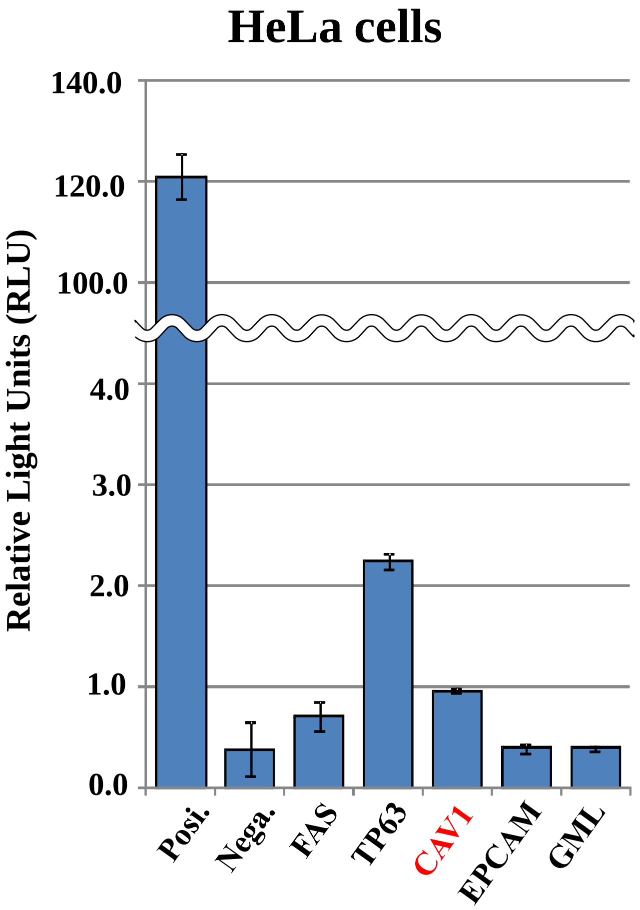
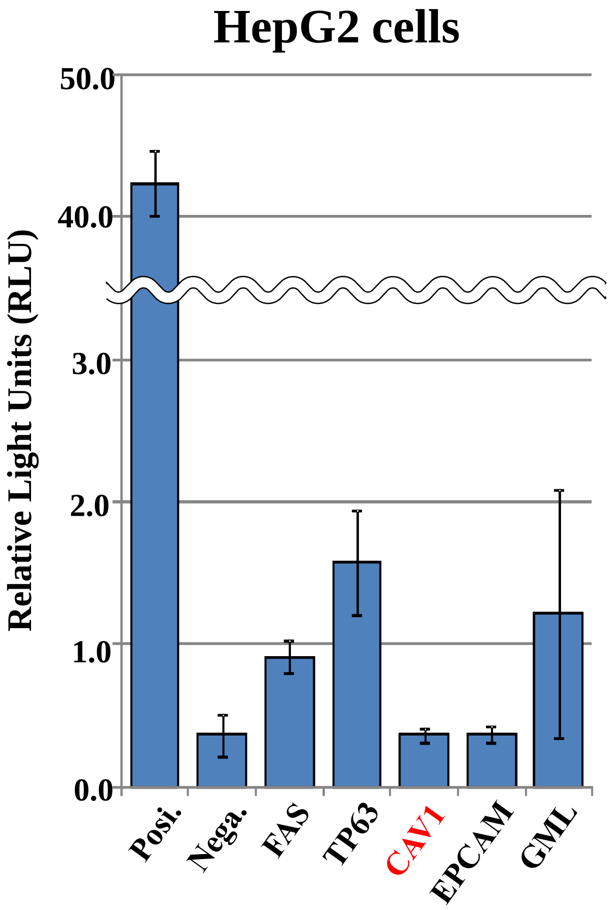
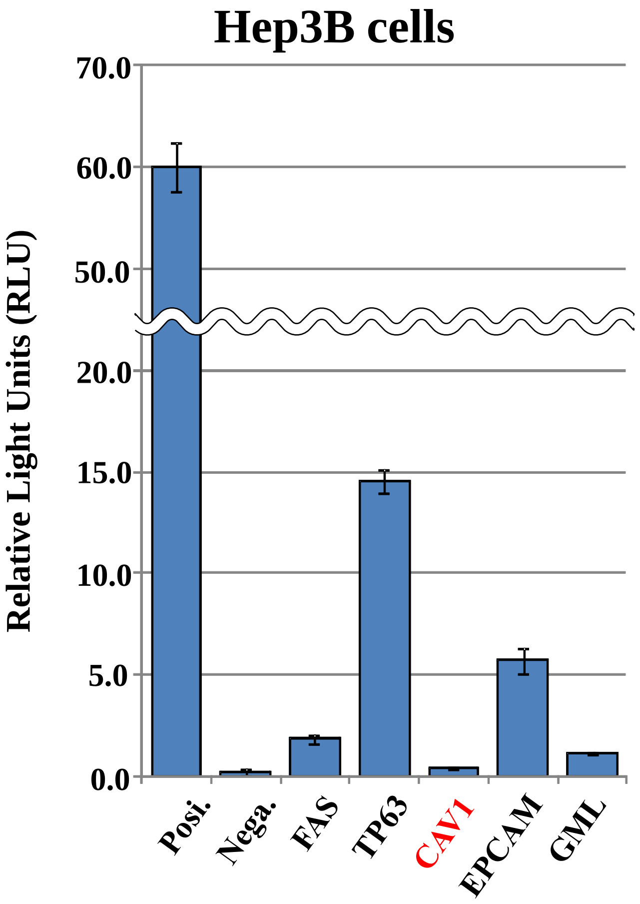
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

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

FAS: pGL4-phFAS (RDB# 7349)
TP63: pGL4-phTP63 (RDB# 7350)
CAV1: pGL4-phCAV1 (RDB# 7364)
EPCAM: pGL4-phEPCAM (RDB#7367)
GML: pGL4-phGML (RDB# 7371)

2009, 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.gnu
  Sequence Size    : 5551

2nd Nucleotide Sequence
  File Name        : RDB7364F.fasta
  Sequence Size    : 380

  Unit Size to Compare = 1
  Pick up Location     = 1



[93.939% / 363 bp]     INT/OPT.Score : <    868/  1236 >

      1’                          GGCCTAA C-TGGCCGGT ACCTGAGCTC GCTAGCCTC-
                                   ****** * ******** ********** *********
      1″ GGTGCCAGAA CATATTCATC ATGTGCCTAA CATGGCCGGT ACCTGAGCTC GCTAGCCTCA

     36’ -GAGGATTGT GACACTTTCC CTGCCATTCT TAGTTAAAAC TGATCTTTTG TTCCAAAAAT
           ******** ********** ********** ********** ********** **********
     61″ GAAGGATTGT GACACTTTCC CTGCCATTCT TAGTTAAAAC TGATCTTTTG TTCCAAAAAT

     95’ TTTTGCTACC AACAATAGCC TGTCCTTTAT AGTTCTTTTA TACTTTTGTG TCTTCTCTCT
         ********** ********** ********** ********** ********** **********
    121″ TTTTGCTACC AACAATAGCC TGTCCTTTAT AGTTCTTTTA TACTTTTGTG TCTTCTCTCT

    155’ AACTAAATAA TCAACTCTTT CAGCATTCCA TCCATTTCCC TTTCTCCTCC CTCTTACTCC
         ********** ********** ********** ********** ********** **********
    181″ AACTAAATAA TCAACTCTTT CAGCATTCCA TCCATTTCCC TTTCTCCTCC CTCTTACTCC

    215’ CAACCCACAT TCCCCTCTCC ATTTTAATTT TAACCTGTGC CCCTTCAAGT GTACTCCAGC
         ********** ********** * ******** ********** ********** **********
    241″ CAACCCACAT TCCCCTCTCC A-TTTAATTT TAACCTGTGC CCCTTCAAGT GTACTCCAGC
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275’ TTTTTTTTTA AAATAATTTC AAGTGATACT TTGACTTTTG ACTGCATATG GAAGCATAAG
     *********   **  ***** *********  ***** **** ********** ***   ****
300″ TTTTTTTTTT TAAATATTTC AAGTGATAC- TTGAC-TTTG ACTGCATATG GAA--CTAAG

335’ TAACATGTCC TTTCATTTTT GGATAATGAG TTTCCTGATT AATTACAGCT CAAGAGTAAA
     * ** ***** **** ***      ****
356″ T-AC-TGTCC TTTCTTTTGA TATTAAT




1st Nucleotide Sequence
  File Name       : Reference Seq.gnu
  Sequence Size   : 5551

2nd Nucleotide Sequence
  File Name       : RDB7364R.fasta (Complementary)
  Sequence Size   : 619

  Unit Size to Compare = 1
  Pick up Location     = 1



[87.171% / 608 bp]     INT/OPT.Score : <   1180/  1786 >

841’ CACCCACACA GATTCCTTCC ATAAGGGATC CACAAAGTTT AGATGTGAAA TGTACCTAAA
                           *.*  * *  .*  **..*  *  * * **   **  *   *
  1″         TT CCAATNANAT TTNACAGTTA NAATAANNTA ACCTTTTAAG GGTTTCCGTA

901’ GGTTCCTAGC CGTCTTTCAT CCCTCCCTCT GTGAAACAGG GAGACA-CAT GT----GTTT
      *  **       *.  **   * * ** **  ** ** **** * **.* **   *     .**
 53″ AG-CCCGTTT TTTNAATCCC CTCCCCTTCA GT-AACCAGG GTGANACCAA CTAGACANTT

956’ TAAGGCAG-- AGATGGAA-C TTGGGCG-AT -GGGC-GGGG GGT-GGGGGA GGTGGGAAGG
     ********   * ****** * ******* **  **** **** *** ****** **********
111″ TAAGGCAGAA AAATGGAACC TTGGGCGAAT GGGGCGGGGG GGTGGGGGGA GGTGGGAAGG
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1009' G--AC--GGC -TTA-GGACA -GGGCAGGAT TGTGGATT-G TTTCTGCCGC CTTGGTTGCC
      *  **  ***  *** *****  ********* ******** * ********** **********
 171″ GTGACGGGGC TTTAGGGACA GGGGCAGGAT TGTGGATTGG TTTCTGCCGC CTTGGTTGCC

1061' CATACTGGGC ATCTCTGCAG GCGCGTC-GG CTCCCTCCAC CCCTGCTGAG ATGATGCACT
      ********** ********** ******* ** ********** ********** **********
 231″ CATACTGGGC ATCTCTGCAG GCGCGTCGGG CTCCCTCCAC CCCTGCTGAG ATGATGCACT

1120' GCGAAAACAT TCGCTCTCCC CGG-GACGCC TCTCGGTGGT TCAGAGCAGG GAAAATGTTG
      ********** ********** *** ****** ********** ********** **********
 291″ GCGAAAACAT TCGCTCTCCC CGGTGACGCC TCTCGGTGGT TCAGAGCAGG GAAAATGTTG

1179' CCTCAGGTTT AAAATAATCT GCCCAAGCAC CCCAGCGCGG GAGAAACGTT CTCACTCGCT
      ********** ********** ********** ********** ********** **********
 351″ CCTCAGGTTT AAAATAATCT GCCCAAGCAC CCCAGCGCGG GAGAAACGTT CTCACTCGCT

1239' CTCTGCTCGC TGCGGGCGCT CCCCGCCCTC TGCTGCCAGA ACCTTGGGGA TGTGCCTAGA
      ********** ********** ********** ********** ********** **********
 411″ CTCTGCTCGC TGCGGGCGCT CCCCGCCCTC TGCTGCCAGA ACCTTGGGGA TGTGCCTAGA

1299' CCCGGCGCAG CACACGTCCG GGCCAACCGC GAGCAGAACA AACCTTTGGC GGATCAAGAT
      ********** ********** ********** ********** ********** **********
 471″ CCCGGCGCAG CACACGTCCG GGCCAACCGC GAGCAGAACA AACCTTTGGC GGATCAAGAT

1359' CTGGCCTCGG CGGCCAAGCT TGGCAATCCG GTACTGTTGG TAAAGCCACC ATGGAAGATG
      ********** ********** ********** ********** ********** **********
 531″ CTGGCCTCGG CGGCCAAGCT TGGCAATCCG GTACTGTTGG TAAAGCCACC ATGGAAGATG

1419' CCAAAAACAT TAA-GAAGGG CCCAGCGCCA TTCTACCCAC TCGAAGACGG GACCGCCGGC
      ********** *** ** *   **  **.**
 591″ CCAAAAACAT TAATGAGGAA CCTCGCNCC
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