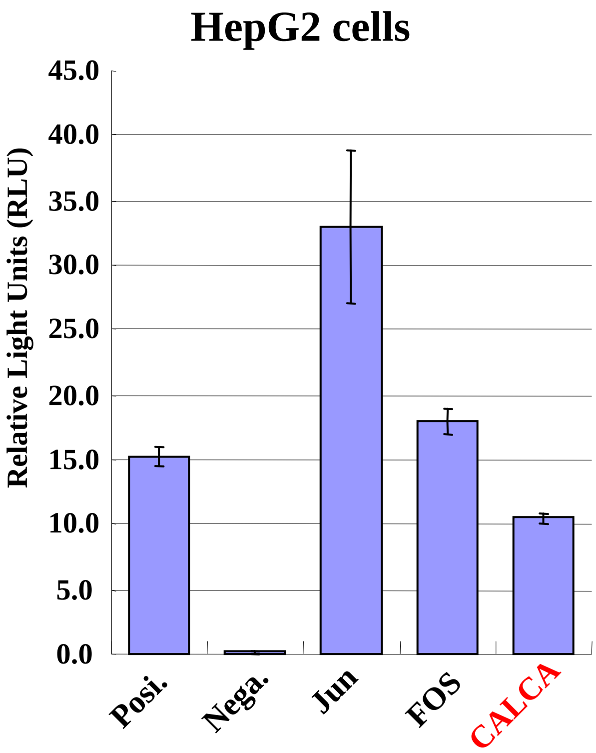
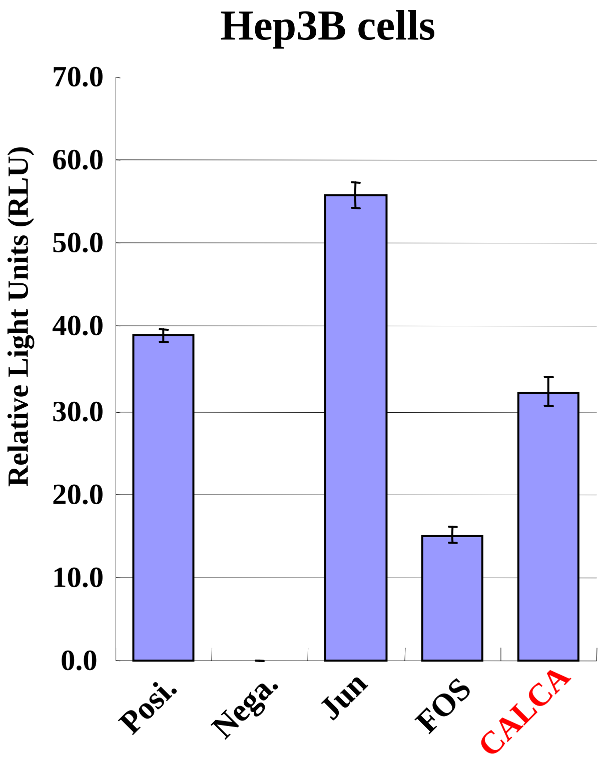
The Promoter Activities of Reporter Constructs







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 : 2009.07.02

1st Nucleotide Sequence
  File Name         : Reference Seq.GNU
  Sequence Size     : 5588

2nd Nucleotide Sequence
  File Name         : RDB7291F.fasta
  Sequence Size     : 644

  Unit Size to Compare = 1
  Pick up Location     = 1



[97.319% / 634 bp]     INT/OPT.Score : <    244/  2300 >

     1’                      G GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT
                             * ********** ********** ********** **********
     1″ GGTGCCAGAA CATTTCTCTG GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT

    42’ TTGGGACACG TTTGAGTGAN ACACCTCAGG ATACTCTTCT GGCCAGTATC TGTTTTTTAG
        ********** *********  ********** ********** ********** **********
    61″ TTGGGACACG TTTGAGTGA- ACACCTCAGG ATACTCTTCT GGCCAGTATC TGTTTTTTAG

   102’ TGTCTGTGAT NTCAGAGTGG GCACATGTTG GGAGACAGTA ATGGGTTTGG GTGTGTGTAA
        **********  ********* ********** ********** ********** **********
   120″ TGTCTGTGAT -TCAGAGTGG GCACATGTTG GGAGACAGTA ATGGGTTTGG GTGTGTGTAA

   162’ ANTGAGTGTG ACCGGAAGCG AGTGTGAGCT TGATCTAGGC AGGGACCACA CANGCACTGT
        * ******** ********** ********** ********** ********** ** *******
   179″ A-TGAGTGTG ACCGGAAGCG AGTGTGAGCT TGATCTAGGC AGGGACCACA CA-GCACTGT

   222’ CACACCTGCC TGCTCTTTAG TAGAGGACTG AAGTGCGGGG GTGNGGGGTA CGGGGCCGGA
        ********** ********** ********** ********** *** ****** **********
   237″ CACACCTGCC TGCTCTTTAG TAGAGGACTG AAGTGCGGGG GTG-GGGGTA CGGGGCCGGA
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282' ATAGAATGTC TCTGGGACAT CTTGGCAAAC AGCANGCCGG AAGCAAAGGG GCAGCTGTGC
     ********** ********** ********** **** ***** ********** **********
296″ ATAGAATGTC TCTGGGACAT CTTGGCAAAC AGCA-GCCGG AAGCAAAGGG GCAGCTGTGC

342' AAACGGCTCA GGCAGGTGAT GGATGNGCAG GGTAGGAAGG GGGAGGTCCA GAGGTCTGGA
     ********** ********** ***** **** ********** ********** **********
355″ AAACGGCTCA GGCAGGTGAT GGATG-GCAG GGTAGGAAGG GGGAGGTCCA GAGGTCTGGA

402' TGGAGGCTTC CGCATCNTGT ACCTTGCAAC TCACCCCTCA GGCCCAGCAG GTCATCGGCC
     ********** ****** *** ********** ********** ********** **********
414″ TGGAGGCTTC CGCATC-TGT ACCTTGCAAC TCACCCCTCA GGCCCAGCAG GTCATCGGCC

462' CCCTCCTNCA CACATGTAAT GGATCTGAAG AGTACCCCGG GACAGTCCGG GGAGATGGNA
     ******* ** ********** ********** ********** ********** ******** *
473″ CCCTCCT-CA CACATGTAAT GGATCTGAAG AGTACCCCGG GACAGTCCGG GGAGATGG-A

522' GATTCGGAAA GTATCCATGG AGATCTTACA GAATCCCCTG TGCGGACCAN GGAAACTCTT
     ********** ********** ********** *********  *********  **********
531″ GATTCGGAAA GTATCCATGG AGATCTTACA GAATCCCCTA TGCGGACCA- GGAAACTCTT

582' GTAGATCCCT G-CCTATCTG A-GGCCCAGG CGCT-GGGCT GTTNTCTCAC AATATTCCTT
     ********** * ******** * ******** **** ***** ***.****** **.
590″ GTAGATCCCT GCCCTATCTG AGGGCCCAGG CGCTGGGGCT GTTTTCTCAC AANTA
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1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5588

2nd Nucleotide Sequence
  File Name        : RDB7291R.fasta (Complementary)
  Sequence Size    : 621

  Unit Size to Compare = 1
  Pick up Location     = 1
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[97.120% / 625 bp]     INT/OPT.Score : <    551/  2253 >

   841' TCTTGGGCCC AGAA-CCCA- -CCCTTA-GG GGCATTAACC NTTTAAAATC TCACTTGGGC
                **  **** ****   ** *** ** ********** .********* **********
     1″    CCCCCCA AGAACCCCAC CCCTTTAGGG GGCATTAACC TTTTAAAATC TCACTTGGGC

   897' AGGGGTCTGG GATCAGAGTT GGAAGAGTCC CNTACAATCC TGGACCCTTT CCGCCAAATC
        ********** ********** ********** * ******** ********** **********
    58″ AGGGGTCTGG GATCAGAGTT GGAAGAGTCC C-TACAATCC TGGACCCTTT CCGCCAAATC

   957' GTGAAACCAG GGGTGGAGTG GGNGCGAGGG TTCAAAACCA GGCCGGACTG AGAGGTGAAA
        ********** ********** ** ******* ********** ********** **********
   117″ GTGAAACCAG GGGTGGAGTG GG-GCGAGGG TTCAAAACCA GGCCGGACTG AGAGGTGAAA

  1017' TTCACCATGA CGTNCAAACT GCCCTCAAAT TCCCGCTCAC TTTAAGGGCG TTACTTGTTG
        ********** *** ****** ********** ********** ********** **********
   176″ TTCACCATGA CGT-CAAACT GCCCTCAAAT TCCCGCTCAC TTTAAGGGCG TTACTTGTTG

  1077' GTGCNCCCCA CCATCCCCCA CCATTTCCAT CAATGACCTC AATGCAAATA CAAGTNGGGA
        **** ***** ********** ********** ********** ********** ***** ****
   235″ GTGC-CCCCA CCATCCCCCA CCATTTCCAT CAATGACCTC AATGCAAATA CAAGT-GGGA

  1137' CGGTCCTGCT GGATCCTCCA GGTTCTGGAA GCATGAGGGT GACGCANACC CAGGGGCAAA
        ********** ********** ********** ********** ****** *** **********
   293″ CGGTCCTGCT GGATCCTCCA GGTTCTGGAA GCATGAGGGT GACGCA-ACC CAGGGGCAAA

  1197' GGACCCCTCC GCCCATTGGT TGCTGTGCAC TGGCGGANAC TTTCCCGACC CACAGCGGCG
        ********** ********** ********** ******* ** ********** **********
   352″ GGACCCCTCC GCCCATTGGT TGCTGTGCAC TGGCGGA-AC TTTCCCGACC CACAGCGGCG

  1257' GGAATAAGAG CAGTCGCTGG CGCTGGGANG GCATCAGAGA CACTGCCCAG CCCAAGTGTC
        ********** ********** ******** * ********** ********** **********
   411″ GGAATAAGAG CAGTCGCTGG CGCTGGGA-G GCATCAGAGA CACTGCCCAG CCCAAGTGTC

  1317' GCCGCCGCTT CCACAGGGCT CTGGCTGGAC GCCGCCGCCG CCGCTGCCAC CGCCTCTGAT
        ********** ********** ********** ********** ********** **********
   470″ GCCGCCGCTT CCACAGGGCT CTGGCTGGAC GCCGCCGCCG CCGCTGCCAC CGCCTCTGAT
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1377' CCAAGCCACC TATCAAGATC TGGCCTCGGC GGCCAAGCTT GGC-AATCCG GTACTGTTGG
      ********** ********** ********** ********** *** ****** **********
 530″ CCAAGCCACC TATCAAGATC TGGCCTCGGC GGCCAAGCTT GGCAAATCCG GTACTGTTGG

1436' TAAAGCCACC ATGGAA-GAT GCCAAA-AAC ATTAAGAAGG GCCCAGCGCC ATTCTACCCA
      ********** ****** *** ****** *** **
 590″ TAAAGCCACC ATGGAACGAT GCCAAACAAC AT
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