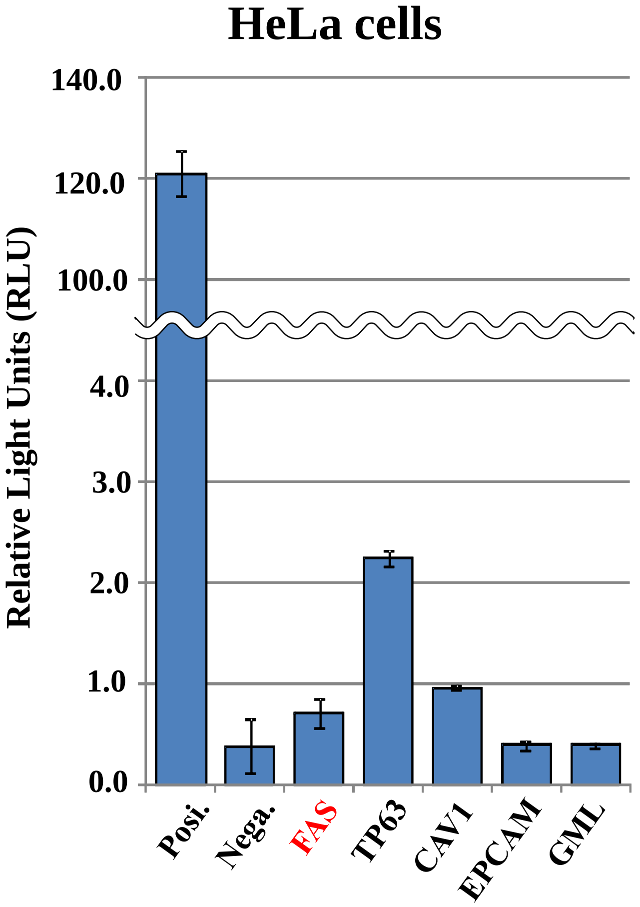
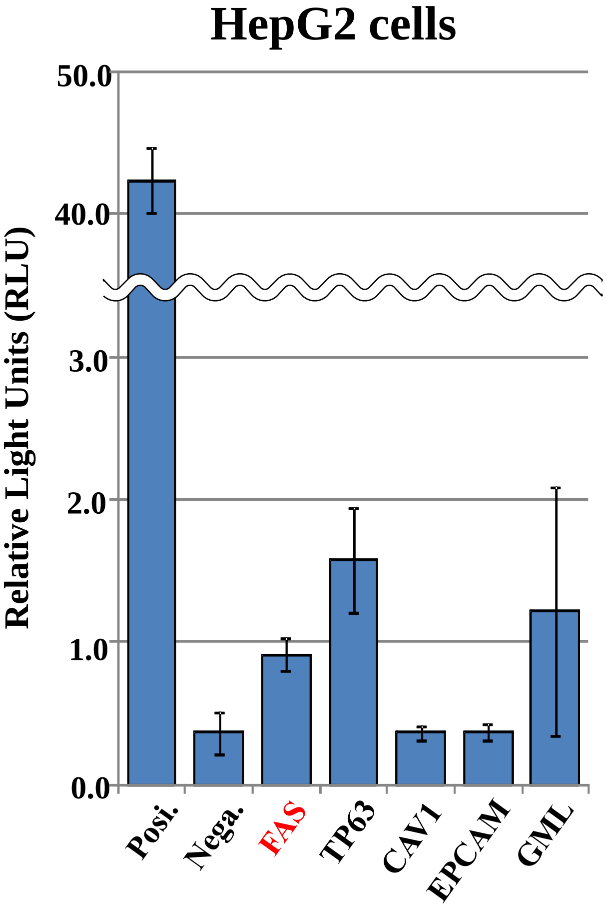
The Promoter Activities of Reporter Constructs

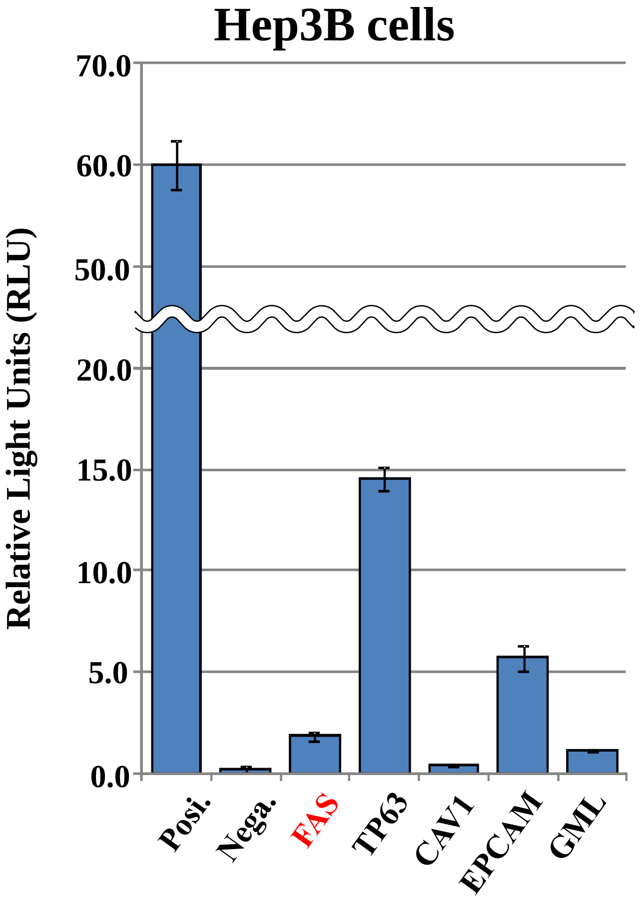
HeLa cells



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

```
[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.03.02

1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5573

2nd Nucleotide Sequence
  File Name        : RDB7349F.fasta
  Sequence Size    : 527

  Unit Size to Compare = 1
  Pick up Location     = 1



[98.024% / 506 bp]     INT/OPT.Score : <    932/  1945 >

      1’                     GG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTC-GAGGAT
                             ** ********** ********** ********** *** ******
      1″ GTGCCAGAAC ATTTCTCTGG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCAGAGGAT

     42’ CACACCCCTT TTCCTTCCTT CTTTTTACAT TTTTTTATTT AAATGAACTT TTCATTTTGG
         ********** ********** ********** ********** ********** **********
     61″ CACACCCCTT TTCCTTCCTT CTTTTTACAT TTTTTTATTT AAATGAACTT TTCATTTTGG

    102’ AATAGTTTTA GGATTTCAAA AAATTTGCAG AGATAATACA GAGAATGCCC ATATACCATC
         ********** ********** ********** ********** ********** **********
    121″ AATAGTTTTA GGATTTCAAA AAATTTGCAG AGATAATACA GAGAATGCCC ATATACCATC

    162’ CTCCTTATCC CACTTCTTTT TGTGTCTATT AGATGCTCAG AGTGTGTGCA CAAGGCTGGC
         ********** ********** ********** ********** ********** **********
    181″ CTCCTTATCC CACTTCTTTT TGTGTCTATT AGATGCTCAG AGTGTGTGCA CAAGGCTGGC

    222’ ACGCCCAGGG TCTTCCTCAT GGCACTAACA GTCTACTGAA AGG--TGGAA CAGAGACAAG
         ********** ********** ********** ********** ***   **** **********
    241″ ACGCCCAGGG TCTTCCTCAT GGCACTAACA GTCTACTGAA AGGTTGGGAA CAGAGACAAG
```

```
    280’ CCTATCAACA CCTACAAGAC TGGTGGTAAG TGCAGTGACA GATGCAAAAC ACAGGGTGAT
         ********** ********** ********** ********** ********** **********
    301″ CCTATCAACA CCTACAAGAC TGGTGGTAAG TGCAGTGACA GATGCAAAAC ACAGGGTGAT

    340’ GGAAAGCCCT CAGGAGGGTA ACCTAACCTA GATTTGAGGG CCCAAACAGG CTCCAGAAGA
         ********** ********** ********** ********** ********** **********
    361″ GGAAAGCCCT CAGGAGGGTA ACCTAACCTA GATTTGAGGG CCCAAACAGG CTCCAGAAGA

    400’ AAATGTCAAC TGAGAGGAAG CCTGAAGGAT GAACAGTGGG CTAAGCAAAG GGTTATTAAT
         ********** ********** ********** ********** ********** **********
    421″ AAATGTCAAC TGAGAGGAAG CCTGAAGGAT GAACAGTGGG CTAAGCAAAG GGTTATTAAT

    460’ GTGTTATTAA TGGGTTGAAT CTAATTGGGA AGGGAGAGAG GTTGCAGAGT GAGGTGCAGA
         ********** ********** *********  * ** *****    .*
    481″ GTGTTATTAA TGGGTTGAAT CTAATTGGGG AAGGGGAGAG AGNGTTT
```

```
1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5573

2nd Nucleotide Sequence
  File Name        : RDB7349R.fasta (Complementary)
  Sequence Size    : 669

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

```
[98.651% / 667 bp]     INT/OPT.Score : <   2416/  2555 >

    781’ TGAATGTTTA ATATA-GCT- GGGGCTATGC GA-TTTGGC- -TTAAGTTGT TAGCTTT-GT
                    ***** ***  ****.*****  * ******   ********* ******* **
      1″         GT ATATAGGCTG GGGGNTATGC AATTTTGGCT TTTAAGTTGT TAGCTTTGGT
```

```
 835' TTTCCTCTTG AG-AAATAAA AACTAAGGGG CCCTCCCTTT TCAGAGCCCT ATGGCGCAAC
      ********** ** ******* ********** ********** ********** **********
  53″ TTTCCTCTTG AGAAAATAAA AACTAAGGGG CCCTCCCTTT TCAGAGCCCT ATGGCGCAAC

 894' ATCTGTACTT TTTCATATGG TTAACTGTCC ATTCCAGAAA CGTCTGTGAG CCTCTCATGT
      ********** ********** ********** ********** ********** **********
 113″ ATCTGTACTT TTTCATATGG TTAACTGTCC ATTCCAGAAA CGTCTGTGAG CCTCTCATGT

 954' TGCAGCCACA ACATGGACAG CCCAGTCAAA TGCCCCGCAA GTCTTTCTCT GAGTGACTCC
      ********** ********** ********** ********** ********** **********
 173″ TGCAGCCACA ACATGGACAG CCCAGTCAAA TGCCCCGCAA GTCTTTCTCT GAGTGACTCC

1014' AGCAATTAGC CAAGGCTCCT GTACCCAGGC AGGACCTCTG CGCTCTGAGC TCCATTCTCC
      ********** ********** ********** ********** ********** **********
 233″ AGCAATTAGC CAAGGCTCCT GTACCCAGGC AGGACCTCTG CGCTCTGAGC TCCATTCTCC

1074' TTCAAGACCT CCCCAACTTC CCAGGTTGAA CTACAGCAGA AGCCTTTAGA AAGGGCAGGA
      ********** ********** ********** ********** ********** **********
 293″ TTCAAGACCT CCCCAACTTC CCAGGTTGAA CTACAGCAGA AGCCTTTAGA AAGGGCAGGA

1134' GGCCGGCTCT CGAGGTCCTC ACCTGAAGTG AGCATGCCAG CCACTGCAGG AACGCCCCGG
      ********** ********** ********** ********** ********** **********
 353″ GGCCGGCTCT CGAGGTCCTC ACCTGAAGTG AGCATGCCAG CCACTGCAGG AACGCCCCGG

1194' GACAGGAATG CCCATTTGTG CAACGAACCC TGACTCCTTC CTCACCCTGA CTTCTCCCCC
      ********** ********** ********** ********** ********** **********
 413″ GACAGGAATG CCCATTTGTG CAACGAACCC TGACTCCTTC CTCACCCTGA CTTCTCCCCC

1254' TCCCTACCCG CGCGCAGGCC AAGTTGCTGA ATCAATGGAG CCCTCCCCAA CCCGGGCGTT
      ********** ********** ********** ********** ********** **********
 473″ TCCCTACCCG CGCGCAGGCC AAGTTGCTGA ATCAATGGAG CCCTCCCCAA CCCGGGCGTT

1314' CCCCAGCGAG GCTTCCTTCC CATCCTCCTG ACCACCGGGG CTTTTCGTGA GCTCGTCTCA
      ********** ********** ********** ********** ********** **********
 533″ CCCCAGCGAG GCTTCCTTCC CATCCTCCTG ACCACCGGGG CTTTTCGTGA GCTCGTCTCA

1374' TCAAGATCTG GCCTCGGCGG CCAAGCTTGG CAATCCGGTA CTGTTGGTAA AGCCACCATG
      ********** ********** ********** ********** ********** **********
 593″ TCAAGATCTG GCCTCGGCGG CCAAGCTTGG CAATCCGGTA CTGTTGGTAA AGCCACCATG
```

```
1434’ GAAGATGCCA AAAACATTAA GAAGGGCCCA GCGCCATTCT ACCCACTCGA AGACGGGACC
      ********** *******
 653″ GAAGATGCCA AAAACAT
```