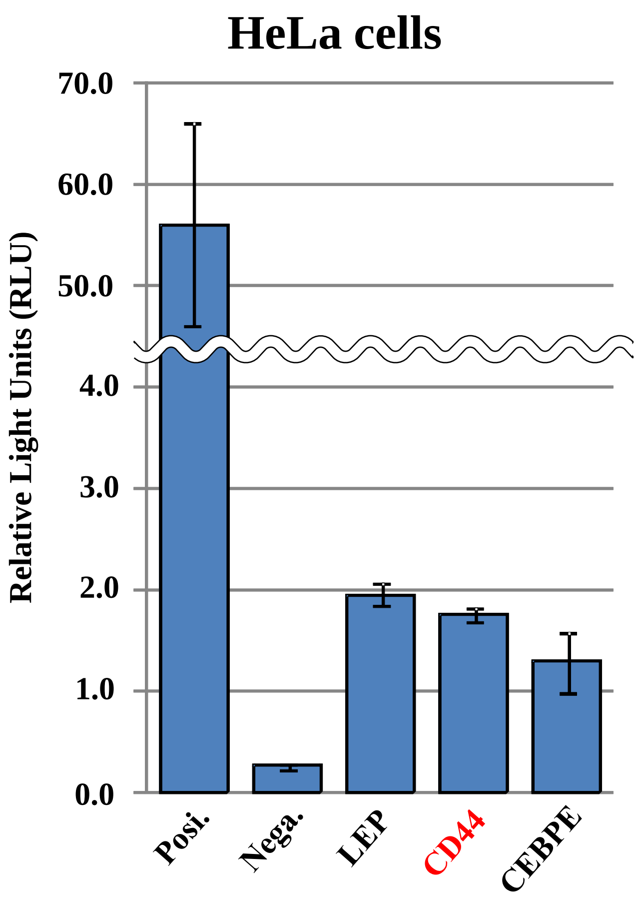
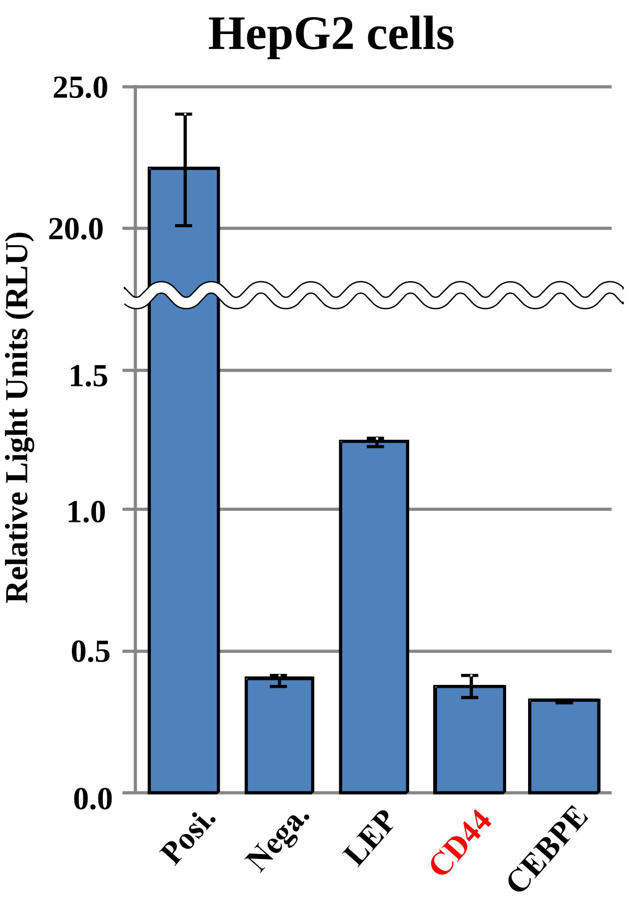
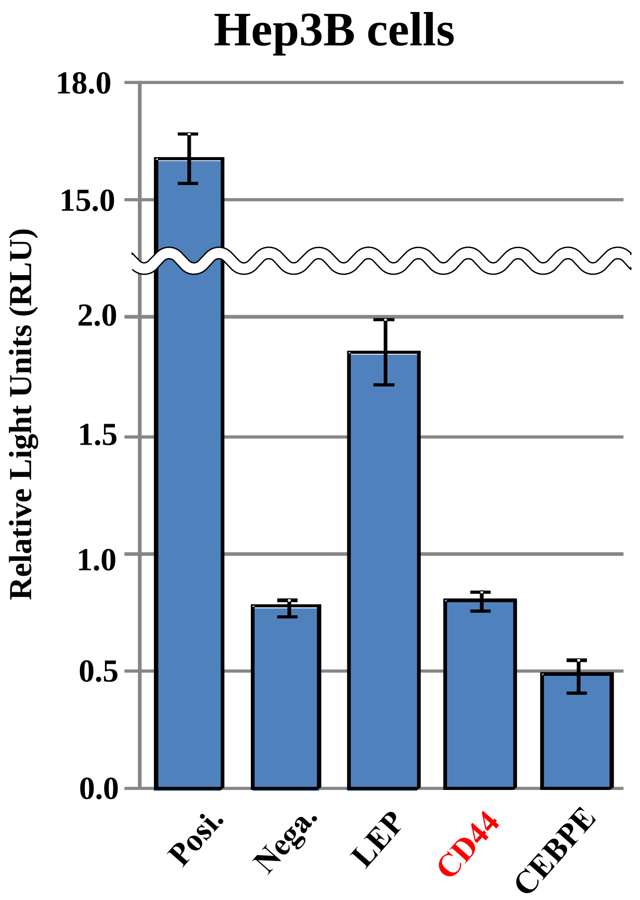
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

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

LEP: pGL4-phLEP (RDB# 7688)
CD44: pGL4-phCD44(RDB# 7685)
CEBPE: pGL4-phCEBPE (RDB# 7713)

2010, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.01.07

1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5702

2nd Nucleotide Sequence
  File Name        : RDB7685F.fasta
  Sequence Size    : 679

  Unit Size to Compare = 1
  Pick up Location     = 1



[100.000% / 660 bp]     INT/OPT.Score : <   2640/  2640 >

     1'                   GGC CTAACTGGCC GGTACCTGAG CTCGCTAGCC TCGAGGATCT
                          *** ********** ********** ********** **********
     1" GGTGCCGAAC TTTCTCTGGC CTAACTGGCC GGTACCTGAG CTCGCTAGCC TCGAGGATCT

    44' CAGAAGTCCT GGCATGGTTC CTTTCATCTT GCCACAGCCA CTGATAATCA CTTTCATTTT
        ********** ********** ********** ********** ********** **********
    61" CAGAAGTCCT GGCATGGTTC CTTTCATCTT GCCACAGCCA CTGATAATCA CTTTCATTTT

   104' CTGTGTAACT CACCAGGCAA GAAGTCCATG CAGATTTACT TTTAGTAGTT CACATGACAA
        ********** ********** ********** ********** ********** **********
   121" CTGTGTAACT CACCAGGCAA GAAGTCCATG CAGATTTACT TTTAGTAGTT CACATGACAA

   164' ATAAATACTG CGTTTGATTT CCAAACATTA AACCATAGTA TATTATAGAT AGATATAGAG
        ********** ********** ********** ********** ********** **********
   181" ATAAATACTG CGTTTGATTT CCAAACATTA AACCATAGTA TATTATAGAT AGATATAGAG

   224' TTATCATTCA AAGTATGATA TTTCAATCTC AAAAGGCTTC CCCTGAAGAA TATTACAAAC
        ********** ********** ********** ********** ********** **********
   241" TTATCATTCA AAGTATGATA TTTCAATCTC AAAAGGCTTC CCCTGAAGAA TATTACAAAC
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    284’ TCTTCCTCTC TTTAAGATCT GCTGGGTAGG AAAGATGGGA GAAAATGAAT TAATGTTTAC
         ********** ********** ********** ********** ********** **********
    301″ TCTTCCTCTC TTTAAGATCT GCTGGGTAGG AAAGATGGGA GAAAATGAAT TAATGTTTAC

    344’ ACAGAAAGGA GGATAATGGG GGCAAAAATA ATAGATGAAC GTATGGGTGG ATGAGAGAAT
         ********** ********** ********** ********** ********** **********
    361″ ACAGAAAGGA GGATAATGGG GGCAAAAATA ATAGATGAAC GTATGGGTGG ATGAGAGAAT

    404’ GGATAAAATG ATAGGTGGAT ATGTTGATCT TGGACAGATG GGAAATGAGT GGATATATCA
         ********** ********** ********** ********** ********** **********
    421″ GGATAAAATG ATAGGTGGAT ATGTTGATCT TGGACAGATG GGAAATGAGT GGATATATCA

    464’ ATAAACAGAT ATGTGGGTGG ATGGGTGGAG AAGAGGATGG TGGATGGTTG TGGTTTTATG
         ********** ********** ********** ********** ********** **********
    481″ ATAAACAGAT ATGTGGGTGG ATGGGTGGAG AAGAGGATGG TGGATGGTTG TGGTTTTATG

    524’ AAGAGATGTG AAAAAGGAAG TGTGGAATGA TGGATGAGAA GTTGTATGGG AAGATGAATA
         ********** ********** ********** ********** ********** **********
    541″ AAGAGATGTG AAAAAGGAAG TGTGGAATGA TGGATGAGAA GTTGTATGGG AAGATGAATA

    584’ GAAGAATAGG TGGTTGAATA AATTAAAAGG TGTGTGGTTG GATGAATGAA TGAGTGGGAT
         ********** ********** ********** ********** ********** **********
    601″ GAAGAATAGG TGGTTGAATA AATTAAAAGG TGTGTGGTTG GATGAATGAA TGAGTGGGAT

    644’ GATAGATGGA CCTAAGTGGT TAGTGGATGG ACAGGAGGAT GGATGGATGT GAGAGCCCCA
         ********** *******
    661″ GATAGATGGA CCTAAGTTT








1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5702

2nd Nucleotide Sequence
  File Name        : RDB7685R.fasta (Complementary)
  Sequence Size    : 747
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 Unit Size to Compare = 1
 Pick up Location     = 1



[98.018% / 757 bp]     INT/OPT.Score : <   2400/  2841 >

  781' GTGGAGAGAG GTGCCCATTC ACACTGGCTT GAACACATGG GTTAGCTGAG CCAAATGCCA
                                                    ****** ** ** **  .**
    1″                                              TTAGCT-AG CCCAAATNCA

  841' GCCCTATGAC AGGCCATCAG TAGCTTTCCC TGAGCTGTTC TGCCAAGAAG CTAAAATTCA
       ********** ********** **** ***** ******* ** ******* ** ****** ***
   19″ GCCCTATGAC AGGCCATCAG TAGC-TTCCC TGAGCTG-TC TGCCAAG-AG CTAAAA-TCA

  901' TTCAAGCCAT GTGGACTTGT TATTGAGGGG AAAAAGAATG AGCTCTCCCT CTTTCCACTT
       *** *** ** ****** *** **********  ********* ********** * ********
   75″ TTC-AGCAAT GTGGAC-TGT TATTGAGGGG -AAAAGAATG AGCTCTCCCT C-TTCCACTT

  961' GGAAGATTCA CCAACTCCCC ACCCCTCACT CCCCACTGTG GGCACGGAGG CACTGCGCCA
       ********** ********** ********** ********** ********** **********
  131″ GGAAGATTCA CCAACTCCCC ACCCCTCACT CCCCACTGTG GGCACGGAGG CACTGCGCCA

 1021' CCCAGGGCAA GACCTCGCCC TCTCTCCAGC TCCTCTCCCA GGATATCCAA CATCCTGTGA
       ********** ********** ********** ********** ********** **********
  191″ CCCAGGGCAA GACCTCGCCC TCTCTCCAGC TCCTCTCCCA GGATATCCAA CATCCTGTGA

 1081' AACCCAGAGA TCTTGCTCCA GCCGGATTCA GAGAAATTTA GCGGGAAAGG AGAGGCCAAA
       ********** ********** ********** ********** ********** **********
  251″ AACCCAGAGA TCTTGCTCCA GCCGGATTCA GAGAAATTTA GCGGGAAAGG AGAGGCCAAA

 1141' GGCTGAACCC AATGGTGCAA GGTTTTACGG TTCGGTCATC CTCTGTCCTG ACGCCGCGGG
       ********** ********** ********** ********** ********** **********
  311″ GGCTGAACCC AATGGTGCAA GGTTTTACGG TTCGGTCATC CTCTGTCCTG ACGCCGCGGG

 1201' GCCAGCGGGA GAAGAAAGCC AGTGCGTCTC TGGGCGCAGG GGCCAGTGGG GCTCGGAGGC
       ********** ********** ********** ********** ********** **********
  371″ GCCAGCGGGA GAAGAAAGCC AGTGCGTCTC TGGGCGCAGG GGCCAGTGGG GCTCGGAGGC
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1261’ ACAGGCACCC CGCGACACTC CAGGTTCCCC GACCCACGTC CCTGGCAGCC CCGATTATTT
      ********** ********** ********** ********** ********** **********
 431″ ACAGGCACCC CGCGACACTC CAGGTTCCCC GACCCACGTC CCTGGCAGCC CCGATTATTT

1321’ ACAGCCTCAG CAGAGCACGG GGCGGGGGCA GAGGGGCCCG CCCGGGAGGG CTGCTACTTC
      ********** ********** ********** ********** ********** **********
 491″ ACAGCCTCAG CAGAGCACGG GGCGGGGGCA GAGGGGCCCG CCCGGGAGGG CTGCTACTTC

1381’ TTAAAACCTC TGCGGGCTGC TTAGTCACAG CCCCCCTTGC TTGGGTGTGT CCTTCGCTCG
      ********** ********** ********** ********** ********** **********
 551″ TTAAAACCTC TGCGGGCTGC TTAGTCACAG CCCCCCTTGC TTGGGTGTGT CCTTCGCTCG

1441’ CTCCCTCCCT CCGTCTTAGG TCACTGTTTT CAACCTCGAA TAAAAACTGC AGCCAACTTC
      ********** ********** ********** ********** ********** **********
 611″ CTCCCTCCCT CCGTCTTAGG TCACTGTTTT CAACCTCGAA TAAAAACTGC AGCCAACTTC

1501’ CATCAAGATC TGGCCTCGGC GGCCAAGCTT GGCAATCCGG TACTGTTGGT AAAGCCACCA
      ********** ********** ********** ********** **********  *********
 671″ CATCAAGATC TGGCCTCGGC GGCCAAGCTT GGCAATCCGG TACTGTTGGT -AAGCCACCA

1561’ TGGAAGATGC CAAAAACATT AAGAAGGGCC CAGCGCCATT CTACCCACTC GAAGACGGGA
      ********** ********
 730″ TGGAAGATGC CAAAAACA
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