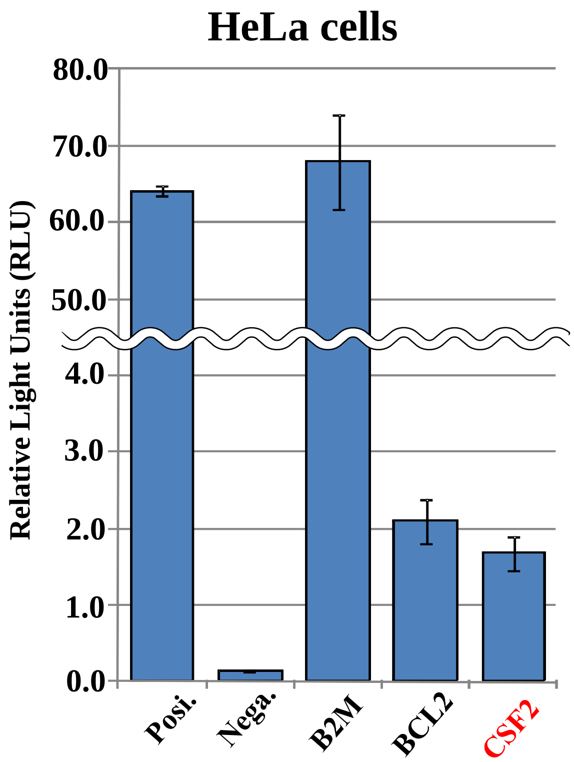
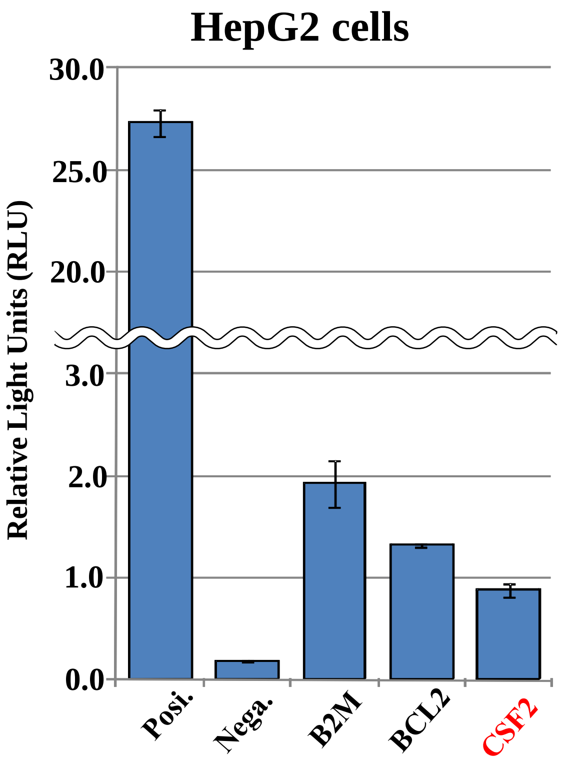
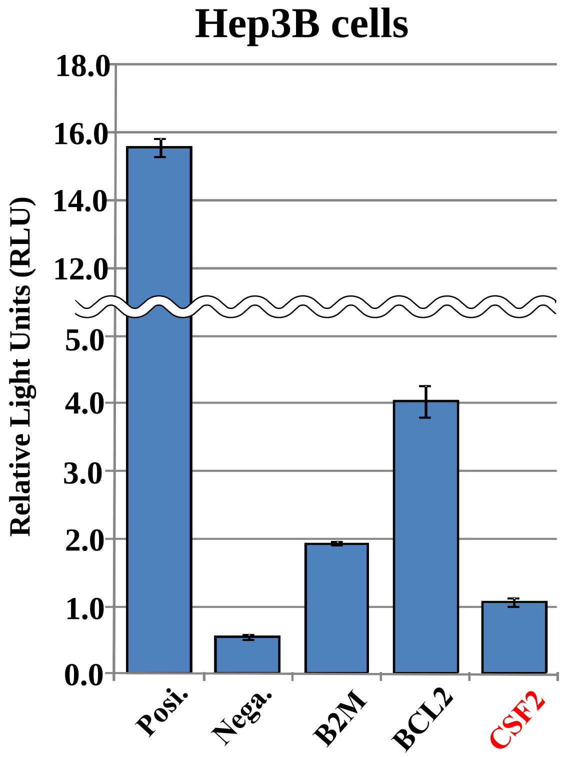
The Promoter Activities of Reporter Constructs







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

B2M: pGL4-phB2M (RDB# 7479)
BCL2: pGL4-phBCL2 (RDB# 7567)
CSF2: pGL4-phCSF2 (RDB# 7482)

2010, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.08.17

1st Nucleotide Sequence
  File Name         : Reference Seq.GNU
  Sequence Size     : 5688

2nd Nucleotide Sequence
  File Name         : RDB7482F.fasta
  Sequence Size     : 711

  Unit Size to Compare = 1
  Pick up Location     = 1



[97.585% / 704 bp]     INT/OPT.Score : <    368/  2577 >

      1'                     G GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT
                             * ********** ********** ********** **********
      1" GGTGCCAGAA CATTTCTCTG GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT

     42' CTCCACCTGC TCTCTGAAGG CTCGCCAACC TGAGTCNCAG CAGAATGTTC TCGCTTGTGT
         ********** ********** ********** ****** *** ********** **********
     61" CTCCACCTGC TCTCTGAAGG CTCGCCAACC TGAGTC-CAG CAGAATGTTC TCGCTTGTGT

    102' CCAACCCCAC TGGTTTAGGC TGAATCANGC CTCTAGGGCC CAGAGGCACT GCACCTGGAG
         ********** ********** ******* ** ********** ********** **********
    120" CCAACCCCAC TGGTTTAGGC TGAATCA-GC CTCTAGGGCC CAGAGGCACT GCACCTGGAG

    162' TAGGGAGCTT CTCCAGTANT CAGAGTCACC TTCAGAGGCC TGGAGCCTTT CATAAAGCAG
         ********** ******** * ********** ********** ********** **********
    179" TAGGGAGCTT CTCCAGTA-T CAGAGTCACC TTCAGAGGCC TGGAGCCTTT CATAAAGCAG

    222' GTAAGAGGAN CTCAATAGAT GCATCTGCAT GGAAAACATC CTCCCCTCTA CCAGGCACCT
         *********  ********** ********** ********** ********** **********
    238" GTAAGAGGA- CTCAATAGAT GCATCTGCAT GGAAAACATC CTCCCCTCTA CCAGGCACCT
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282’ NGTATGTACA ACCAATCACA GCAGCACACA TACACCCAGA AATGGGCACG TNGTGGGCCC
      ********* ********** ********** ********** ********** * ********
297″ -GTATGTACA ACCAATCACA GCAGCACACA TACACCCAGA AATGGGCACG T-GTGGGCCC

342’ ACACCCCTTT AGCTATGAAA CCCAGGCATG GGGCAGCTTG AGNCCAGATA CCTTGTGCAA
     ********** ********** ********** ********** ** ******* **********
355″ ACACCCCTTT AGCTATGAAA CCCAGGCATG GGGCAGCTTG AG-CCAGATA CCTTGTGCAA

402’ ACACAAACTC GTGCTGTCTT CTCTGAACTC CATNTGTGAA AATCAAACAC TTGTCAGCCC
     ********** ********** ********** *** ****** ********** **********
414″ ACACAAACTC GTGCTGTCTT CTCTGAACTC CAT-TGTGAA AATCAAACAC TTGTCAGCCC

462’ CTCAAGAGCC TTTAGATTTC CTACNTTCCA CACTTCCACA GAAAGGCCTC TGGAGTTGGG
     ********** ********** **** ***** ********** ********** **********
473″ CTCAAGAGCC TTTAGATTTC CTAC-TTCCA CACTTCCACA GAAAGGCCTC TGGAGTTGGG

522’ GGATGCTGGG GTTATNGTAG GAAATTAAGC CTGGAGGGCC TTGCTGGGGA AGCCATTGTC
     ********** ***** **** ********** *** ****** ********** **********
532″ GGATGCTGGG GTTAT-GTAG GAAATTAAGC CTGAAGGGCC TTGCTGGGGA AGCCATTGTC

582’ CCTGTANCCT GAGATGGATG CAGCCACAGC CCTGGAGCCA GCCTGAAGCT CCTGGTGNTC
     ****** *** ********** ********** ********** ********** ******* **
591″ CCTGTA-CCT GAGATGGATG CAGCCACAGC CCTGGAGCCA GCCTGAAGCT CCTGGTG-TC

642’ TTCT-GGGGG CTACATATAG GAGTGTAGTC CGAACCTCAG AGGGGCAAAN CCTGCTCTGC
     **** ***** ********** ********** ********** ****** **. **********
649″ TTCTGGGGGG CTACATATAG GAGTGTAGTC CGAACCTCAG AGGGGC-AAC CCTGCTCTGC

701’ AGAGGGAATC AAGGTTCACA TAACCAGAGA GGGGAGTCAC NTCAGGAAGG TGGCTCCAGA
     * *
708″ AAAA
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1st Nucleotide Sequence

File Name : Reference Seq.GNU

Sequence Size : 5688

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2nd Nucleotide Sequence
  File Name        : RDB7482R.fasta (Complementary)
  Sequence Size    : 710

  Unit Size to Compare = 1
  Pick up Location     = 1



[97.642% / 721 bp]     INT/OPT.Score : <    448/  2655 >

    841’ TGNCTGGATG TGCAC-ATGG TGGTCATTCC CTCTGCTCAC AGGGGCAGGG GTCCNCCCCT
                *.* ***** **** * ******** ********** **********  *** *****
      1″       AANG TGCACAATGG TTGTCATTCC CTCTGCTCAC AGGGGCAGGG TTCC-CCCCT

    900’ TACTGGACTG AGGTTGCCCC CTGCTCCAGG TCCTGGGTGG GAGCCNCATG TGAACTGTCA
         ********** *** ****** ********** ********** ***** **** **********
     54″ TACTGGACTG AGGGTGCCCC CTGCTCCAGG TCCTGGGTGG GAGCC-CATG TGAACTGTCA

    960’ GTGGGGCAGG TCTGTGAGAG CTCCCCTCAC ACTCAANGTC TCTCACAGTG GCCAGAGAAG
         ********** ********** ********** ****** *** ********** **********
    113″ GTGGGGCAGG TCTGTGAGAG CTCCCCTCAC ACTCAA-GTC TCTCACAGTG GCCAGAGAAG

   1020’ AGGAAGGCTG GAGTCAGAAT GAGGCACNCA GGGCGGGCAT AGCCTGCCCA AAGGCCCCTG
         ********** ********** ******* ** ********** ********** **********
    172″ AGGAAGGCTG GAGTCAGAAT GAGGCAC-CA GGGCGGGCAT AGCCTGCCCA AAGGCCCCTG

   1080’ GGATTACAGG CAGGATGGNG GAGCCCTATC TAAGTGTCTC CCACGCCCCA CCCCAGCCAT
         ********** ******** * ********** ********** ********** **********
    231″ GGATTACAGG CAGGATGG-G GAGCCCTATC TAAGTGTCTC CCACGCCCCA CCCCAGCCAT

   1140’ TCCAGGCCAN GGAAGTCCAA ACTGTGCCCC TCAGAGGGAG GGGGCAGCCT CAGGCCCATT
         *********  ********** ********** ********** ********** **********
    290″ TCCAGGCCA- GGAAGTCCAA ACTGTGCCCC TCAGAGGGAG GGGGCAGCCT CAGGCCCATT

   1200’ NCAGACTGCC CAGGGAGGGC TGGAGAGCCC TCAGGAAGGC GGGTGGGTGG GNCTGTCGGT
          ********* ********** ********** ********** ********** * ********
    349″ -CAGACTGCC CAGGGAGGGC TGGAGAGCCC TCAGGAAGGC GGGTGGGTGG G-CTGTCGGT
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1260' TCTTGGAAAG GTTCATTAAT GAAAACCCCC AAGCCTGACC ACNCTAGGGA AAAGGCTCAC
      ********** ********** ********** ********** ** ******* **********
 407″ TCTTGGAAAG GTTCATTAAT GAAAACCCCC AAGCCTGACC AC-CTAGGGA AAAGGCTCAC

1320' CGTTCCCATG TGTGGCTGAT AAGGGCCAGG AGANTTCCAC AGTTCAGGTA GTTCCCCCGC
      ********** ********** ********** *** ****** ********** **********
 466″ CGTTCCCATG TGTGGCTGAT AAGGGCCAGG AGA-TTCCAC AGTTCAGGTA GTTCCCCCGC

1380' CTCCCTGGCA TTTTGTGGTC ACCANTTAAT CATTTCCTCT GTGTATTTAA GAGCTCTTTT
      ********** ********** **** ***** ********** ********** **********
 525″ CTCCCTGGCA TTTTGTGGTC ACCA-TTAAT CATTTCCTCT GTGTATTTAA GAGCTCTTTT

1440' GCCAGTGAGC CCAGTNACAC AGAGAGAAAG GCTAAAGTTC TCTGGAGGAT CAAGATCTGG
      ********** ***** **** ********** ********** ********** **********
 584″ GCCAGTGAGC CCAGT-ACAC AGAGAGAAAG GCTAAAGTTC TCTGGAGGAT CAAGATCTGG

1500' CCTCGGCGGC CAAGCTTGGC AATCCGGTAC TGTTGGTAAA GCCACCATGG AAGATGCCAA
      ********** ********** ********** ********** ********** **********
 643″ CCTCGGCGGC CAAGCTTGGC AATCCGGTAC TGTTGGTAAA GCCACCATGG AAGATGCCAA

1560' AAACATTAAG AAGGGCCCAG CGCCATTCTA CCCACTCGAA GACGGGACCG CCGGCGAGCA
      ********
 703″ AAACATTA
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