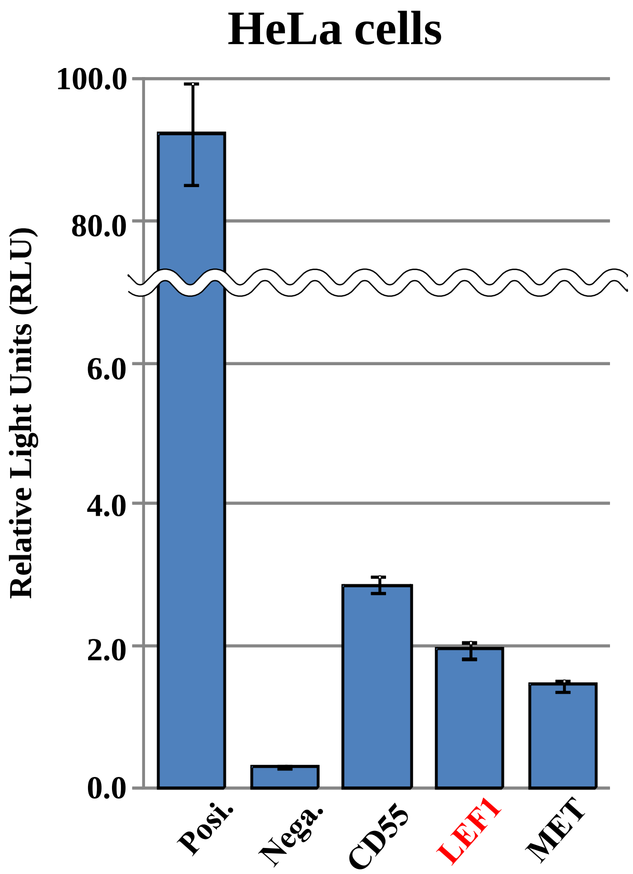
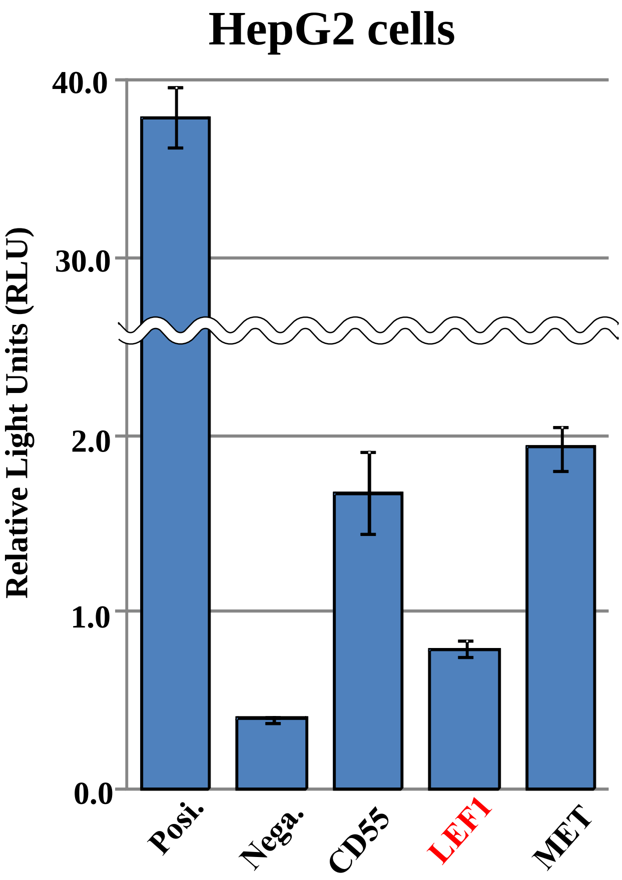
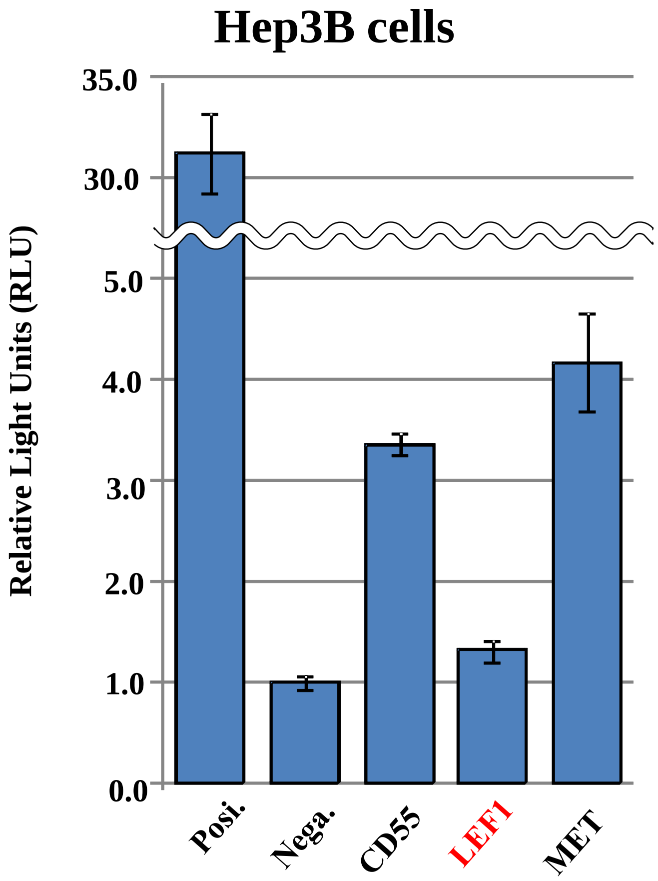
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

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

CD55: pGL4-phCD55(RDB# 7539)
LEF1 : pGL4-phLEF1(RDB# 7553)
MET : pGL4-phMET(RDB# 7554)

2010, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.11.19

1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5766

2nd Nucleotide Sequence
  File Name        : RDB7553F.fasta
  Sequence Size    : 712

  Unit Size to Compare = 1
  Pick up Location     = 1
[96.751% / 708 bp]     INT/OPT.Score : <    242/  2547 >

   1'                   GGC CTAACTGGCC GGTACCTGAG -CTCGCTAGC CTCGAGGATT
                        *** ********** **********  ********  *   ******
   1" GTGCCGAACT TTACTCTGGC CTAACTGGCC GGTACCTGAG ACTCGCTAGA CCTCAGGATT

  43' CCCTCCCTCT TCTGGCTTTG CTCTCCTGAG TCCTTTTGCC TTNCTCTTCC CCCTTCTTGG
      ********** ********** ********** ********** ** ******* **********
  61" CCCTCCCTCT TCTGGCTTTG CTCTCCTGAG TCCTTTTGCC TT-CTCTTCC CCCTTCTTGG

 103' ATTATCTTTT CATTCTCGAT GAGGTTCCCA CACNACTGCG GTGTGTGTCT CTGAAAACCC
      ********** ********** ********** *** ****** ********** **********
 120" ATTATCTTTT CATTCTCGAT GAGGTTCCCA CAC-ACTGCG GTGTGTGTCT CTGAAAACCC

 163' ACTGGAGACC TAGCACAACT CTCCNGTACA TCCCGTGGTG AGAACAGAAT GAAAGATATA
      ********** ********** **** ***** ********** ********** **********
 179" ACTGGAGACC TAGCACAACT CTCC-GTACA TCCCGTGGTG AGAACAGAAT GAAAGATATA

 223' TTGTTTAAAA AGCAANTAAT TAAAATCTAG TCTTCAGTTC CTTCTTCCTC GTCATATTTT
      ********** ***** **** ********** ********** ********** **********
 238" TTGTTTAAAA AGCAA-TAAT TAAAATCTAG TCTTCAGTTC CTTCTTCCTC GTCATATTTT

 283' TTCTCCNGTA AGCCTAGAGA TTTTATTTTC ACTAGTGTGT TCCCTTGTCT CCAAAGANGC
      ****** *** ********** ********** ********** ********** ******* **
 297" TTCTCC-GTA AGCCTAGAGA TTTTATTTTC ACTAGTGTGT TCCCTTGTCT CCAAAGA-GC
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343' GTGTGTGTGA TATTATATTC GGGAAAGCTA CAACTCTCTT TTCCTTGTNC CTTCTGTTCT
     ********** ********** ********** ********** ******** * **********
355″ GTGTGTGTGA TATTATATTC GGGAAAGCTA CAACTCTCTT TTCCTTGT-C CTTCTGTTCT

403' CTCTTAATAG TTGAGCAATG TCTGTTATAT TTTCCCCTTN TTCCTTTTTT TCTCAGTCCC
     ********** ********** ********** *********  ********** **********
414″ CTCTTAATAG TTGAGCAATG TCTGTTATAT TTTCCCCTT- TTCCTTTTTT TCTCAGTCCC

463' AGATTCCCGC CTCTCCCCAC TGTCAGAGCA NTCTATCAAT GTGGTGTCCA TCACAGCGGC
     ********** ********** **********  ********* ********** **********
473″ AGATTCCCGC CTCTCCCCAC TGTCAGAGCA -TCTATCAAT GTGGTGTCCA TCACAGCGGC

523' AGCGGCTTTC TCTTTCATCT TNCCTCCCTC TGCCAGAGCC AGGGAGGGAG AGTGGGAGGC
     ********** *********  * ******** ********** ********** **********
532″ AGCGGCTTTC TCTTTCATC- TCCCTCCCTC TGCCAGAGCC AGGGAGGGAG AGTGGGAGGC

583' GTCAAGGAGG TANGGGGAGA GACTGGCAGA GGAAAAGGAG TGGGTGGGTG GGGGCCAAGT
     ***** **** ** ******* ********** ********** ********** **********
591″ GTCAA-GAGG TA-GGGGAGA GACTGGCAGA GGAAAAGGAG TGGGTGGGTG GGGGCCAAGT

643' AAANTAGATA CTTAGATGAT GAAGTCAAGC CACTGCGGCA ATGTTTCTTG TCAGNTTTCA
     *** ****** ********** ***** **** ****** *** ********** * ** *****
649″ AAA-TAGATA CTTAGATGAT GAAGTTAAGC CACTGCCGCA ATGTTTCTTG TTAG-TTTCA

703' CGCGGGCAAA GCGTGCCTTT CGGTGGGTTA TAAGCAGCGC CCGGTNCCTT CCTTCTCTCG
     *****
707″ CGCGGC
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1st Nucleotide Sequence
  File Name       : Reference Seq.gnu
  Sequence Size   : 5766

2nd Nucleotide Sequence
  File Name       : RDB7553R.fasta (Complementary)
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  Sequence Size    : 720

  Unit Size to Compare = 1
  Pick up Location     = 1
[92.877% / 730 bp]     INT/OPT.Score : <   1792/  2521 >

   901' NCTCCCCCTC ACCCCCCGCC TCCCCTCCAG CGGGCAGCCA AGGAGAGCTA GNAGGCGGGG
                                 ** ***  * *** .**  ** * *.*    .* **  **
     1″                          CCCCCAA C-GGC-NCCC AGAAAANC-- AAAAGC-CGG

   961' GAGGGGAGAG GGAGGAGAAG CGACGCAAGT GGGTAGCTTT TCNAGCGCCG GCGAGGCGCG
        **  *** *   **  * .*. * **.****  *** ***    **.*** **  ** * **.*
    33″ GAAAGGA-AA AGAAAAANAN CCACNCAAG- GGGGAGC--C TCCAGC-CCC GCCAAGCNCC

  1021' GGAGGAGGAG AAGCAGTGGG GAGGCGCAGC CGCTCACCTG CGGGGCAGGG CGCGGA-GGA
        *** *** *  **.******* ***** ** * *** ****** ********** ****** ***
    88″ GGAAGAGAAA AANCAGTGGG GAGGCCCACC CGCGCACCTG CGGGGCAGGG CGCGGAGGGA

  1080' GGGACCCGGG CTGCGCGCTC TCGGGCCGAG GAACCAGGAC GCGCCCGGAG CCTCGCACGC
        ********** ********** ********** ********** ********** * ********
   148″ GGGACCCGGG CTGCGCGCTC TCGGGCCGAG GAACCAGGAC GCGCCCGGAG CTTCGCACGC

  1140' GGCCAAGCTC GGGGCGTCCC CTCCCCTCGG CCGGGCGAAC TCAAGGGGCG CAGCTCTTT-
        ********** ********** ********** ********** ********** *********
   208″ GGCCAAGCTC GGGGCGTCCC CTCCCCTCGG CCGGGCGAAC TCAAGGGGCG CAGCTCTTTG

  1199' GCTTTGACAG AGCTGGCCGG CGGAGGCGTG CAGAGCGGCG AGCCGGCGAG CCAGGCTGAG
        ********** ********** ********** ********** ********** **********
   268″ GCTTTGACAG AGCTGGCCGG CGGAGGCGTG CAGAGCGGCG AGCCGGCGAG CCAGGCTGAG

  1259' AAACTCGAGC CGGGAACAAA GAGGGGTCGG ACTGAGTGTG TGTGTCGGCT CGAGCTCCGG
        ********** ********** ********** *** ****** ********** **********
   328″ AAACTCGAGC CGGGAACAAA GAGGGGTCGG ACTCAGTGTG TGTGTCGGCT CGAGCTCCGG

  1319' GCAGAGGCAT TTGGGCCCGA GGCCCCCGCT GTGACTCCCC GAGACTCCGC AGTGCCCTCC
        ********** ********** ********** ********** ********** **********
   388″ GCAGAGGCAT TTGGGCCCGA GGCCCCCGCT GTGACTCCCC GAGACTCCGC AGTGCCCTCC

  1379' ACTGCGGAGT CCCCGCGCTT GCCGGCAAAA ACTTTATTCT TGGCAAACTT CTCTTTCTCT
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      ********** ********** ********** ********** ********** **********
 448″ ACTGCGGAGT CCCCGCGCTT GCCGGCAAAA ACTTTATTCT TGGCAAACTT CTCTTTCTCT

1439' TCCCCTCCTC CTCGGCCCCC ATCTTCTGCT CCTCCTCCTT CTCTAGCAGA TTAAATGAGC
      ********** ********** ********** ********** ********** **********
 508″ TCCCCTCCTC CTCGGCCCCC ATCTTCTGCT CCTCCTCCTT CTCTAGCAGA TTAAATGAGC

1499' CTCGAGAAGA AAAACCGAAG CGAAAGGGAA GAAAATAAGA AGATCTAAAA CGGACATCTC
      ********** ********** ********** ********** ********** **********
 568″ CTCGAGAAGA AAAACCGAAG CGAAAGGGAA GAAAATAAGA AGATCTAAAA CGGACATCTC

1559' CAGCGTGATC AAGATCTGGC CTCGGCGGCC AAGCTTGGCA ATCCGGTACT GTTGGTAAAG
      ********** ********** ********** ********** ********** **********
 628″ CAGCGTGATC AAGATCTGGC CTCGGCGGCC AAGCTTGGCA ATCCGGTACT GTTGGTAAAG

1619' CCACCATGGA AGATGCCAAA AACATTAA-G AAGGGCCCAG CGCCATTCTA CCCACTCGAA
      ********** ********** ******** * ***
 688″ CCACCATGGA AGATGCCAAA AACATTAATG AAG
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