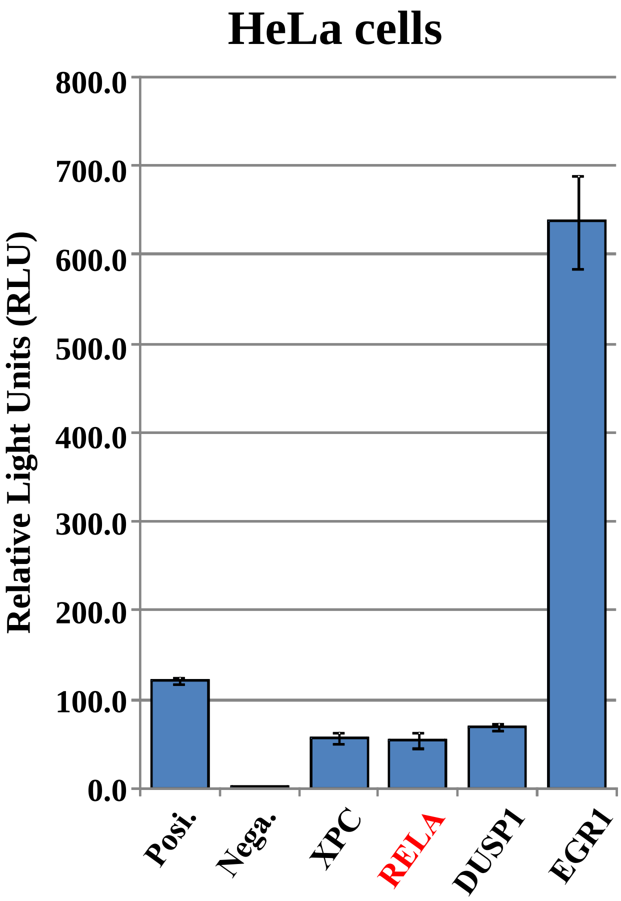
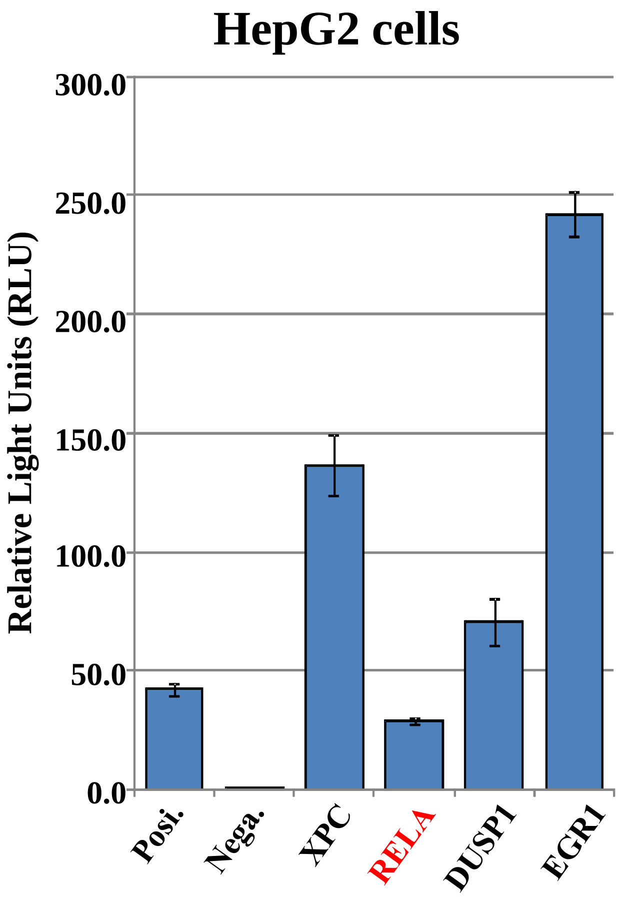
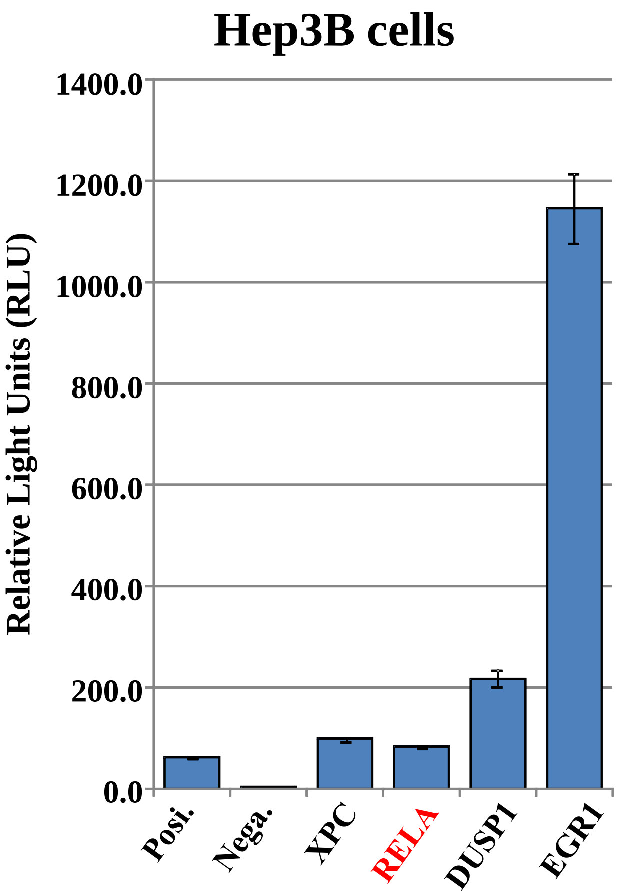
The Promoter Activities of Reporter Constructs







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

XPC: pGL4-phXPC (RDB# 7351)
RELA: pGL4-phRELA (RDB# 7366)
DUSP1: pGL4-phDUSP1 (RDB# 7368)
EGR1: pGL4-phEGR1 (RDB#7369)

2010, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.05.29

1st Nucleotide Sequence
  File Name        : Reference Seq GNU
  Sequence Size    : 5391

2nd Nucleotide Sequence
  File Name        : RDB7366F.fasta
  Sequence Size    : 400

  Unit Size to Compare = 2
  Pick up Location     = 1



[97.500% / 400 bp]     INT/OPT.Score : <    818/  1520 >

    1’ GGCCTAACTG GCCGGTACCT GAGCTCGCTA GCCTCGAGGA TAGCCTGGGA AACAAGTCAG
                                                 ********* **********
   67″                                            AGCCTGGGA AACAAGTCAG

   61’ AATTTCCAAT CTTTTCCAAT TCCCACATGA TTTCCTAATT TAAGACGAAT TCAGAGAAAA
       ********** ** ******* ********** ********** ********** **********
   86″ AATTTCCAAT CTATTCCAAT TCCCACATGA TTTCCTAATT TAAGACGAAT TCAGAGAAAA

  121’ TAAAAAAGTC TTTCTCCATC TGGAGAAGAC TCCGCCCCCT GCAGTGGAGC ATCCTCCT-T
       ********** ********** ********** ********** ********** ******** *
  146″ TAAAAAAGTC TTTCTCCATC TGGAGAAGAC TCCGCCCCCT GCAGTGGAGC ATCCTCCTAT

  180’ TGGGGATGAG GCCTGGGGTG GGGGTGCGTC AGCCCCAGCC TCCACACGGA CGCGCCTTGG
        *** ***** ********** ********** ********** ********** ******* **
  206″ AGGGAATGAG GCCTGGGGTG GGGGTGCGTC AGCCCCAGCC TCCACACGGA CGCGCCTAGG

  240’ GCTTGGTCTT GGGGGAGCTA CCTGCACTGT GGGGTCACAT GACAGAATTA GTGGTCAGCC
       *** *****  ********** ********** ********** ******** * **********
  266″ GCTAGGTCTA GGGGGAGCTA CCTGCACTGT GGGGTCACAT GACAGAATAA GTGGTCAGCC
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    300' CTAGCTGGAG GTCCAGGGCA AACACAGGCG GGGGCAGGGG GGTGGGGGGT CGTGAGCCTG
         ********** ********** ********** ********** ********** **********
    326″ CTAGCTGGAG GTCCAGGGCA AACACAGGCG GGGGCAGGGG GGTGGGGGGT CGTGAGCCTG

    360' CTGATTCAAG TGTCCCTGTG GGTCCCGCAC CTT-CTGAGA CACAAGCGCC AGGCTTCAGA
         ********** ********** ********** *** ****** *** ****** **********
    386″ CTGATTCAAG TGTCCCTGTG GGTCCCGCAC CTTACTGAGA CACTAGCGCC AGGCTTCAGA

    419' GACGAGGCTC CGGGATTTAC CCCTGGGGGC CTCCTGCTCC CACAGCCGAT GAGAGCCGGC
         ********** ********** *
    446″ GACGAGGCTC CGGGATTTAC C
```

```
1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5391

2nd Nucleotide Sequence
  File Name        : RDB7366R.fasta (Complementary)
  Sequence Size    : 400

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

```
[97.236% / 398 bp]     INT/OPT.Score : <    658/  1492 >

    781' TCCCTGCGCG GGGCGGGCGG CCGCAGCCCA GTAGCCCTGG CTTTGCTCCA GACCCGGCCC
                         *.**   * ******* *********   ********* .*********
     87″               CGCGNCGC GCCCAGCCCA GTAGCCCTGC TTTTGCTCCA NACCCGGCCC

    841' AGAGTGACAT CACCAAACTC CGCCG-ATCG GCGGGAGGGG GCCCTGAAAT CCCCTAAAAA
         ***** **** ********** ***** **** ********** ********** **********
    135″ AGAGT-ACAT CACCAAACTC CGCCGAATCG GCGGGAGGGG GCCCTGAAAT CCCCTAAAAA
```

```
 900’ CAAAGTGAGT AATCGGCGGA CCCACCCTCC AGGCGGGGCC GGGACCCGGG AGCTAGCCGA
      ********** ********** ********** ********** ********** **********
 194″ CAAAGTGAGT AATCGGCGGA CCCACCCTCC AGGCGGGGCC GGGACCCGGG AGCTAGCCGA

 960’ GCCACCGGGC ACGCCAGCCT CTTCGTCCTC -GGCGAGGCG CGCACTTGGC CCCGACCCCC
      ********** ********** **********  ********* ********** **********
 254″ GCCACCGGGC ACGCCAGCCT CTTCGTCCTC GGGCGAGGCG CGCACTTGGC CCCGACCCCC

1019’ GGCAGCGGCT GTGCGTGCAG CCTCTTCGTC CTCCGCGC-G GCGTGCACTT GCTCCCGGCC
      ********** ********** ********** ******** * ********** **********
 314″ GGCAGCGGCT GTGCGTGCAG CCTCTTCGTC CTCCGCGCGG GCGTGCACTT GCTCCCGGCC

1078’ CCTGCGCCGG GCGGCGGCGG GGCAGCGCGC AGGCGCGGCC GGATTCCGGG CAGTGACGCG
      ********** ********** ********** ********** ********** **********
 374″ CCTGCGCCGG GCGGCGGCGG GGCAGCGCGC AGGCGCGGCC GGATTCCGGG CAGTGACGCG

1138’ ACGGCGGGCC GCGCGGCGCA TTTCCGCCTC TGGCGAATGG CTCGTCTGTA GTGATCAAGA
      ********** ********** ********** ********** ********** ***
 434″ ACGGCGGGCC GCGCGGCGCA TTTCCGCCTC TGGCGAATGG CTCGTCTGTA GTG
```