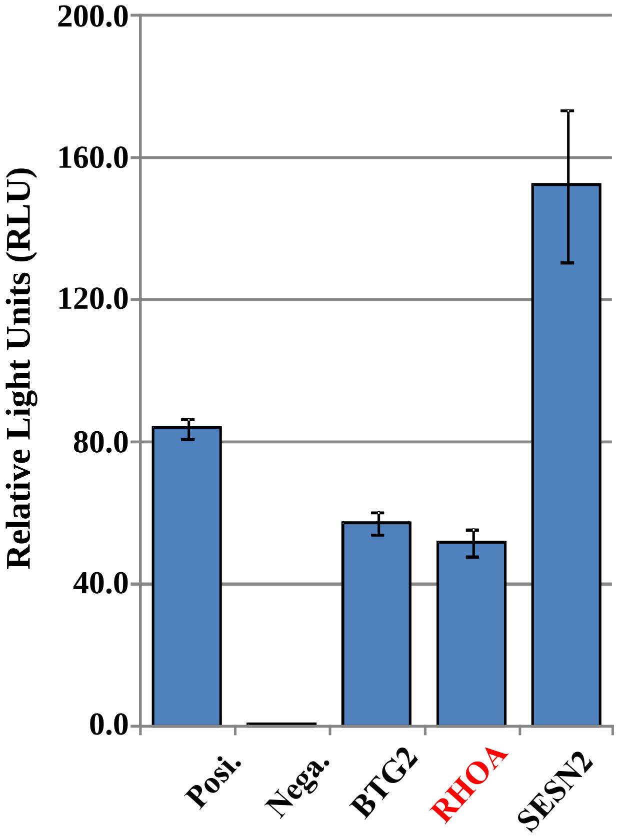
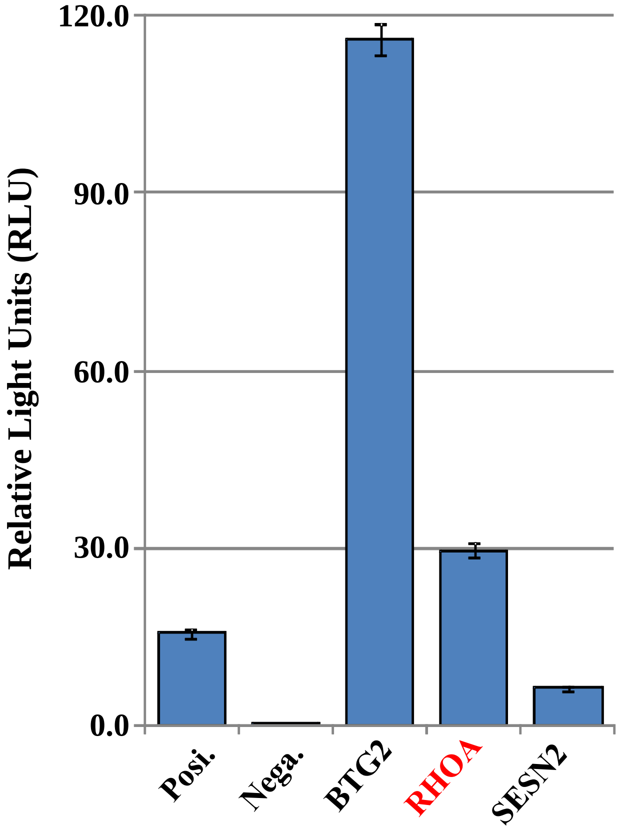
The Promoter Activities of Reporter Constructs

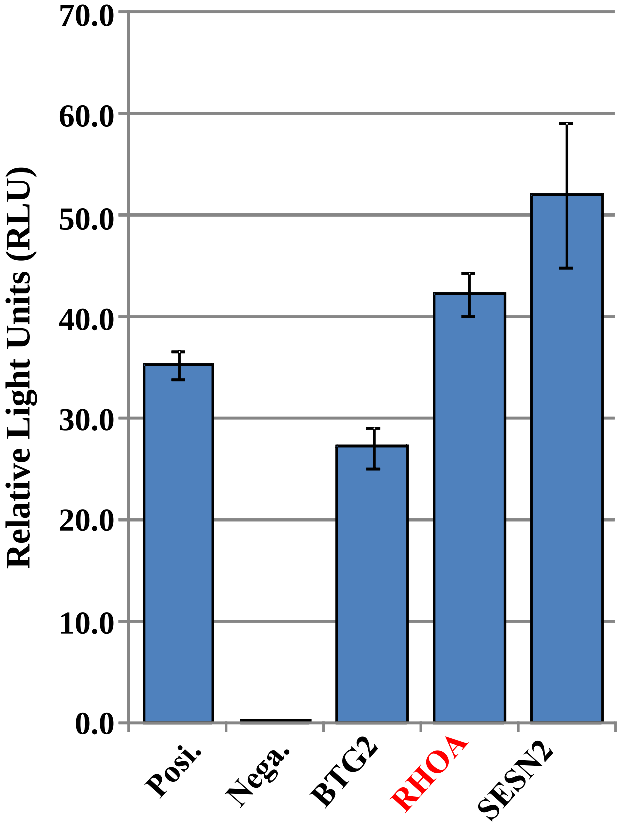
HeLa cells



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 : 2009.06.30

1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5558

2nd Nucleotide Sequence
  File Name        : RDB7404F.fasta
  Sequence Size    : 631

  Unit Size to Compare = 1
  Pick up Location     = 1



[97.097% / 620 bp]     INT/OPT.Score : <   2060/  2337 >

      1'                 GGCCTA ACTGGCCGGT ACCTGAGCTC GCTAGCCTCG AGGAT-CAAA
                         ****** ********** ********** ********** ***** ****
      1" CAGAACATTT CTCTGGCCTA ACTGGCCGGT ACCTGAGCTC GCTAGCCTCG AGGATGCAAA

     46' GGCCATTAAG CTGGTGGGCT TAAAGCCTGA GAACTCCCCT CTCTGTCACC AGCACAGGAG
         ********** ********** ********** ********** ********** **********
     61" GGCCATTAAG CTGGTGGGCT TAAAGCCTGA GAACTCCCCT CTCTGTCACC AGCACAGGAG

    106' TGTCCTTGGA ATGCCAAGCA TGGGGTTGCG GTATGGACAG ATTTACTCAC CACGAAGGGA
         ********** ********** ********** ********** ********** **********
    121" TGTCCTTGGA ATGCCAAGCA TGGGGTTGCG GTATGGACAG ATTTACTCAC CACGAAGGGA

    166' AATGCGTGGA GCCATCAGGC GTGGATCCAT TCTGACCACC CAGACCTGGA GGCAGAAACA
         ********** ********** ********** ********** ********** **********
    181" AATGCGTGGA GCCATCAGGC GTGGATCCAT TCTGACCACC CAGACCTGGA GGCAGAAACA

    226' CATCCAGAGC TGCAGAAGGC TGGGGTGGGA ATCTGAGCAG GCATCAGCCC AGGTCAGGTT
         ********** ********** **** ***** ********** ********** **********
    241" CATCCAGAGC TGCAGAAGGC TGGGATGGGA ATCTGAGCAG GCATCAGCCC AGGTCAGGTT
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286’ AGAGACCACT GGTATTGTTT GGTGAAGTCT GGTGAGGGTC CTAAGGGACT AATGGTATTG
     ********** ********** ********** ********** ********** **********
301″ AGAGACCACT GGTATTGTTT GGTGAAGTCT GGTGAGGGTC CTAAGGGACT AATGGTATTG

346’ CCAGGTGAGA GTTCTGAGGA ACAGATACAA TGTGATGGGT GGACTGGTGG GGATTCTGGC
     ********** ********** ********** ********** ********** **********
361″ CCAGGTGAGA GTTCTGAGGA ACAGATACAA TGTGATGGGT GGACTGGTGG GGATTCTGGC

406’ GTAAAATGGT ATGGTGGCAT GAGTCAGGGC ACAACGTTAA GTTCTCCCAT CCAAGTACCT
     ********** ********** ********** ********** ********** **********
421″ GTAAAATGGT ATGGTGGCAT GAGTCAGGGC ACAACGTTAA GTTCTCCCAT CCAAGTACCT

466’ GGCTTAGCTT CCGAGGTCAG ATGCGTTCAG GGTAGTAAGG CCGTGAACCA ATGTTAAGTT
     ********** ********** ********** ********** ********** **********
481″ GGCTTAGCTT CCGAGGTCAG ATGCGTTCAG GGTAGTAAGG CCGTGAACCA ATGTTAAGTT

526’ CTGATGAGCC TCTTGCAGGA TAGTGGGGAA CCCAATGGTA CAGTCGGGAG AGGGTGGGGG
     ********** ********** **********  ********* ********** * ****** *
541″ CTGATGAGCC TCTTGCAGGA TAGTGGGGAA -CCAATGGTA CAGTCGGGAG A-GGTGGGCG

586’ CGGGGGCGGC CAGCCCACGG AGGTTCGTAG GAAGCCTCAC CTGGACGGTG ATACAACCCG
      ******  * *  ***** * * ****.. * ...*
599″ GGGGGGCCCC CCCCCCAC-G A-GTTCNNGG NNNGG



1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5558

2nd Nucleotide Sequence
  File Name        : RDB7404R.fasta (Complementary)
  Sequence Size    : 604

  Unit Size to Compare = 1
  Pick up Location     = 1
```

```
[99.005% / 603 bp]     INT/OPT.Score : <   2300/  2346 >

  781’ GCGCCCAGCA CCGTGGCCGG CAGAGCCTGC AAGGCCTGCC CAGACCAGGA CTCCGCCATG
                                                                      **
    1″                                                              TTG

  841’ ACTGG-CCCT CGCCCCA-CC CGGGGTACTG TCACCGTAGT CCCCACCACG CACGCGTGTG
       ***** ** * ******* ** ********** ********** ********** **********
    4″ ACTGGTCCTT CGCCCCACCC CGGGGTACTG TCACCGTAGT CCCCACCACG CACGCGTGTG

  899’ GTCTTCCGGG ACCAGGCCCG TTAGTGCGCA CGCGTAAACC CAGCCAGGGT GGGGCCTACT
       ********** ********** ********** ********** ********** **********
   64″ GTCTTCCGGG ACCAGGCCCG TTAGTGCGCA CGCGTAAACC CAGCCAGGGT GGGGCCTACT

  959’ TCGCGTGCGT GAAGAGTTGG CAGTTCGGGG AGGAGTATTA AAACCGCGCA CGCGCACCTA
       ********** ********** ********** ********** ********** **********
  124″ TCGCGTGCGT GAAGAGTTGG CAGTTCGGGG AGGAGTATTA AAACCGCGCA CGCGCACCTA

 1019’ ACCCCACCCT GCTTGCTTAA GGGATGAGTG ACTCCGGGAG TACAAAATAG CAACCAGGTC
       ********** ********** ********** ********** ** ******* **********
  184″ ACCCCACCCT GCTTGCTTAA GGGATGAGTG ACTCCGGGAG TATAAAATAG CAACCAGGTC

 1079’ TTTTATAGCC CCGGAGTTCC CGTGATGCCC CACGCGGCTG CAATGATTGG TTAAGGGTTT
       ********** ********** ********** ********** ********** **********
  244″ TTTTATAGCC CCGGAGTTCC CGTGATGCCC CACGCGGCTG CAATGATTGG TTAAGGGTTT

 1139’ TGCTTTTAGG GCGTGGACGG GCTCCTGAGC AATAGTGGAT GAGCTGTGAG TGCGCGCGCG
       ********** ********** ********** ********** ********** **********
  304″ TGCTTTTAGG GCGTGGACGG GCTCCTGAGC AATAGTGGAT GAGCTGTGAG TGCGCGCGCG

 1199’ TGCGCGGGGC CGCGACCTGT GCCGGCTCGA GCCCGCTGGG CACTCGGAGG CGCGCACGTC
       ********** ********** ********** ********** ********** **********
  364″ TGCGCGGGGC CGCGACCTGT GCCGGCTCGA GCCCGCTGGG CACTCGGAGG CGCGCACGTC

 1259’ GTTCCCCGCC CTCCCGCCGC CGCCCGCCCT CGCTCTCTCG CGCTACCCTC CCGCCGCCCG
       ********** ********** ********** ********** ********** **********
  424″ GTTCCCCGCC CTCCCGCCGC CGCCCGCCCT CGCTCTCTCG CGCTACCCTC CCGCCGCCCG
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```
1319' CGGTCCTCCG TCGGTTCTCT CGTTAGTCCA CGGTCTGGTA TCAAGATCTG GCCTCGGCGG
      ********** ********** ********** ********** ********** **********
 484" CGGTCCTCCG TCGGTTCTCT CGTTAGTCCA CGGTCTGGTA TCAAGATCTG GCCTCGGCGG

1379' CCAAGCTTGG CAATCCGGTA CTGTTGGTAA AGCCACCATG GAAGATGCCA A-AAACATTA
      ********** ********** ********** ********** ********** * ***** **
 544" CCAAGCTTGG CAATCCGGTA CTGTTGGTAA AGCCACCATG GAAGATGCCA ACAAACACTA

1438' AGAAGGGCCC AGCGCCATTC TACCCACTCG AAGACGGGAC CGCCGGCGAG CAGCTGCACA
      *
 604" A
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