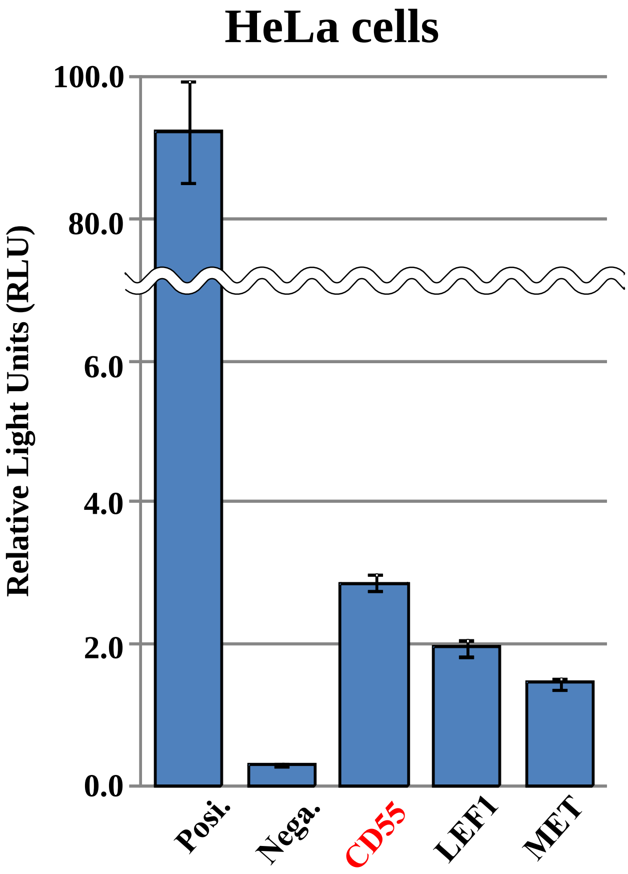
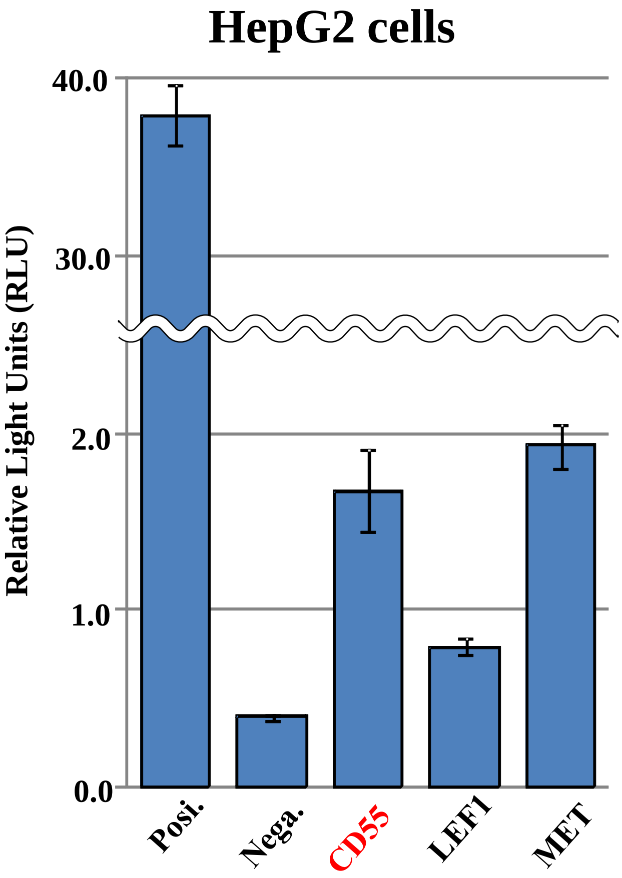
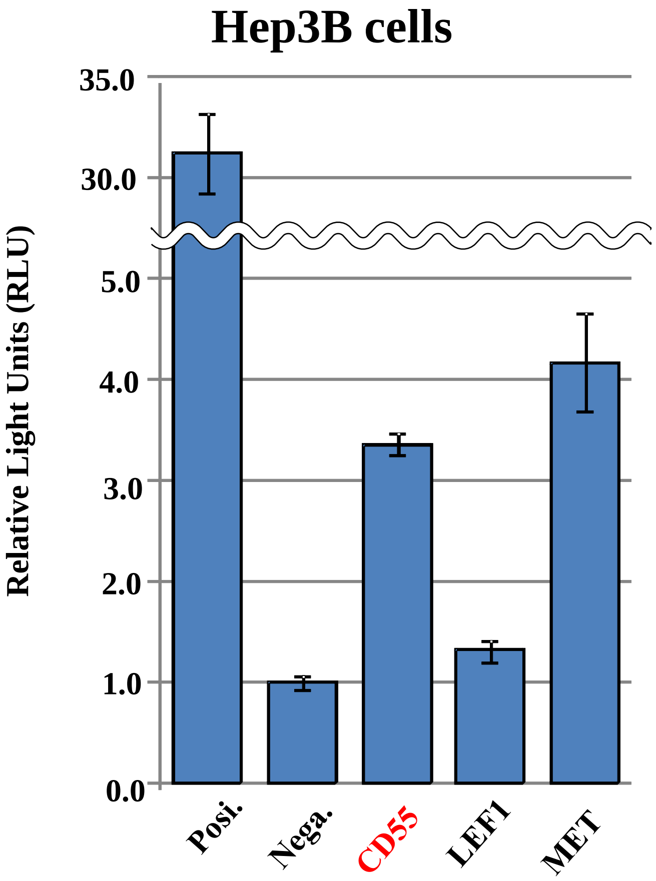
The Promoter Activities of Reporter Constructs







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 : 2009.11.13

1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5701

2nd Nucleotide Sequence
  File Name        : RDB7539F.fasta
  Sequence Size    : 384

  Unit Size to Compare = 1
  Pick up Location     = 1



[98.365% / 367 bp]     INT/OPT.Score : <    352/  1372 >

      1'                          GGCCTAA CTGGCCGGTA CCTGAGCTCG CTAGCCTCGA
                                  ******* ********** ********** **********
      1" TTCAGGTGCC AGAACATTTC TCTGGCCTAA CTGGCCGGTA CCTGAGCTCG CTAGCCTCGA

     38' GGATAGGGGT GGTCCTAAGC TGGATAGATC TTTACTCTGA CCAGTACCAT ANTAGGTCTG
         ********** ********** ********** ********** ********** * ********
     61" GGATAGGGGT GGTCCTAAGC TGGATAGATC TTTACTCTGA CCAGTACCAT A-TAGGTCTG

     98' TGGTTCTCAA ACCTGGCTGC ACAGTGTGGC ACTTTAAGTA ATNCCTGATA CCCAGTCCCA
         ********** ********** ********** ********** ** ******* **********
    120" TGGTTCTCAA ACCTGGCTGC ACAGTGTGGC ACTTTAAGTA AT-CCTGATA CCCAGTCCCA

    158' TCCCCAAAGA TGCTGATTTA ATTTGTCTAA GGTNGCAGTT TGGGCCTCTG GATTGGAACC
         ********** ********** ********** *** ****** ********** **********
    179" TCCCCAAAGA TGCTGATTTA ATTTGTCTAA GGT-GCAGTT TGGGCCTCTG GATTGGAACC

    218' AACCCATATA CCCATCAATG ATAGNACTGG ATAAAGAAAA TGTGGCACAT ATACACCATA
         ********** ********** **** ***** ********** ********** **********
    238" AACCCATATA CCCATCAATG ATAG-ACTGG ATAAAGAAAA TGTGGCACAT ATACACCATA
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    278’ GAATACTACA CAGCCNATAA AAAAGGATGA GTTCATGTCC TATGCAGGGA CATGGATGAA
         ********** ***** **** ********** ********** ********** **********
    297″ GAATACTACA CAGCC-ATAA AAAAGGATGA GTTCATGTCC TATGCAGGGA CATGGATGAA

    338’ GCTGGANAAC CATCAACCTC AGCAAACTAA CATAAGACCA GAAAACCAAA CACTGCANTG
         ****** *** ********** **********
    356″ GCTGGA-AAC CATCAACCTC AGCAAACTAA




1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5701

2nd Nucleotide Sequence
  File Name        : RDB7539R.fasta (Complementary)
  Sequence Size    : 790

  Unit Size to Compare = 1
  Pick up Location     = 1



[92.725% / 811 bp]     INT/OPT.Score : <    701/  2648 >

    781’ ACCACCATTC AGCGTTTTGG GGNTCTGTTT G-TTTTTA-T TGTTAT-CCC ACCCCACACC
                                .******* * ****** * ****** *** **********
      1″                        TTCTGTTT GTTTTTTATT TGTTATCCCC ACCCCACACC

    838’ GCCCCGAGGC GCGCGCNGCG CGCGCGCACA CACACACACA CACACACACA CACACATACA
         ***** **   *****   ** ********** ********** ****** *** *****
     39″ GCCCC-AGAG GCGCG---CG CGCGCGCACA CACACACACA CACACATACA CACAC-----

    898’ CACACGCNAC ACTGGTGAAT TTCTCTCTAC AGTCAGTCTG GAGTAAT-CC CAAAGTGGTN
              ** ** ******* ** ********** ********** ******* ** *********
     90″ -----GC-AC ACTGGTGCAT TTCTCTCTAC AGTCAGTCTG GAGTAATCCC CAAAGTGGT-
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 957' GTCTTTCGTA AATAAGGAGA ACCCGGGTGA AGAAAATGAC TCCCACCCGA NACAAGGCAT
      **********  ********* ********** ********** **********  *********
 143″ GTCTTTCGTA CATAAGGAGA ACCCGGGTGA AGAAAATGAC TCCCACCCGA -ACAAGGCAT

1017' GAACAATGTT CACTCCCTAC TGTGTTATTC AACCTGTTTC CNCCAGGTCT CTGTTTTCAC
      ********** ****** *** ******* ** ********** * ******** **********
 202″ GAACAATGTT CACTCCATAC TGTGTTACTC AACCTGTTTC C-CCAGGTCT CTGTTTTCAC

1077' ATTAGAGAGT GTTCTAGGAG ATGACGCCC- ---------- -----TTCNC TCCTT----A
      ********** ********** *********                 * *.* *****    *
 261″ ATTAGAGAGT GTTCTAGGAG ATGACGCCCT TCCTCCTTAG TTACTTCCCC TCCTTCCCTA

1117' GTTATTTCCC CACCCTCGTG CTGGCCTTTG ACAGACCTCC CAGNTAGAGG GCCCAAGACG
      ********** ********** ********** ********** *** ****** **********
 321″ GTTATTTCCC CACCCTCGTG CTGGCCTTTG ACAGACCTCC CAG-TAGAGG GCCCAAGACG

1177' CGGGTAGAGC ACCGCGTCTC AGCGCCTGAG TCTCNAGCCC CCGAACTCCA CCGCACCTGC
      ********** ********** ********** **** ***** ********** **********
 380″ CGGGTAGAGC ACCGCGTCTC AGCGCCTGAG TCTC-AGCCC CCGAACTCCA CCGCACCTGC

1237' AGGTCCCCTT GGCAGCACTC AAGCGNCGGG GATGCTCCGC TTAGACGAAC TCACGTGCGG
      ********** ********** ***** **** ********** ********** **********
 439″ AGGTCCCCTT GGCAGCACTC AAGCG-CGGG GATGCTCCGC TTAGACGAAC TCACGTGCGG

1297' GCAGCAAGGC CTGCGANTAC TTGAGCACCC CTCCCCCTCT CCCGTTTACA CCCCGTTTGT
      ********** ****** *** ********** ********** ********** **********
 498″ GCAGCAAGGC CTGCGA-TAC TTGAGCACCC CTCCCCCTCT CCCGTTTACA CCCCGTTTGT

1357' GTTTACGNTA GCGAGGAGAT ATTTAGGTTT CTAGAAGGCA GGTCATCGCA GGCCCCACNC
      ******* ** ********** ********** ********** ********** ******** *
 557″ GTTTACG-TA GCGAGGAGAT ATTTAGGTTT CTAGAAGGCA GGTCATCGCA GGCCCCAC-C

1417' CAGCAGTGGA GAGAGTGAGT CCCAGAGGGT GTTGCCAGCG AGCTCCTCCT CCTTCCCCTC
      ********** ********** ********** ********** ********** **********
 615″ CAGCAGTGGA GAGAGTGAGT CCCAGAGGGT GTTGCCAGCG AGCTCCTCCT CCTTCCCCTC

1477' CCCACTCTCC CCGAGTCTAG GGCCATCAAG ATCTGGCCTC GGCGGCCAAG CTTGGCAATC
      ********** ********** ********** ********** ********** **********
 675″ CCCACTCTCC CCGAGTCTAG GGCCATCAAG ATCTGGCCTC GGCGGCCAAG CTTGGCAATC
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1537' CGGTACTGTT GGTAAAGCCA CCATGGAAGA TGCCAAAAAC ATTAAGAAGG GCCCAGCGCC
      ********** ********** ********** ********** *********  ***
 735" CGGTACTGTT GGTAAAGCCA CCATGGAAGA TGCCAAAAAC ATTAAGAAGA GCCACN
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