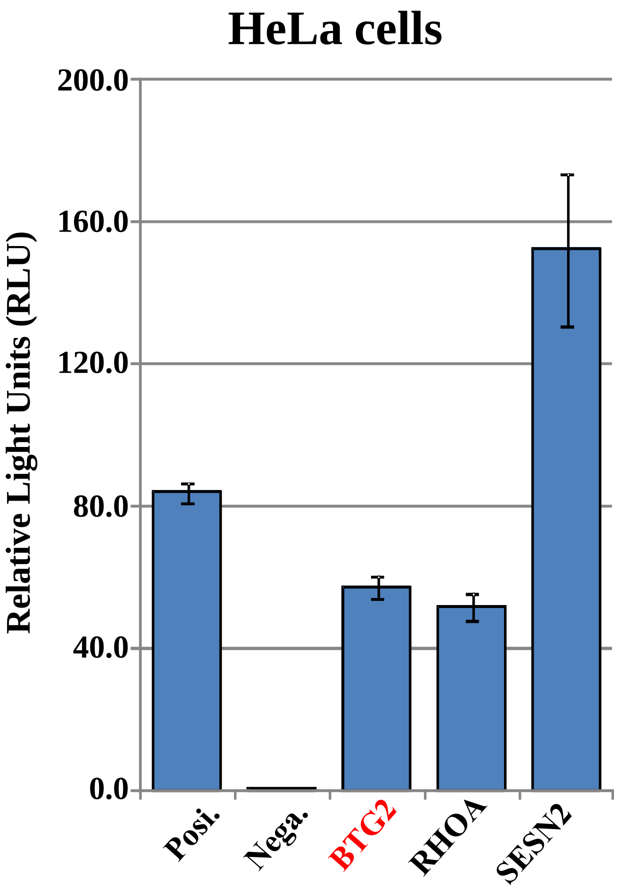
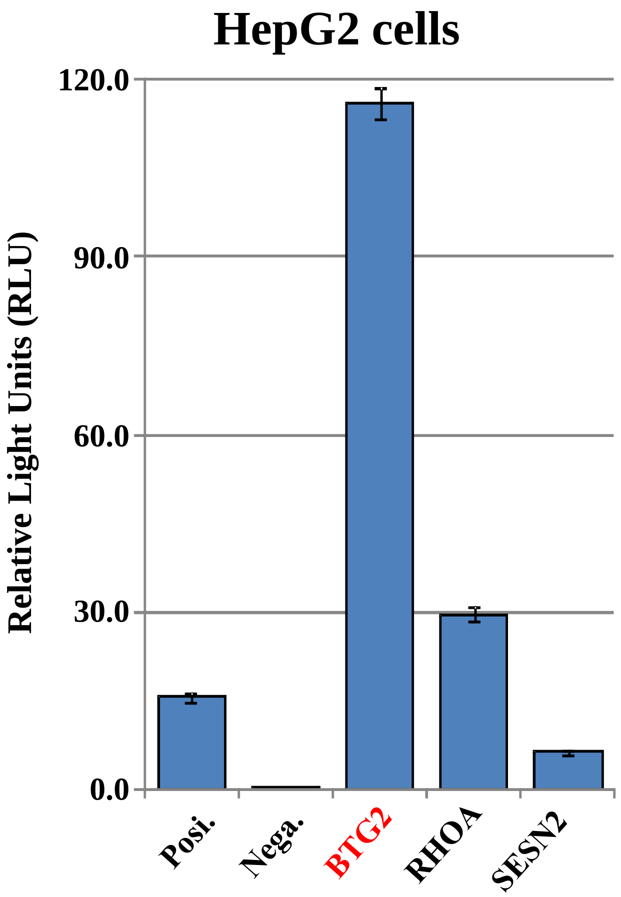
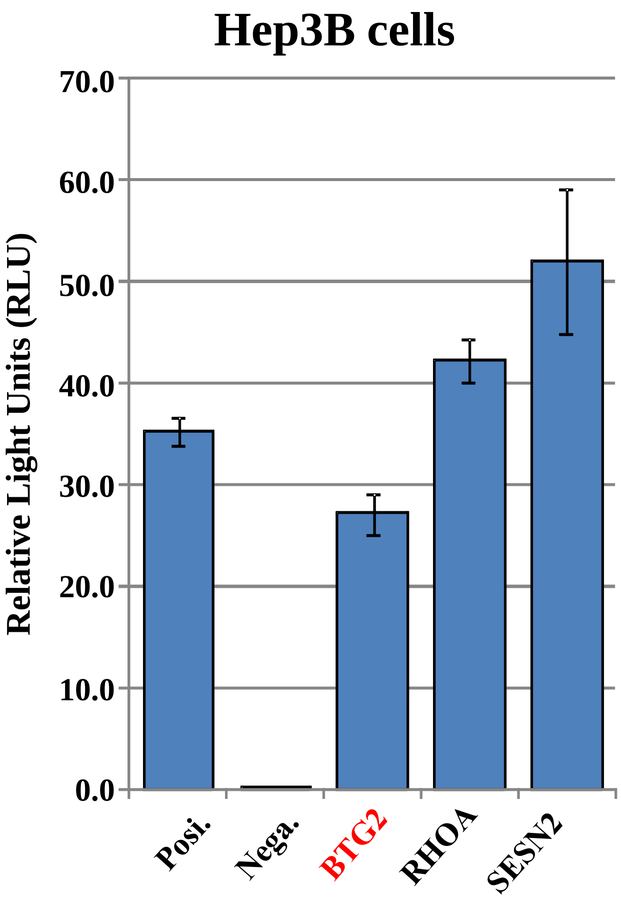
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

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

BTG2: pGL4-phBTG2 (RDB# 7402)
RHOA: pGL4-phRHOA (RDB# 7404)
SESN2: pGL4-phSESN2 (RDB# 7413)

2010, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.03.02

1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5598

2nd Nucleotide Sequence
  File Name        : RDB7402F.fasta
  Sequence Size    : 592

  Unit Size to Compare = 1
  Pick up Location     = 1



[99.475% / 571 bp]     INT/OPT.Score : <   1745/  2249 >

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

    42' GAACAGGAGC AGGATGGAAA GACAGGAGGA CAGACTATGC AGATGAGAAA AGCCACTGTA
        ********** ********** ********** ********** ********** **********
    61" GAACAGGAGC AGGATGGAAA GACAGGAGGA CAGACTATGC AGATGAGAAA AGCCACTGTA

   102' AAACAGTAAA CA-TCAAGAC AGGCTACATG CA-TAGGACC TCTCCAAGGA AAGGCAGCCT
        ********** ** ******* ********** ** ******* ********** **********
   121" AAACAGTAAA CATTCAAGAC AGGCTACATG CATTAGGACC TCTCCAAGGA AAGGCAGCCT

   160' AGAGAAAAGG GAGGAGGACT GAGGAGACAT AGTGCGGGGA ACGGGGCACG AAGGGATCCA
        ********** ********** ********** ********** ********** **********
   181" AGAGAAAAGG GAGGAGGACT GAGGAGACAT AGTGCGGGGA ACGGGGCACG AAGGGATCCA

   220' GGGGCAGCAC AGCCAGACAG GGGGGTGGAG AAGCCTGGGG CACAAGGAAA AAAGACAGGG
        ********** ********** ********** ********** ********** **********
   241" GGGGCAGCAC AGCCAGACAG GGGGGTGGAG AAGCCTGGGG CACAAGGAAA AAAGACAGGG
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    280’ ACACGGCTTC CAGAAGGTGG TCAGAGGGCT CAGAGTCCAA GGAAAATAGG AATTTACAGA
         ********** ********** ********** ********** ********** **********
    301″ ACACGGCTTC CAGAAGGTGG TCAGAGGGCT CAGAGTCCAA GGAAAATAGG AATTTACAGA

    340’ GGCCACTGGG TTTTAGTCAC CTTACAAACA CGGCATCTGT ATGCCAGACC CTGGGCCAGG
         ********** ********** ********** ********** ********** **********
    361″ GGCCACTGGG TTTTAGTCAC CTTACAAACA CGGCATCTGT ATGCCAGACC CTGGGCCAGG

    400’ CTTCACGGTG TTGGGTAGAA GTTATCCTCA TTCAGCAGAC ATCTACCGAG TGCCTGTGAT
         ********** ********** ********** ********** ********** **********
    421″ CTTCACGGTG TTGGGTAGAA GTTATCCTCA TTCAGCAGAC ATCTACCGAG TGCCTGTGAT

    460’ GGTGGCGGTC CCTGAGTGTG GAAGAGGGAG ACTGAGGCCA GATTCTTTCT CGAGAAGGTC
         ********** ********** ********** ********** ********** **********
    481″ GGTGGCGGTC CCTGAGTGTG GAAGAGGGAG ACTGAGGCCA GATTCTTTCT CGAGAAGGTC

    520’ CAAACCACAA TGAGGAAGGA AGACGGCTGG GGGAAGGAGG GAGTGGACGG AAAAATACGT
         ********** ********** ********** ********** ********.*
    541″ CAAACCACAA TGAGGAAGGA AGACGGCTGG GGGAAGGAGG GAGTGGACNG GG
    500″ CTGTCCTCCT GTCTTTCCAT CCTGCTCCTG TTCATCCTCG AGGCTAGCGA GCTCAGGTAC
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1st Nucleotide Sequence
  File Name       : Reference Seq.gnu
  Sequence Size   : 5598

2nd Nucleotide Sequence
  File Name       : RDB7402R.fasta (Complementary)
  Sequence Size   : 638

  Unit Size to Compare = 1
  Pick up Location     = 1


[97.561% / 574 bp]     INT/OPT.Score : <   1200/  2138 >
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 841' AGAGACGAGG CAAAGCGGTA AAATGGTGAC AACACGTCCT GGTGAGTGGT TCTGACCGTG

   1″          A GGGTGGGGGG TTTTTCCTTG GAACCCCCGG GTGGGAAAAT TGGGTTTGGG

 901' AATGGTTGGA AAATGCTGTG GGAATC-AGA AA--GGGGAA -CCGTCTGGG AGAGGTGGTG
                 ** ** *   **** *** **  ******   ********* **********
  52″ GAAAAAAATG GCTTGGTGGG AAAATCAAGA AAGGGGGGAA CCCGTCTGGG AGAGGTGGTG

 957' TCACCGAAGG CTTCTCGGAG GAGGTGGCCT CTAACTCGAG CCTTAAAAAT GGGCGAAGAG
      ********** ********** ********** ********** ********** **********
 112″ TCACCGAAGG CTTCTCGGAG GAGGTGGCCT CTAACTCGAG CCTTAAAAAT GGGCGAAGAG

1017' GCGAGGCCGG GGCCTGCCCC GCGCGGAGTA CTCGGGAGCC GCCTCCCTCC TTTCAGAGCT
      ********** *********  ********** ********** ********** **********
 172″ GCGAGGCCGG GGCCTGCCCG GCGCGGAGTA CTCGGGAGCC GCCTCCCTCC TTTCAGAGCT

1077' CTCAGTCCCG TCCCCGGGCC TCGCTTTCTC CTCTCGCCTC GCTCAGCTCA GCCGGGCGCA
      ********** ********** ********** ********** ********** **********
 232″ CTCAGTCCCG TCCCCGGGCC TCGCTTTCTC CTCTCGCCTC GCTCAGCTCA GCCGGGCGCA

1137' GGTTCCTAGC ACTGACGACA GCGAGCGATG ACCTCAGCGC CGCCAAGGCT GCGAGGGCGG
      ********** ********** ********** ********** ********** **********
 292″ GGTTCCTAGC ACTGACGACA GCGAGCGATG ACCTCAGCGC CGCCAAGGCT GCGAGGGCGG

1197' GGGCTGGGGT GGCGGGGGCG GGGAAAAGCG CCGGA--GCG GGGCCGAGCG GAGCGGCTCC
      ********** ********** ********** *****  *** ********** **********
 352″ GGGCTGGGGT GGCGGGGGCG GGGAAAAGCG CCGGAGCGCG GGGCCGAGCG GAGCGGCTCC

1255' GGGCCCCGCC CCCATCCTCT GGCCGCGACC AATGAGCGCC GCCGCCGGCT GCCCCCCTAC
      ********** ********** ********** ********** ********** **********
 412″ GGGCCCCGCC CCCATCCTCT GGCCGCGACC AATGAGCGCC GCCGCCGGCT GCCCCCCTAC

1315' CTCCCTGGAC CTCCTGAAAA ACGCTGCCCG GGGAAAGTCC GGGCAGAGCC CGAGCAGCGG
      ********** ********** ********** ********** ********** **********
 472″ CTCCCTGGAC CTCCTGAAAA ACGCTGCCCG GGGAAAGTCC GGGCAGAGCC CGAGCAGCGG

1375' CCAGGGTAAC GCTGTCTTGT GGAATCAAGA TCTGGCCTCG GCGGCCAAGC TTGGCA-ATC
      ********** ********** ********** ********** ********** ****** ***
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 532″ CCAGGGTAAC GCTGTCTTGT GGAATCAAGA TCTGGCCTCG GCGGCCAAGC TTGGCACATC

1434' CGGTACTGTT GGTAAAGCCA CCATGGAA-G ATGCCAAA-A ACATTAAGAA GGGCCCAGCG
      ********** ********** ******** * ******** * *******
 592″ CGGTACTGTT GGTAAAGCCA CCATGGAACG ATGCCAAACA ACATTAA
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