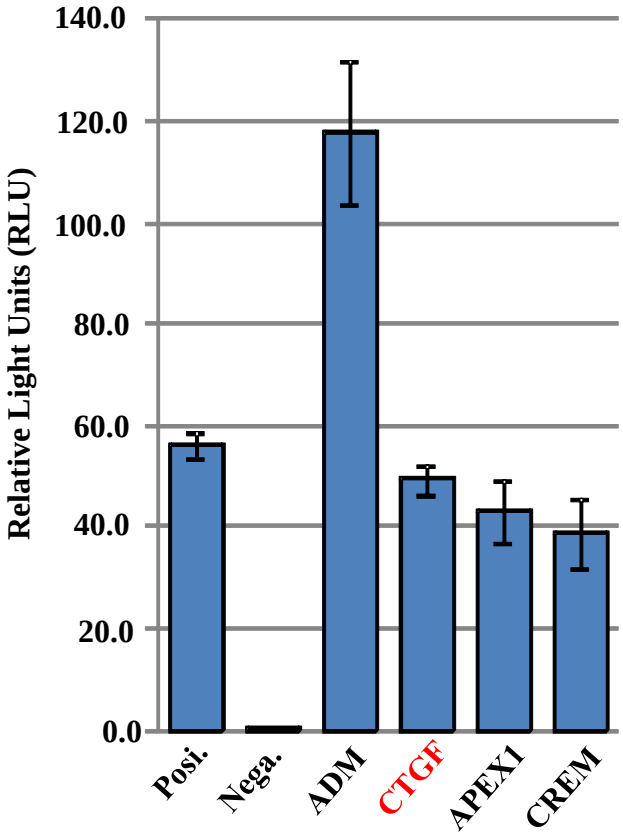
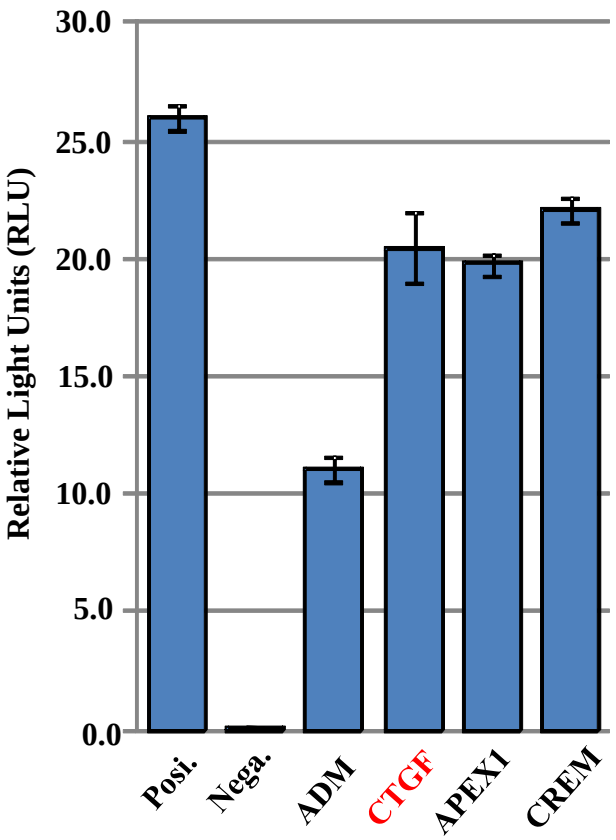
The Promoter Activities of Reporter Constructs

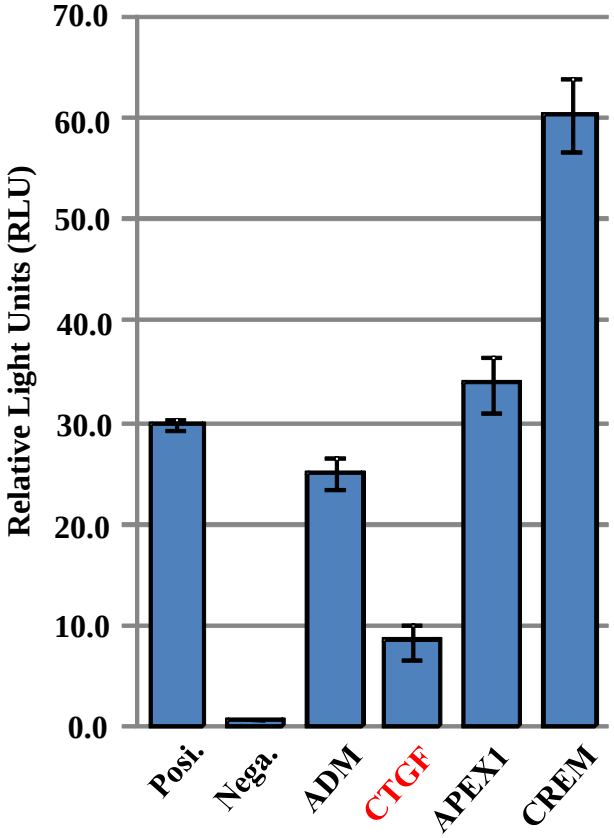
HeLa cells



HepG2 cells



Hep3B cells



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

ADM: pGL4-phADM (RDB# 7808)
CTGF: pGL4-phCTGF (RDB# 7807)
APEX1: pGL4-phAPEX1 (RDB# 7729)
CREM: pGL4-phCREM (RDB#7811)

2010, DNA Bank, RIKEN BioResource Center

```
[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.04.13

1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5735

2nd Nucleotide Sequence
  File Name        : RDB7807F.fasta
  Sequence Size    : 711

  Unit Size to Compare = 1
  Pick up Location     = 1
[95.983% / 697 bp]     INT/OPT.Score : <   2564/  2582 >

      1'                    G GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT
                            * ********** ********** ********** **********
      1" GGTGCCAGAA CATTTCTCTG GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT

     42' CCATGCTCTG AAGCATCAAC AACTTAAAGG AATCTACTCA TTGGTAACAC CAATGTCAAA
         ********** ********** ********** ********** ********** **********
     61" CCATGCTCTG AAGCATCAAC AACTTAAAGG AATCTACTCA TTGGTAACAC CAATGTCAAA

    102' TGATGCGGCA TTACAGAATA CAAAAATGGT ATGGCCCTAG AATCACTCTC TTTATATAAA
         ********** ********** ********** ********** ********** **********
    121" TGATGCGGCA TTACAGAATA CAAAAATGGT ATGGCCCTAG AATCACTCTC TTTATATAAA

    162' ATGGGAACTG GAGGTATTAA CAAAAAAGCC ACTAAACAAC ATAGATTCCA AATGAAAGCA
         ********** ********** ********** ********** ********** **********
    181" ATGGGAACTG GAGGTATTAA CAAAAAAGCC ACTAAACAAC ATAGATTCCA AATGAAAGCA

    222' CAGTGAATTA GTTGGGTCTT TAGTGAAGCT AAGTAGCACT ATATTAAGAA ATGGAGATAT
         ********** ********** ********** ********** ********** **********
    241" CAGTGAATTA GTTGGGTCTT TAGTGAAGCT AAGTAGCACT ATATTAAGAA ATGGAGATAT

    282' GCTTAGGTTT ATTGGCCATA TTCAACATCT GCACACACCC AGGGAGAATA AAGCCTATTC
         ********** ********** ********** ********** ********** **********
    301" GCTTAGGTTT ATTGGCCATA TTCAACATCT GCACACACCC AGGGAGAATA AAGCCTATTC
```

```
    342' TTTCCTTGTC CTGACCTCAC TCCCTCAGGC TGCATGTTCC TTGGGTAATG AGAAGTCACA
         ********** ********** ********** ********** ********** **********
    361" TTTCCTTGTC CTGACCTCAC TCCCTCAGGC TGCATGTTCC TTGGGTAATG AGAAGTCACA

    402' ATCACTATTC ATAGATGTGT GGGGAGTCAC TAAAAATATA TTATTCACTG TCAATCTTAG
         ********** ********** ********** ********** ********** **********
    421" ATCACTATTC ATAGATGTGT GGGGAGTCAC TAAAAATATA TTATTCACTG TCAATCTTAG

    462' TTTATATCCA GATACAACAG GGTACACTGC TCTTGTAATG GAATCAGACT TCTTATTTTA
         ********** ********** ********** ********** ********** **********
    481" TTTATATCCA GATACAACAG GGTACACTGC TCTTGTAATG GAATCAGACT TCTTATTTTA

    522' ACAAGACAAA CCAAATCCAA TCCACATTTG AAGATTATAG GTTTTAATAT AAGAAAATGC
         ********** ********** ********** ********** ********** **********
    541" ACAAGACAAA CCAAATCCAA TCCACATTTG AAGATTATAG GTTTTAATAT AAGAAAATGC

    582' ACTCATTTCT CAAAGACCCT AGTGAAGCTG TGTTTAAATG CTCCTAGGTG AACCCCCTTT
         ********** ********** ********** ********** ********** **********
    601" ACTCATTTCT CAAAGACCCT AGTGAAGCTG TGTTTAAATG CTCCTAGGTG AACCCCCTTT

    642' GCATCCCAGT GTTCCCACCC TGACACCCAG AGCCCCTACC TACCCAACAC AGAATCATTT
           *  *  *  * ****         ***   * *****     * *** * * **** *
    661" ---TGGCCAT -TCCCCAGTT GTTTTCCCCC ACCCCCT--- GAACCACCCC AGAAGCCC
```

```
1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5735

2nd Nucleotide Sequence
  File Name        : RDB7807R.fasta (Complementary)
  Sequence Size    : 776

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

[96.512% / 774 bp] INT/OPT.Score : < 1384/ 2747 >

```
  841' CTGAGTCACA CGCGTCTTTG TTCTCTTTCT TGT-CCCAAA A-CCGTTA-- CCTC-AAGTG
                               ***** *** ****** * ******   * ** *****
    1"                         TTTTCT TGTCCCCAAA ACCCGTTACC CTTCAAAGTG

  896' -ACA-AATGA --TCAAA--T CTC-AAATAT ---AGAATTC A-GGGTTTT- ACA-GGTA-G
        *** *****   *****  * *** ******    * * *** * *******  *** **** *
   37" AACANAATGA TTTCAAATTT CTCAAAATAT AAGAAATTTC AGGGGTTTTA ACAGGGTANG

  942' GCA-TCTTGA GGA-TTTCAA ATGGTT-AAA AGCAACTCAC TCCTTTTCTA CTCTTTGGAG
       *** ****** *** *****. ****** *** ********** ********** **********
   97" GCATTCTTGA GGATTTTCAN ATGGTTAAAA AGCAACTCAC TCCTTTTCTA CTCTTTGGAG

  999' AGTTTCAAGA GCCTATAGCC TCTAAAACGC AAATCATTGC TAAGGGTTGG GGGGGAGAAA
       ********** ********** ********** ********** ********** **********
   157" AGTTTCAAGA GCCTATAGCC TCTAAAACGC AAATCATTGC TAAGGGTTGG GGGGGAGAAA

 1059' CCTTTTCGAA TTTTTTAGGA ATTCCTGCTG TTTGCCTCTT CAGCTACCTA CTTCCTAAAA
       ********** ********** ********** ********** ********** **********
   217" CCTTTTCGAA TTTTTTAGGA ATTCCTGCTG TTTGCCTCTT CAGCTACCTA CTTCCTAAAA

 1119' AGGATGTATG TCAGTGGACA GAACAGGGCA AACTTATTCG AAAAAGAAAT AAGAAATAAT
       ********** ********** ********** ********** ********** **********
   277" AGGATGTATG TCAGTGGACA GAACAGGGCA AACTTATTCG AAAAAGAAAT AAGAAATAAT

 1179' TGCCAGTGTG TTTATAAATG ATATGAATCA GGAGTGGTGC GAAGAGGATA GGGAAAAAAA
       ********** ********** ********** ********** ********** **********
   337" TGCCAGTGTG TTTATAAATG ATATGAATCA GGAGTGGTGC GAAGAGGATA GGGAAAAAAA

 1239' AATTCTATTT GGTGCTGGAA ATACTGCGCT TTTTTTTTTC CTTTTTTTTT TTTTCTGTGA
       ********** ********** ********** ********** * ******** **********
   397" AATTCTATTT GGTGCTGGAA ATACTGCGCT TTTTTTTTTC C-TTTTTTT TTTTCTGTGA

 1299' GCTGGAGTGT GCCAGCTTTT TCAGACGGAG GAATGCTGAG TGTCAAGGGG TCAGGATCAA
       ********** ********** ********** ********** ********** **********
   456" GCTGGAGTGT GCCAGCTTTT TCAGACGGAG GAATGCTGAG TGTCAAGGGG TCAGGATCAA
```

2010 DNA Bank, RIKEN BioResource Center

```
1359'  TCCGGTGTGA GTTGATGAGG CAGGAAGGTG GGGAGGAATG CGAGGAATGT CCCTGTTTGT
       ********** ********** ********** ********** ********** **********
 516"  TCCGGTGTGA GTTGATGAGG CAGGAAGGTG GGGAGGAATG CGAGGAATGT CCCTGTTTGT

1419'  GTAGGACTCC ATTCAGCTCA TTGGCGAGCC GCGGCCGCCC GGAGCGTATA AAAGCCTCGG
       ********** ********** ********** ********** ********** **********
 576"  GTAGGACTCC ATTCAGCTCA TTGGCGAGCC GCGGCCGCCC GGAGCGTATA AAAGCCTCGG

1479'  GCCGCCCGCC CCAAACTCAC ACAACAACTC TTCCCCGCTG AGAGGAGACA GCCAGTATCA
       ********** ********** ********** ********** ********** **********
 636"  GCCGCCCGCC CCAAACTCAC ACAACAACTC TTCCCCGCTG AGAGGAGACA GCCAGTATCA

1539'  AGATCTGGCC TCGGCGGCCA AGCTTGGCAA TCCGGTACTG TTGGTAAAGC CACCATGGAA
       ********** ********** ********** ********** ********** **********
 696"  AGATCTGGCC TCGGCGGCCA AGCTTGGCAA TCCGGTACTG TTGGTAAAGC CACCATGGAA

1599'  GATGCCAAAA ACATTAAGAA GGGCCCAGCG CCATTCTACC CACTCGAAGA CGGGACCGCC
       ********** **********
 756"  GATGCCAAAA ACATTAAGAG A
```

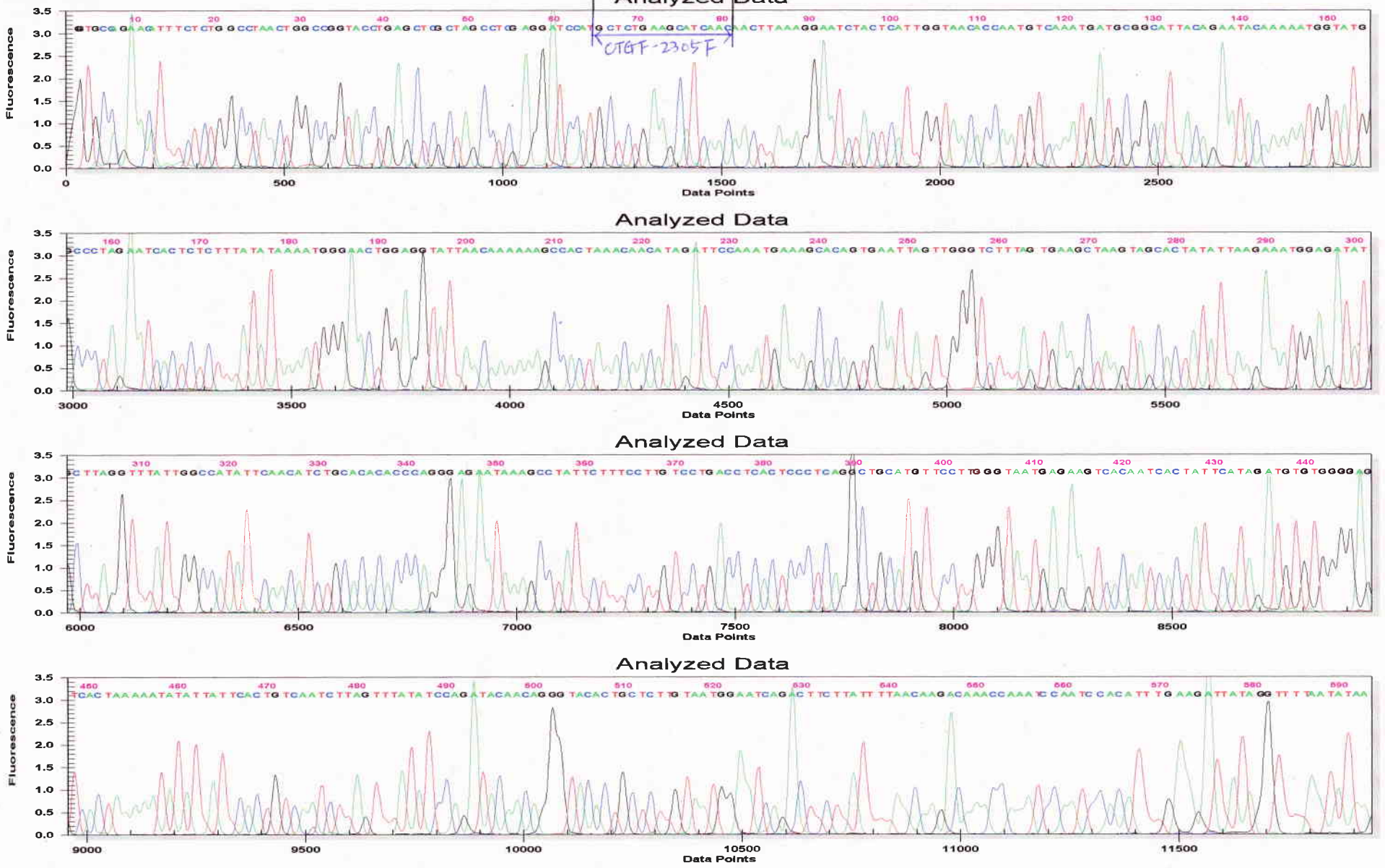
Project : Promoter RDB 7807 (pGL4-CTGF)
Sample : U2927-12F.E07_10041218ML
Result : U2927-12F.E07_10041218ML

System : CEQ System
Operator : 3.100412Kusa
Instrument : CEQ System (Ver. 9.0.25)

Vector region — Insert region

PCR cloning primer sequence

CTGF-2305F



Project : Promoter RDB 7807 (pGL4-CTGF)
Sample : U2927-12R.F07_10041218ML
Result : U2927-12R.F07_10041218ML

System : CEQ System
Operator : 3.100412Kusa
Instrument : CEQ System (Ver. 9.0.25)

Vector region — Insert region
PCR cloning primer sequence

