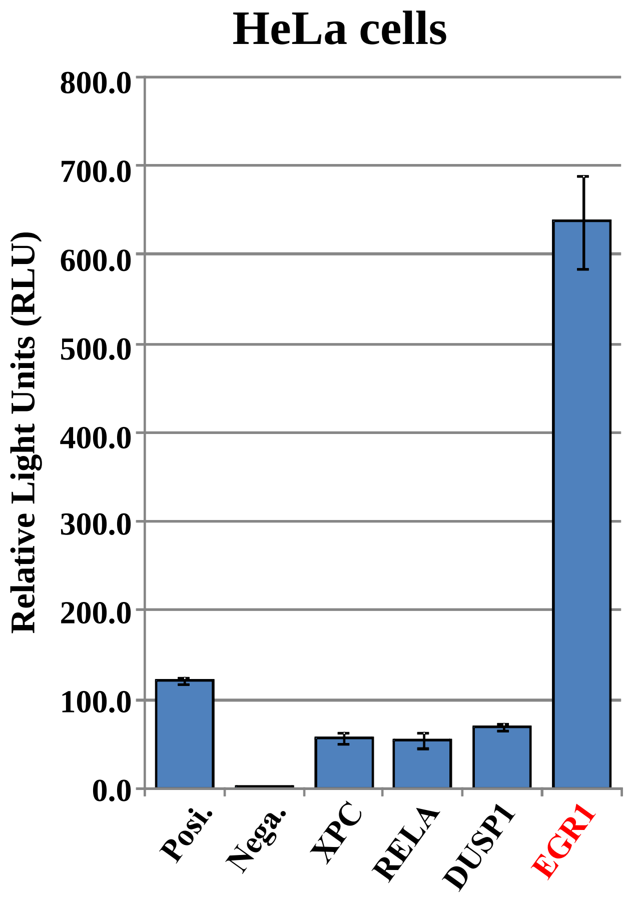
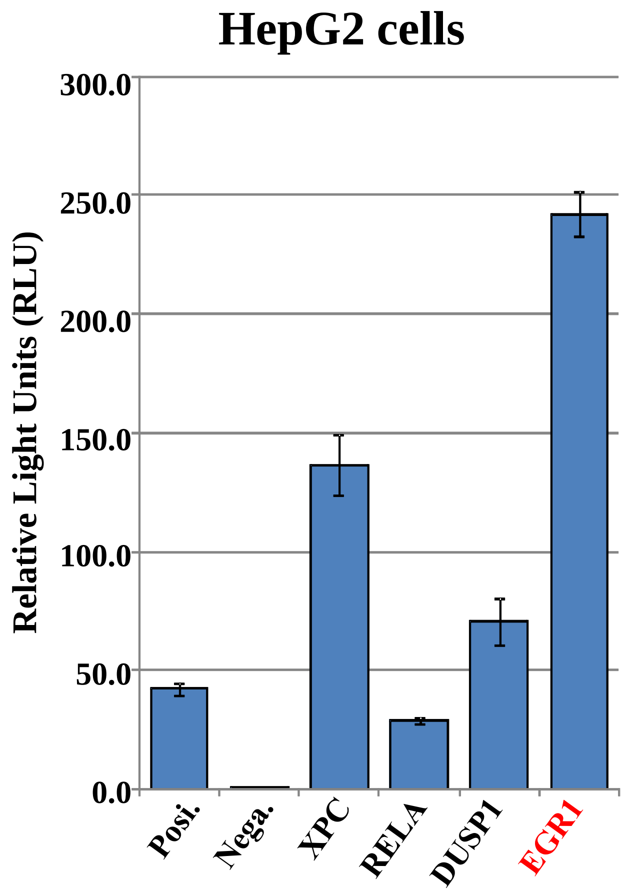
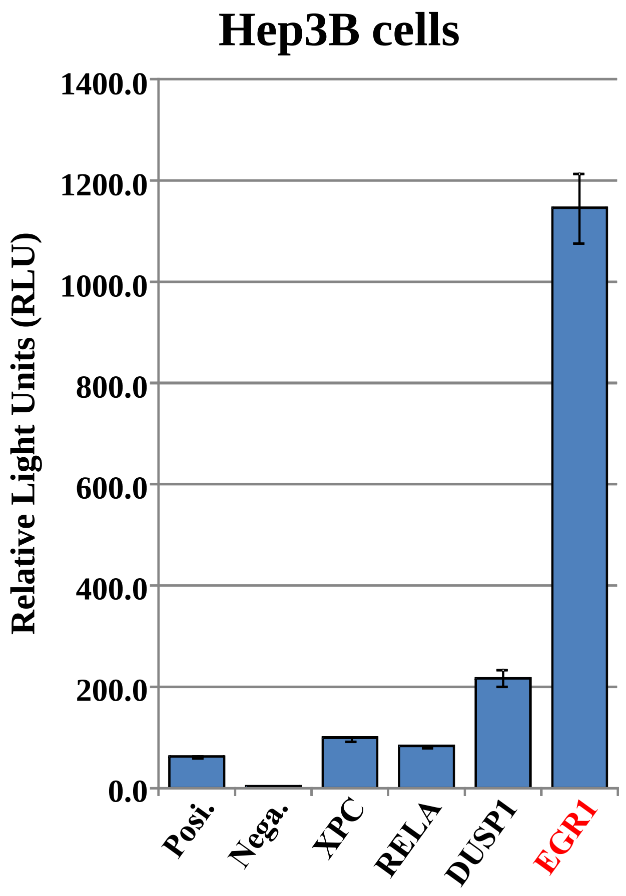
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

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    : 5552

2nd Nucleotide Sequence
  File Name        : RDB7369F.fasta
  Sequence Size    : 400

  Unit Size to Compare = 1
  Pick up Location     = 1



[100.000% / 400 bp]     INT/OPT.Score : <   1600/  1600 >

      1’ GGCCTAACTG GCCGGTACCT GAGCTCGCTA GCCTCGAGGA TCATAGGGAA GCCCCTCTTT
                                                   ********* **********
     55″                                            CATAGGGAA GCCCCTCTTT

     61’ CGGATTCCCG CAGTGTGGGC CGGCCCTCCA CCTGGACTGG ATAAAGGGGG GAAAGTGACC
         ********** ********** ********** ********** ********** **********
     74″ CGGATTCCCG CAGTGTGGGC CGGCCCTCCA CCTGGACTGG ATAAAGGGGG GAAAGTGACC

    121’ CCTCACCACA AGGACCATTA TCTCCTGGTG AGAACAAGAA TCAGGCCTCT CTTGGGGCAA
         ********** ********** ********** ********** ********** **********
    134″ CCTCACCACA AGGACCATTA TCTCCTGGTG AGAACAAGAA TCAGGCCTCT CTTGGGGCAA

    181’ TCAGCTTCCC CACTTCGGTC CCCCAAAGGT GGGCTCTTTG CCGGCGGGGA CTAGGGAACA
         ********** ********** ********** ********** ********** **********
    194″ TCAGCTTCCC CACTTCGGTC CCCCAAAGGT GGGCTCTTTG CCGGCGGGGA CTAGGGAACA

    241’ GCCTTTCGGT TCCGGGGGAG CACAGGGGAC CCCAGGCACC AGCAGCCCCA TCCCACCGAC
         ********** ********** ********** ********** ********** **********
    254″ GCCTTTCGGT TCCGGGGGAG CACAGGGGAC CCCAGGCACC AGCAGCCCCA TCCCACCGAC
```

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    301’ AGGTGGCAGA GGCAAGGCAG CTCACTGCTA TACAGTGTCC CAAGAACCAA GTGGCCGTGA
         ********** ********** ********** ********** ********** **********
    314″ AGGTGGCAGA GGCAAGGCAG CTCACTGCTA TACAGTGTCC CAAGAACCAA GTGGCCGTGA

    361’ CTTCCTATCC TCAATTTCCC AGCGACACCC GGAAAGACAC CGTGCCATAG ATCGAGGCCC
         ********** ********** ********** ********** ********** **********
    374″ CTTCCTATCC TCAATTTCCC AGCGACACCC GGAAAGACAC CGTGCCATAG ATCGAGGCCC

    421’ GGGGTCAAGG CCCCGCCTCT CCTGGGCGGC CCCTGCCCAG GCGGGCCCAG CCGCTCCTCC
         ********** ********** *
    434″ GGGGTCAAGG CCCCGCCTCT C




1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5552

2nd Nucleotide Sequence
  File Name        : RDB7369R.fasta (Complementary)
  Sequence Size    : 400

  Unit Size to Compare = 1
  Pick up Location     = 1



[100.000% / 400 bp]     INT/OPT.Score : <   1600/  1600 >

    901’ CTCCGGAGCT GCGCGGGTCC CGGAGGCCCC GGCGGCGGCT AGAGCTCTAG GCTTCCCCGA
                                                               ********
     84″                                                       TTCCCCGA

    961’ AGCCTGGGCG CCTGGGATGC GGGCGCGGGC GCGGGCCCTA GGGTGCAGGA TGGAGGTGCC
         ********** ********** ********** ********** ********** **********
     92″ AGCCTGGGCG CCTGGGATGC GGGCGCGGGC GCGGGCCCTA GGGTGCAGGA TGGAGGTGCC
```

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1021’ GGGCGCTGTC GGATGGGGGG CTTCACGTCA CTCCGGGTCC TCCCGGCCGG TCCTGCCATA
      ********** ********** ********** ********** ********** **********
 152″ GGGCGCTGTC GGATGGGGGG CTTCACGTCA CTCCGGGTCC TCCCGGCCGG TCCTGCCATA

1081’ TTAGGGCTTC CTGCTTCCCA TATATGGCCA TGTACGTCAC GACGGAGGCG GACCCGTGCC
      ********** ********** ********** ********** ********** **********
 212″ TTAGGGCTTC CTGCTTCCCA TATATGGCCA TGTACGTCAC GACGGAGGCG GACCCGTGCC

1141’ GTTCCAGACC CTTCAAATAG AGGCGGATCC GGGGAGTCGC GAGAGATCCC AGCGCGCAGA
      ********** ********** ********** ********** ********** **********
 272″ GTTCCAGACC CTTCAAATAG AGGCGGATCC GGGGAGTCGC GAGAGATCCC AGCGCGCAGA

1201’ ACTTGGGGAG CCGCCGCCGC CATCCGCCGC CGCAGCCAGC TTCCGCCGCC GCAGGACCGG
      ********** ********** ********** ********** ********** **********
 332″ ACTTGGGGAG CCGCCGCCGC CATCCGCCGC CGCAGCCAGC TTCCGCCGCC GCAGGACCGG

1261’ CCCCTGCCCC AGCCTCCGCA GCCGCGGCGC GTCCACGCCC GCCCGCGCCC AGGGCGAGTC
      ********** ********** ********** ********** ********** **********
 392″ CCCCTGCCCC AGCCTCCGCA GCCGCGGCGC GTCCACGCCC GCCCGCGCCC AGGGCGAGTC

1321’ GGGGTCGCCG CCTGCACGCT TCTCAGTGTT CATCAAGATC TGGCCTCGGC GGCCAAGCTT
      ********** ********** ********** **
 452″ GGGGTCGCCG CCTGCACGCT TCTCAGTGTT CA
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