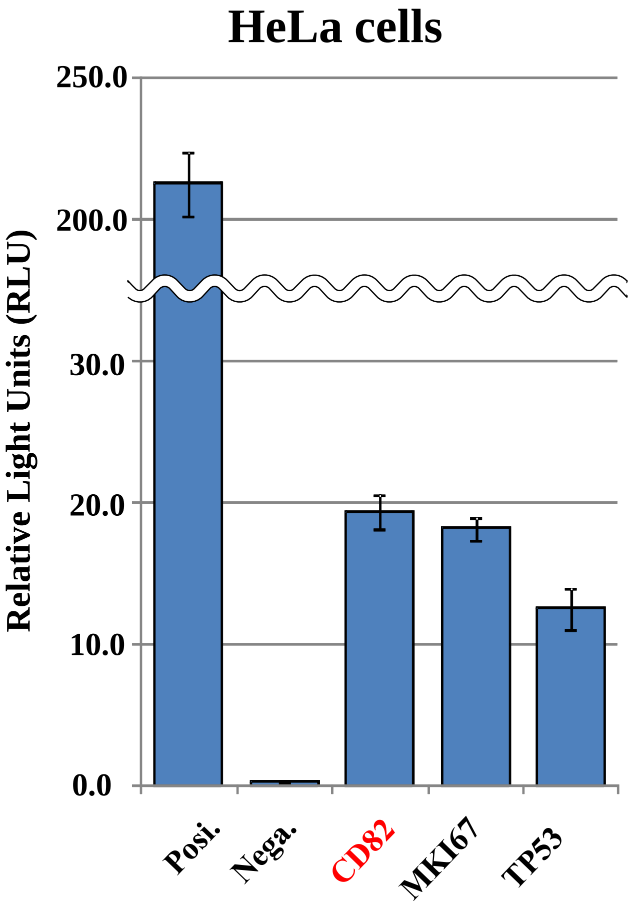
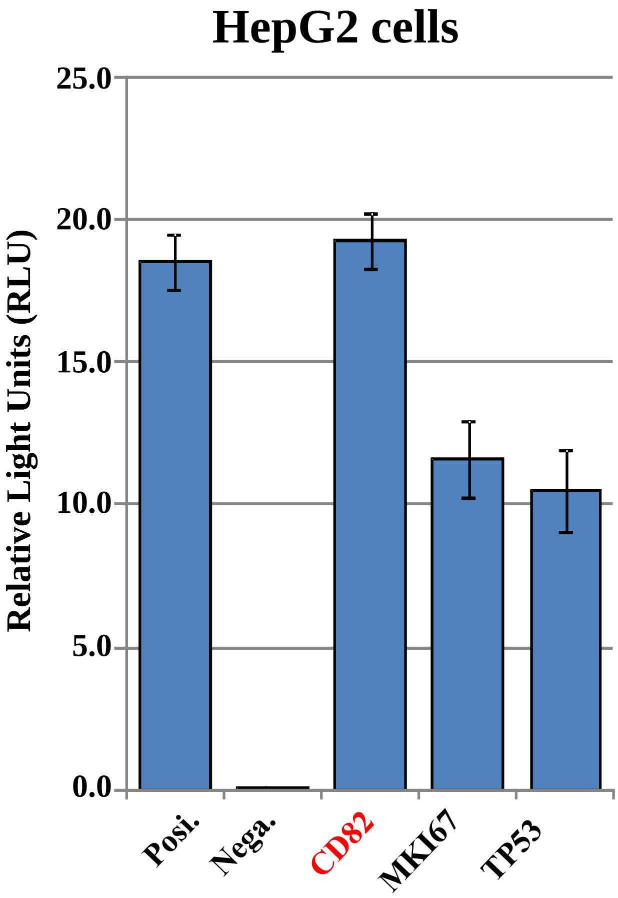
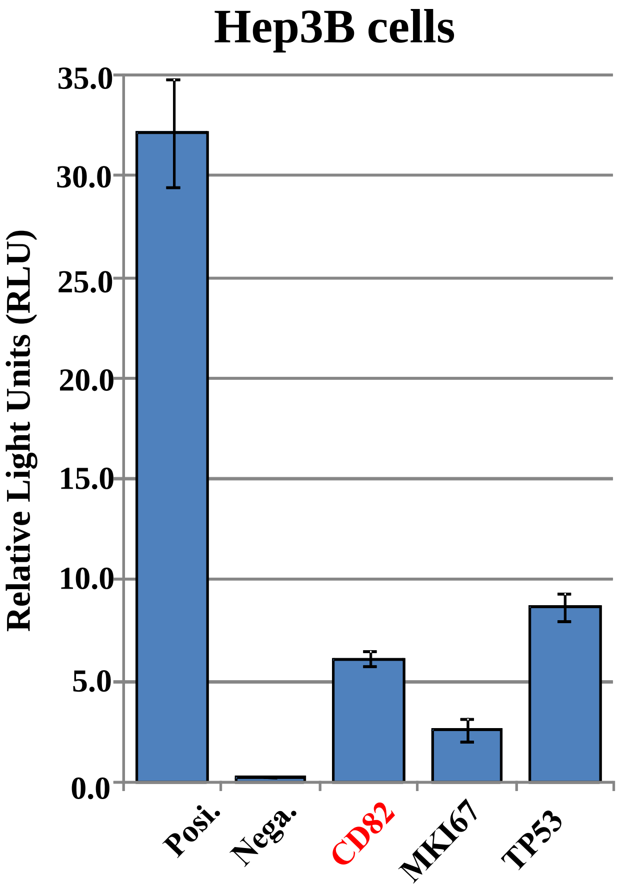
The Promoter Activities of Reporter Constructs







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

CD82: pGL4-phCD82 (RDB# 7416)
MKI67: pGL4-phMKI67 (RDB# 7323)
TP53: pGL4-phPTP53 (RDB# 7330)

2010, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.06.26

1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5561

2nd Nucleotide Sequence
  File Name        : RDB7416F.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 TCAACGGTGT GTTGTGAGAG
                                                     ********* **********
    57″                                              CAACGGTGT GTTGTGAGAG

    61' GACATTGTGA TAATGGAAGT GAAAGAGCTT TGTCAGCTGC ACAGGTGAAT GCCCCTGGTC
        ********** ********** ********** ********** ********** **********
    76″ GACATTGTGA TAATGGAAGT GAAAGAGCTT TGTCAGCTGC ACAGGTGAAT GCCCCTGGTC

   121' ATTAACCAGG TAATCTGCCT GAGGCTAGTC CTCTGGAGCC TGGGAGGGCA GAGGGCTGGG
        ********** ********** ********** ********** ********** **********
   136″ ATTAACCAGG TAATCTGCCT GAGGCTAGTC CTCTGGAGCC TGGGAGGGCA GAGGGCTGGG

   181' ACGCAGGGTG GGCACCGCAG CCACCTAGAG AGCTCTTGCA GCCCACCTCA ATTTTGGGCC
        ********** ********** ********** ********** ********** **********
   196″ ACGCAGGGTG GGCACCGCAG CCACCTAGAG AGCTCTTGCA GCCCACCTCA ATTTTGGGCC

   241' ACTTTTTCTT CAGGGAGAAA GCCAGCTTTG AGGGCTTAGG CCCACAGCCC CTCCTGCCAC
        ********** ********** ********** ********** ********** **********
   256″ ACTTTTTCTT CAGGGAGAAA GCCAGCTTTG AGGGCTTAGG CCCACAGCCC CTCCTGCCAC
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   301’ TATTCTCATC AACCCACACC TCCTCCCTCA CCTCAGGCAG CTGCTGGGCA CTGCCCCAGC
        ********** ********** ********** ********** ********** **********
   316″ TATTCTCATC AACCCACACC TCCTCCCTCA CCTCAGGCAG CTGCTGGGCA CTGCCCCAGC

   361’ ACTGGTTGTT CTGGGCTACT TCCCCAGGGG CCAGTCCAGG CAAGCTGGGG CAGCTCAAGC
        ********** ********** ********** ********** ********** **********
   376″ ACTGGTTGTT CTGGGCTACT TCCCCAGGGG CCAGTCCAGG CAAGCTGGGG CAGCTCAAGC

   421’ CTGTGACTCA GGACCTGAGG CTGGATCCCG CTCACGCCCG CCTCCATGAG ATTCAGAGCC
        ********** ********** *
   436″ CTGTGACTCA GGACCTGAGG C
```

```
1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5561

2nd Nucleotide Sequence
  File Name        : RDB7416R.fasta (Complementary)
  Sequence Size    : 400

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

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

   961’ GCGGGACCGT TAGGCAGCGC CGTGAGTGGA CAGGGCTGGA GCGGGGCGGG CTTAATCCCC
        ********** ********** ********** ********** ********** **********
    86″ GCGGGACCGT TAGGCAGCGC CGTGAGTGGA CAGGGCTGGA GCGGGGCGGG CTTAATCCCC

  1021’ AGTGTAACCT GGGGGCGGGG CTGCCGGGAT AGAGGAGAGA CTCCGTAGCG GGGCGGGGCC
        ********** ********** ********** ********** ********** **********
   146″ AGTGTAACCT GGGGGCGGGG CTGCCGGGAT AGAGGAGAGA CTCCGTAGCG GGGCGGGGCC
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1081’ TCAGCTCCAG CTGGGCCCGG GGGCGAGGCT GGTTGGGGTA CGGCCATAGT GGGCGGGGCC
      ********** ********** ********** ********** ********** **********
 206″ TCAGCTCCAG CTGGGCCCGG GGGCGAGGCT GGTTGGGGTA CGGCCATAGT GGGCGGGGCC

1141’ TGGCCGGCGG GAGCGCACCG CCTTCCCAAA GGGCTCGGGG GCGGGGCCGG CGGAGGGGGC
      ********** ********** ********** ********** ********** **********
 266″ TGGCCGGCGG GAGCGCACCG CCTTCCCAAA GGGCTCGGGG GCGGGGCCGG CGGAGGGGGC

1201’ GTGTCTTCTG GGGGCGGGGC CTGCCGAGTC CGCGGCGTTC CCCGGCTGCA GCCGGGAGGG
      ********** ********** ********** ********** ********** **********
 326″ GTGTCTTCTG GGGGCGGGGC CTGCCGAGTC CGCGGCGTTC CCCGGCTGCA GCCGGGAGGG

1261’ GGCCGAGGAG TGACTGAGCC CCGGGCTGTG CAGTCCGACG CCGACTGAGG CACGAGCGGG
      ********** ********** ********** ********** ********** **********
 386″ GGCCGAGGAG TGACTGAGCC CCGGGCTGTG CAGTCCGACG CCGACTGAGG CACGAGCGGG

1321’ TGACGCTGGG CCTGCAGCGC GGAGCAGAAA GCAGAACCCG ATCAAGATCT GGCCTCGGCG
      ********** ********** ********** **********
 446″ TGACGCTGGG CCTGCAGCGC GGAGCAGAAA GCAGAACCCG
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