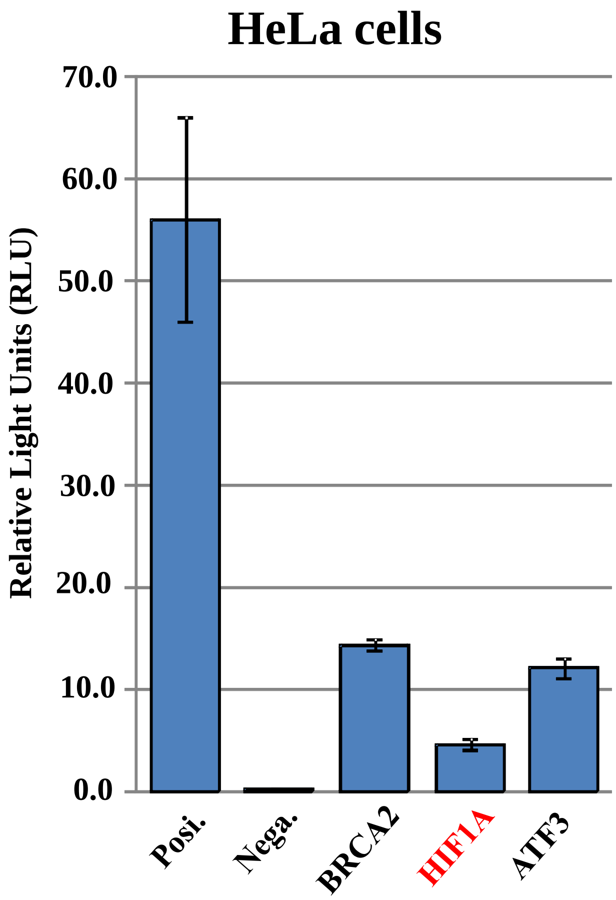
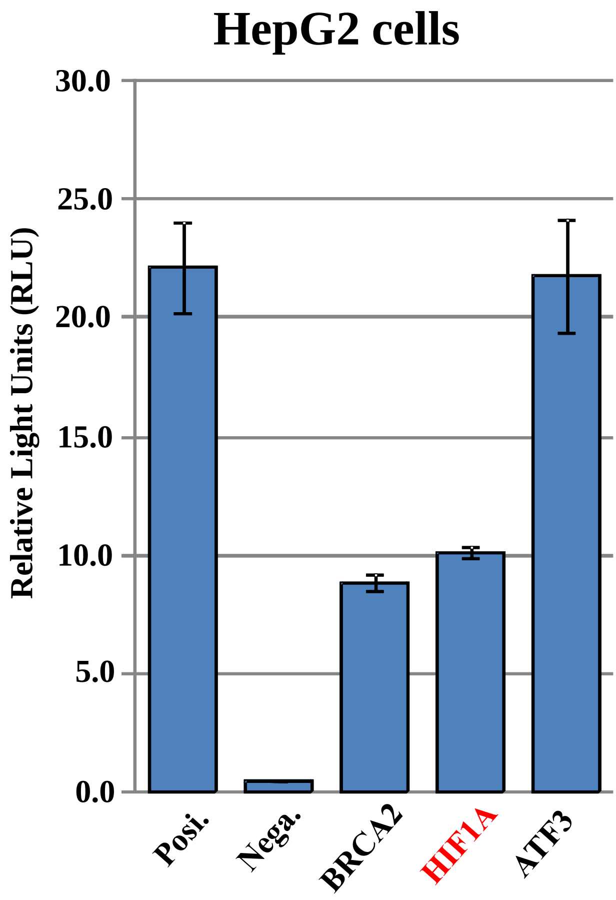
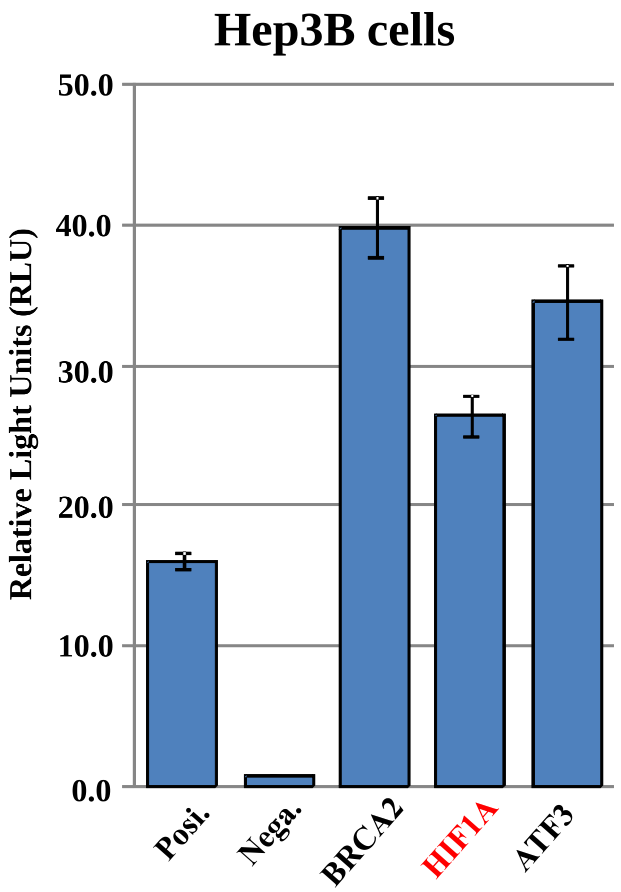
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

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

BRCA2: pGL4-phBRCA2(RDB# 7691)
HIF1A: pGL4-phHIF1A(RDB# 7693)
ATF3: pGL4-phATF3 (RDB# 7710)

2010, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.02.04

1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5711

2nd Nucleotide Sequence
  File Name        : RDB7693F.fasta
  Sequence Size    : 575

  Unit Size to Compare = 1
  Pick up Location     = 1



[99.475% / 571 bp]     INT/OPT.Score : <   2096/  2246 >

   1201' GAGCACGTGA GCGTCGCAGC CCGTCCCAGC TGT-GCCTCA GCTGACCGCC TCCTGATTGG
                                    ***** ***  ***** ********** **********
      1″                         TGGCCAGC TGTAACCTCA GCTGACCGCC TCCTGATTGG

   1260' CTGAGAGCGG CGTGGGCTGG GGTGGGGACT TGCCGCCTGC GTCGCTCGCC ATTGGATCTC
         ********** ********** ********** ********** ********** **********
     39″ CTGAGAGCGG CGTGGGCTGG GGTGGGGACT TGCCGCCTGC GTCGCTCGCC ATTGGATCTC

   1320' GAGGAACCCG CCTCCACCTC AGGTGAGGCG GGCTTGCGGG AGCGCGCGCC GGCCTGGGCA
         ********** ********** ********** ********** ********** **********
     99″ GAGGAACCCG CCTCCACCTC AGGTGAGGCG GGCTTGCGGG AGCGCGCGCC GGCCTGGGCA

   1380' GGCGAGCGGG CGCGCTCCCG CCCCCTCTCC CCTCCCCGCG CGCCCGAGCG CGCCTCCGCC
         ********** ********** ********** ********** ********** **********
    159″ GGCGAGCGGG CGCGCTCCCG CCCCCTCTCC CCTCCCCGCG CGCCCGAGCG CGCCTCCGCC

   1440' CTTGCCCGCC CCCTGACGCT GCCTCAGCTC CTCAGTGCAC AGTGCTGCCT CGTCTGAGGG
         ********** ********** ********** ********** ********** **********
    219″ CTTGCCCGCC CCCTGACGCT GCCTCAGCTC CTCAGTGCAC AGTGCTGCCT CGTCTGAGGG
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 1500' GACAGGAGGA TATCAAGATC TGGCCTCGGC GGCCAAGCTT GGCAATCCGG TACTGTTGGT
       ********** ********** ********** ********** ********** **********
  279″ GACAGGAGGA TATCAAGATC TGGCCTCGGC GGCCAAGCTT GGCAATCCGG TACTGTTGGT

 1560' AAAGCCACCA TGGAAGATGC CAAAAACATT AAGAAGGGCC CAGCGCCATT CTACCCACTC
       ********** ********** ********** ********** ********** **********
  339″ AAAGCCACCA TGGAAGATGC CAAAAACATT AAGAAGGGCC CAGCGCCATT CTACCCACTC

 1620' GAAGACGGGA CCGCCGGCGA GCAGCTGCAC AAAGCCATGA AGCGCTACGC CCTGGTGCCC
       ********** ********** ********** ********** ********** **********
  399″ GAAGACGGGA CCGCCGGCGA GCAGCTGCAC AAAGCCATGA AGCGCTACGC CCTGGTGCCC

 1680' GGCACCATCG CCTTTACCGA CGCACATATC GAGGTGGACA TTACCTACGC CGAGTACTTC
       ********** ********** ********** ********** ********** **********
  459″ GGCACCATCG CCTTTACCGA CGCACATATC GAGGTGGACA TTACCTACGC CGAGTACTTC

 1740' GAGATGAGCG TTCGGCT-GG CAGAAGCTAT GAAGCGCTAT GGGCTGAATA CAAACCATCG
       ********** ******* ** ********** ********** ********** ******
  519″ GAGATGAGCG TTCGGCTGGG CAGAAGCTAT GAAGCGCTAT GGGCTGAATA CAAACCT




1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5711

2nd Nucleotide Sequence
  File Name        : RDB7693R.fasta
  Sequence Size    : 742

  Unit Size to Compare = 1
  Pick up Location     = 1
[99.308% / 723 bp]     INT/OPT.Score : <   2808/  2852 >

    1'                    GG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATC
                          ** ********** ********** ********** **********
    1″ GTGCCAGAAC ATTTCTCTGG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATC
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 43’ CCATGGTTCT TTTCAAGACA TAATACATAT CATTTAGTGT TGTAGATCTG AAAAAACAAA
     ********** ********** ********** ********** ********** **********
 61″ CCATGGTTCT TTTCAAGACA TAATACATAT CATTTAGTGT TGTAGATCTG AAAAAACAAA

103’ AGTAGCGTGA AGATCAAAAA TTTTCTAAAG AGACGGAGTC TCGCTACGTT CCCTAGGCTG
     ********** ********** ********** ********** ********** **********
121″ AGTAGCGTGA AGATCAAAAA TTTTCTAAAG AGACGGAGTC TCGCTACGTT CCCTAGGCTG

163’ GAACACCCAG GCTTCTCCAG CCTCACACCT CTGAGTAGCT GGAACCACCC TGTCCGCTAA
     ********** ********** ********** ********** ********** **********
181″ GAACACCCAG GCTTCTCCAG CCTCACACCT CTGAGTAGCT GGAACCACCC TGTCCGCTAA

223’ GGTCAATGTT TAATCGTATC TTTGTAGGTC TACTGACCAG TTAAAAAGAG GTGCTGTATA
     ********** ********** ********** ********** ********** **********
241″ GGTCAATGTT TAATCGTATC TTTGTAGGTC TACTGACCAG TTAAAAAGAG GTGCTGTATA

283’ CATTGGTTGT TGTCTTGTCA GAGTTTGATG CTTCTATATA GACCATTGTT TTTACATGCT
     ********** ********** ********** ********** ********** **********
301″ CATTGGTTGT TGTCTTGTCA GAGTTTGATG CTTCTATATA GACCATTGTT TTTACATGCT

343’ AATACAATTG AAAGCCACTA CAGATATTTA TATTTACAAC CCAAAGCTAG GTTTTAACAA
     ********** ********** ********** ********** ********** **********
361″ AATACAATTG AAAGCCACTA CAGATATTTA TATTTACAAC CCAAAGCTAG GTTTTAACAA

403’ GAAACTCATA AGGCAAAGGT GAGAAGTAAA ATAATTTAGC GCCAAGTGGA GATATATGTG
     ********** ********** ********** ********** ********** **********
421″ GAAACTCATA AGGCAAAGGT GAGAAGTAAA ATAATTTAGC GCCAAGTGGA GATATATGTG

463’ CAATGCTACT TTGTTGGGCT CAAAACATAT TTTTCTTTTA GAAGACTGAC AGGCTTGAAG
     ********** ********** ********** ********** ********** **********
481″ CAATGCTACT TTGTTGGGCT CAAAACATAT TTTTCTTTTA GAAGACTGAC AGGCTTGAAG

523’ TTTATGCCTC CAAAGACAAA AGTGATTATG TTTTGTTTAG TAGCTTGCAA AGTTGCCAAA
     ********** ********** ******** * ********** ********** **********
541″ TTTATGCCTC CAAAGACAAA AGTGATTACG TTTTGTTTAG TAGCTTGCAA AGTTGCCAAA

583’ GGCCATTTTT TCTACTCTTT CCCTGAAATT GGTTTATATG CTTATTAAAG TCATTTATAC
     ********** ********** ********** ********** ********** **********
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601″ GGCCATTTTT TCTACTCTTT CCCTGAAATT GGTTTATATG CTTATTAAAG TCATTTATAC

643’ CTATTTGCAA ATGCTTAACA TAGTTTCAGA TTTTAAGATT TCCCTGCAAC TTTA-TTTCC
     ******** * ********** ********** ********** ********** **** *****
661″ CTATTTGCCA ATGCTTAACA TAGTTTCAGA TTTTAAGATT TCCCTGCAAC TTTATTTTCC

702’ CTTGAAGTTT ACAGCAACAG GAGTTCATTT TTATTTTTAA TTGCATTTAT TCAGTAAGTA
     **  ****** ********** *
721″ CTGAAAGTTT ACAGCAACAG GG
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