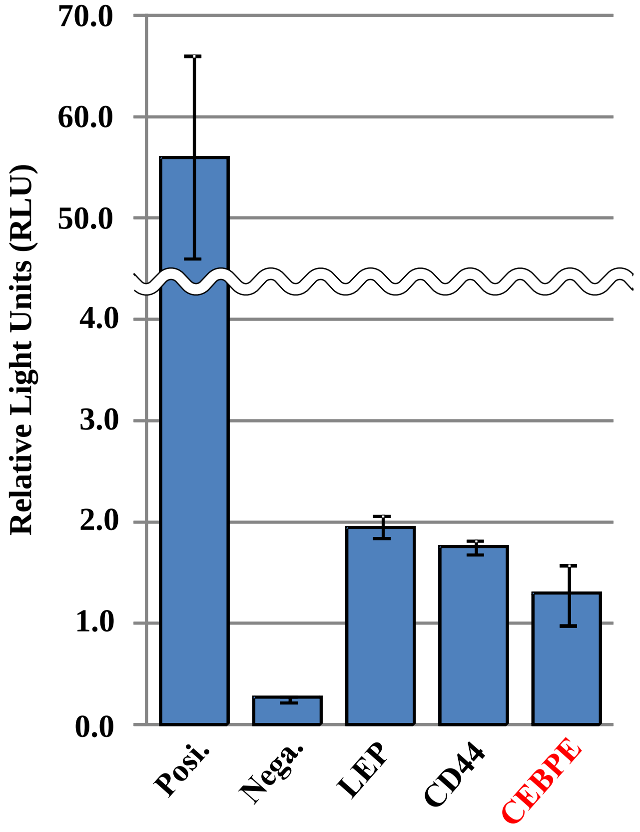
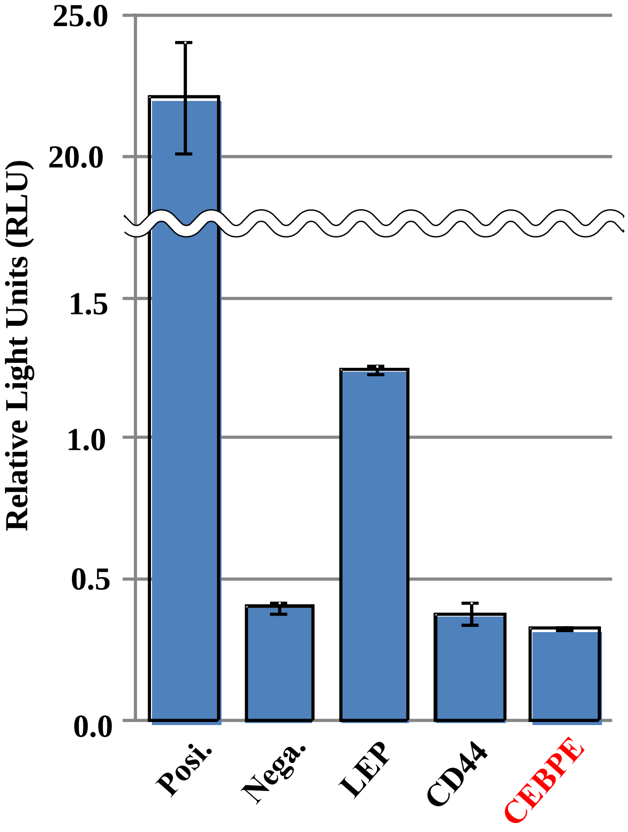
The Promoter Activities of Reporter Constructs

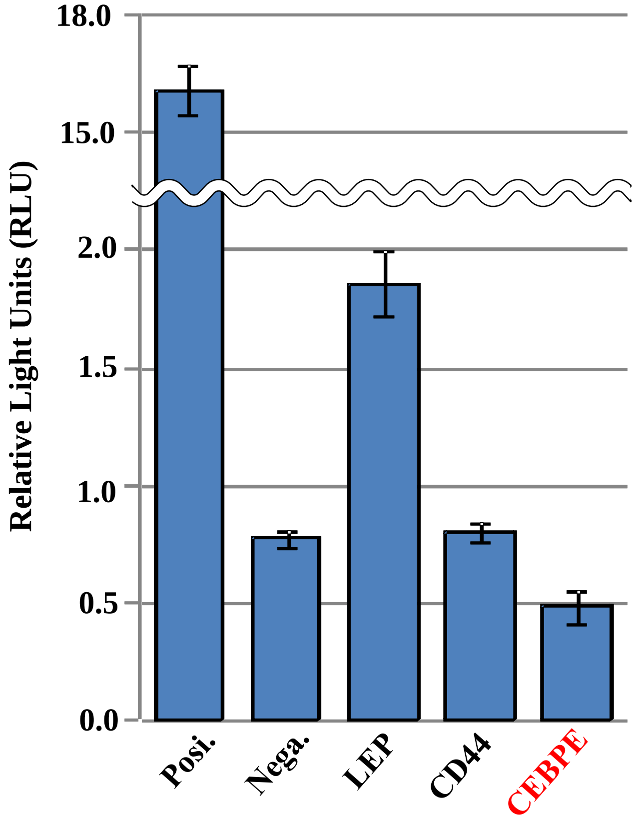
HeLa cells



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 : 2010.03.01

1st Nucleotide Sequence
  File Name        : Reference Seq (insert)
  Sequence Size    : 1464

2nd Nucleotide Sequence
  File Name        : RDB7713F.fasta
  Sequence Size    : 731

Unit Size to Compare : 6

Percent Similarity   : 99.4
Percent Identity     : 99.4


     1’ GTTCAATGCG ACACACATCC TCTCTGCACT TGTCCTACTG TGGCCCACTC ACAGTGAACC
        ********** ********** ********** ********** ********** **********
    66″ GTTCAATGCG ACACACATCC TCTCTGCACT TGTCCTACTG TGGCCCACTC ACAGTGAACC

    61’ ACCCCTTGTT TGGCCCAACT TACAAAAACT TCTGGTCCCT CTGGGGCACC CATAGCACTT
        ********** ********** ********** ********** ********** **********
   126″ ACCCCTTGTT TGGCCCAACT TACAAAAACT TCTGGTCCCT CTGGGGCACC CATAGCACTT

   121’ GCTGGTCATA AAAGAGTCAG TAACATTTCT ATGTGTCCTT CCCCCCCCCC CCCCAACTGG
        ********** ********** ********** ********** ********** **********
   186″ GCTGGTCATA AAAGAGTCAG TAACATTTCT ATGTGTCCTT CCCCCCCCCC CCCCAACTGG

   181’ ACCTACAATC CCTTTTGGAG ATGAAATTCA ACAGGTAAAA GCAGTACCAG AGCAGGTGTC
        ********** ********** ********** ********** ********** **********
   246″ ACCTACAATC CCTTTTGGAG ATGAAATTCA ACAGGTAAAA GCAGTACCAG AGCAGGTGTC

   241’ TCTGAAAGGA GGTAGTGGGG AGTTCCCAAA GGAAAGAGAA AAGGGAAGAG GAGAGCCAGC
        ********** ********** ********** ********** ********** **********
   306″ TCTGAAAGGA GGTAGTGGGG AGTTCCCAAA GGAAAGAGAA AAGGGAAGAG GAGAGCCAGC
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301’ ACAGAACAAA GAATTGCAGA GAGGGAGCCA TGGGCTTCTC CTGGAGACCC TAAAACAGAG
     ********** ********** ********** ********** ********** **********
366″ ACAGAACAAA GAATTGCAGA GAGGGAGCCA TGGGCTTCTC CTGGAGACCC TAAAACAGAG

361’ CCCCAGGAAG AGGTGATGAC ATAAGAGGCT TCTCAAACCT CACAAGAGGA AGTAGACCCA
     ********** ********** ********** ********** ********** **********
426″ CCCCAGGAAG AGGTGATGAC ATAAGAGGCT TCTCAAACCT CACAAGAGGA AGTAGACCCA

421’ AGAGACACGC ATTGGAGATC AGAGAGCGGC CATGCAAAAG GAAAGACAGC AAACGAGCTG
     ********** ********** ********** ********** ********** **********
486″ AGAGACACGC ATTGGAGATC AGAGAGCGGC CATGCAAAAG GAAAGACAGC AAACGAGCTG

481’ CAGCAAGCTC CTAAGCCCTG CAGCCCAGGC ACAGGAAACC AGAGGCAGAG CCTCAGGCCC
     ********** ********** ********** ********** ********** **********
546″ CAGCAAGCTC CTAAGCCCTG CAGCCCAGGC ACAGGAAACC AGAGGCAGAG CCTCAGGCCC

541’ AGGGTGAGGG GCGAAGCACC AGCCTGAGCC T-CTTGCAGC ACAGAGCAGC TGGAAGAGAG
     * ******** ********** ********** * ******** ********** **********
606″ ACGGTGAGGG GCGAAGCACC AGCCTGAGCC TCCTTGCAGC ACAGAGCAGC TGGAAGAGAG

600’ AAGTGCTGGA GCCACCGGAG GATTATGGCT GTCTACTCCG AGGGCAGCAA CCTGCCTAGG
     ********** ********** ********** ** ******* *********  **********
666″ AAGTGCTGGA GCCACCGGAG GATTATGGCT GTTTACTCCG AGGGCAGCAC CCTGCCTAGG

660’ CCTGCG
     * ****
726″ CTTGCG
```

1st Nucleotide Sequence
File Name : Reference Seq (insert)
Sequence Size : 1464

2nd Nucleotide Sequence
File Name : RDB7713R.fasta (Complementary)

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  Sequence Size     : 758

Unit Size to Compare : 6

Percent Similarity   : 99.4
Percent Identity     : 99.1

   783' CTCCTGTGCA AAAACCTAGC AAATGAGCAT GCTCTGGAGC ACCACGCAGG CTCGCGTGTA
         ********* *** *.**** ********** ***** **** ********** **********
   758" GTCCTGTGCA AAACCNTAGC AAATGAGCAT GCTCT-GAGC ACCACGCAGG CTCGCGTGTA

   843' GAGCTTGTTC CTAGGACCTA TCACTACTCC CTAGACCCCT CAAAAAACAA ACCCTGGCCT
        ***** **** ********** ********** ********** *********. **********
   699" GAGCTGGTTC CTAGGACCTA TCACTACTCC CTAGACCCCT CAAAAAACAN ACCCTGGCCT

   903' ACACTCAGAG AATGCTCTGG GAGGTGGGGC TACAAAAGAA ACTTTCTCTT GGGGGTAGGT
        ********** ********** ********** ********** ********** **********
   639" ACACTCAGAG AATGCTCTGG GAGGTGGGGC TACAAAAGAA ACTTTCTCTT GGGGGTAGGT

   963' GGAGCCCAGC AGCAGGGGAG AGCCAGAGGA AGGCGTGTCA AGGGAGGAGG TGAGACCCAA
        ********** ********** ********** ********** ********** **********
   579" GGAGCCCAGC AGCAGGGGAG AGCCAGAGGA AGGCGTGTCA AGGGAGGAGG TGAGACCCAA

  1023' CTGAGGGTAG GCACTGGAAG AGGGCTTTCT CTCTTCACTC TAACTTGGAA CCTCATTCTG
        ********** ********** ********** ********** ********** **********
   519" CTGAGGGTAG GCACTGGAAG AGGGCTTTCT CTCTTCACTC TAACTTGGAA CCTCATTCTG

  1083' CATAGAACTT TTTCAAAGTC GGAGGGAGGA GGTTGCTCAG AGTGGGGTGT TGCCCTCTGC
        ********** ********** ********** ********** ********** **********
   459" CATAGAACTT TTTCAAAGTC GGAGGGAGGA GGTTGCTCAG AGTGGGGTGT TGCCCTCTGC

  1143' GAGGATTTGG AGTCCCCTGG CCTCCCAGCA GGGAGTGGAG AGGCATTCCC AGAAGCATCA
        ********** ********** ********** ********** ********** **********
   399" GAGGATTTGG AGTCCCCTGG CCTCCCAGCA GGGAGTGGAG AGGCATTCCC AGAAGCATCA

  1203' GCTTCGGGCA TCTCCAGAAC CCTGGCTTGG TCCCTGACCA AGGAGTGTCC CCAACTGCTG
        ********** ********** ********** ********** *** ****** **********
   339" GCTTCGGGCA TCTCCAGAAC CCTGGCTTGG TCCCTGACCA AGGGGTGTCC CCAACTGCTG
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1263’ AATAGGCCAG GAGTCGCCTT TCTCTAAGGC TTACATCTCT CCCTCTGGGG TGTGTCCTGC
      ********** ********** ********** ********** ********** **********
 279″ AATAGGCCAG GAGTCGCCTT TCTCTAAGGC TTACATCTCT CCCTCTGGGG TGTGTCCTGC

1323’ CCCTCCCTGA GTCACCCCAA GGGGAGAGAG GGGAAAAAAG GGAAGAGAAG AGAGGCATTG
      ********** ********** ********** ********** ********** **********
 219″ CCCTCCCTGA GTCACCCCAA GGGGAGAGAG GGGAAAAAAG GGAAGAGAAG AGAGGCATTG

1383’ ACTACAGAGG AAGGAAAAGG AAGCAGAGCA GAGGGGGGAG AGAGGCCACA CAGGAGTGGG
      ********** ********** ********** ********** ********** **********
 159″ ACTACAGAGG AAGGAAAAGG AAGCAGAGCA GAGGGGGGAG AGAGGCCACA CAGGAGTGGG

1443’ TGACAGAGGA GACTGCAGAG GG
      ********** ********** **
  99″ TGACAGAGGA GACTGCAGAG GG
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