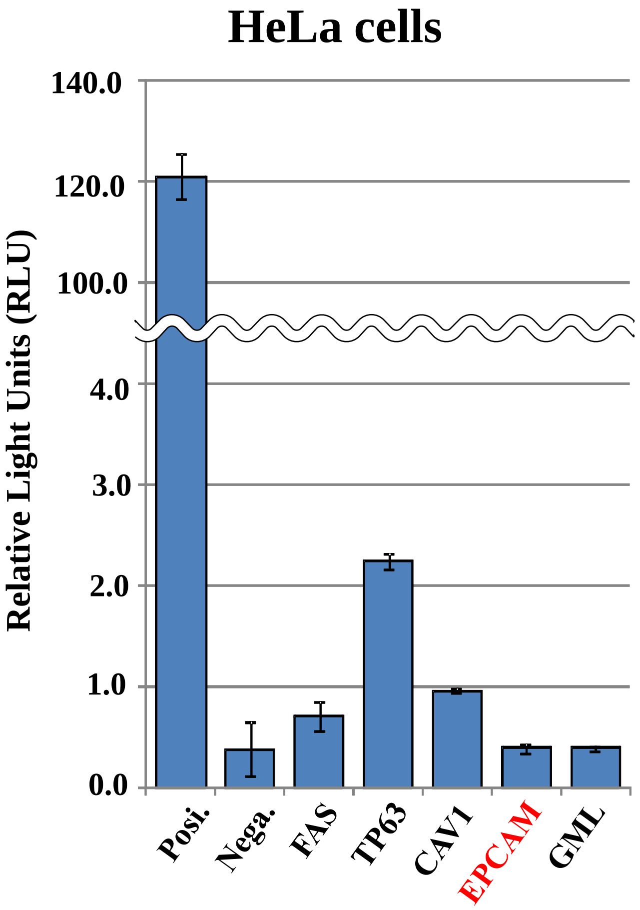
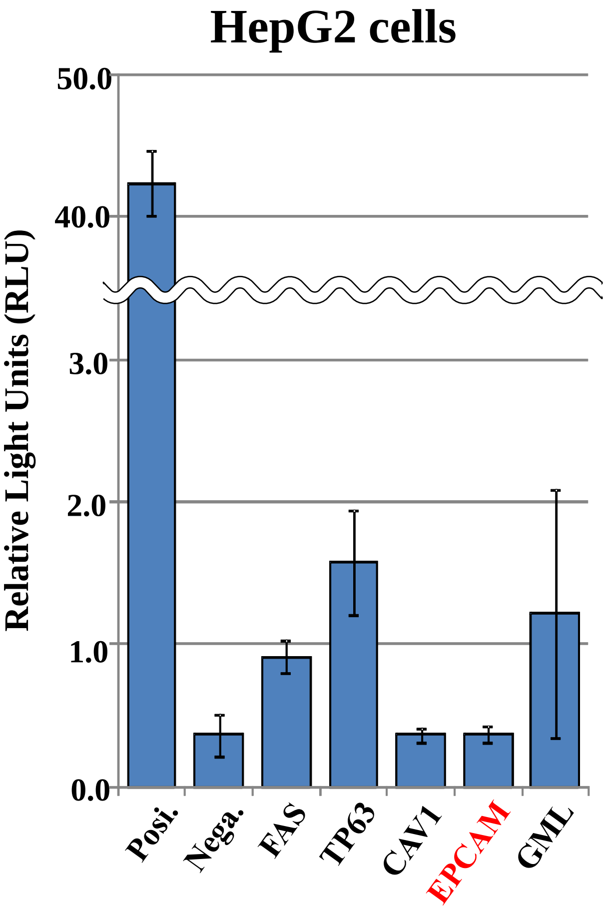
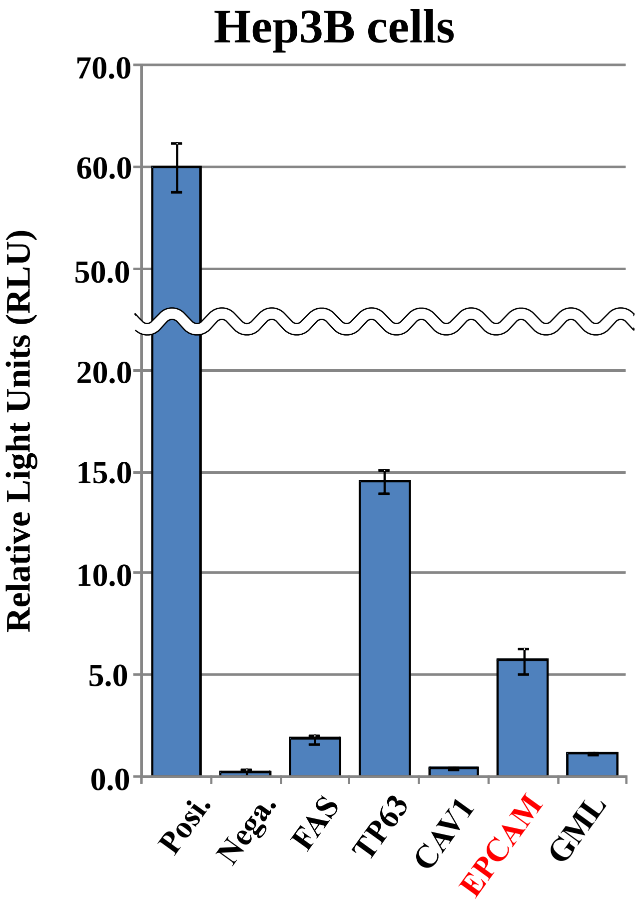
The Promoter Activities of Reporter Constructs







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 : 2009.05.29

1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5753

2nd Nucleotide Sequence
  File Name        : RDB7367F.fasta
  Sequence Size    : 400

  Unit Size to Compare = 2
  Pick up Location     = 1



[99.751% / 401 bp]     INT/OPT.Score : <   1444/  1588 >

    1' GGCCTAACTG GCCGGTACCT GAGCTCGCTA GCCTCGAGGA TCCAGCCTCC TTTCCTCTTT
                                                    ********* **********
   60"                                              CCAGCCTCC TTTCCTCTTT

   61' TTAACTCTTA CTTTTATGAT TTCTTTAGTG GATAAAAAGC TTTTAAAAAA TAGGTTACAA
       ********** ********** ********** ********** ********** **********
   79" TTAACTCTTA CTTTTATGAT TTCTTTAGTG GATAAAAAGC TTTTAAAAAA TAGGTTACAA

  121' TGATATTACA GCTAACAAAA AATAACATTT AAAAACACTA AATAGTATAT ATATGAAGTA
       ********** ********** ********** ********** ********** **********
  139" TGATATTACA GCTAACAAAA AATAACATTT AAAAACACTA AATAGTATAT ATATGAAGTA

  181' TTTATAATTA TTTTAATATT GTAATAATAT AGTGTGTTGT GATTTGAATT CATCTGCACG
       ********** ********** ********** ********** ********** **********
  199" TTTATAATTA TTTTAATATT GTAATAATAT AGTGTGTTGT GATTTGAATT CATCTGCACG

  241' GAAATCGATT ACTGTCCTTT CTTTCTATTT CCCTATATTT TCTTTCCGAA GGCGTCATCA
       ********** ********** ********** ********** ********** **********
  259" GAAATCGATT ACTGTCCTTT CTTTCTATTT CCCTATATTT TCTTTCCGAA GGCGTCATCA
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   301' ACATTTTGGT TCTTTAATAG TAACCAAAAC CCGAAATCAT CTCGGTTCTC AGTATTTGGC
        ********** ********** ********** ********** ********** **********
   319″ ACATTTTGGT TCTTTAATAG TAACCAAAAC CCGAAATCAT CTCGGTTCTC AGTATTTGGC

   361' TCTATGGGAA CACCTTTTCT TTTCTCTCTT TTTTTTTTTT TTTGAGACGG AGTCTTGCTC
        ********** ********** ******** * ********** ********** **********
   379″ TCTATGGGAA CACCTTTTCT TTTCTCTC-T TTTTTTTTTT TTTGAGACGG AGTCTTGCTC

   421' CTGTCGCCCA GGCTGGAGTG TAATGGCACG ATCTCTGCTC ACTGCAACCT CAGCCTCCCC
        ********** ********** **
   438″ CTGTCGCCCA GGCTGGAGTG TA




1st Nucleotide Sequence
  File Name         : Reference Seq.GNU
  Sequence Size     : 5753

2nd Nucleotide Sequence
  File Name         : RDB7367R.fasta (Complementary)
  Sequence Size     : 390

  Unit Size to Compare = 1
  Pick up Location     = 1



[99.744% / 391 bp]     INT/OPT.Score : <   1508/  1548 >

  1141' GGGGGAGGGG AGCCTACTCA CTCCCCCAAC TCCCGGGCGG TGACTCATCA ACGAGCACCA
                               ********* **********  ********* **********
    85″                        TCCCCCAAC TCCCGGGCGG -GACTCATCA ACGAGCACCA

  1201' GCGGCCAGAG GTGAGCAGTC CCGGGAAGGG GCCGAGAGGC GGGGCCGCCA GGTCGGGCAG
        ********** ********** ********** ********** ********** **********
   123″ GCGGCCAGAG GTGAGCAGTC CCGGGAAGGG GCCGAGAGGC GGGGCCGCCA GGTCGGGCAG
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1261’ GTGTGCGCTC CGCCCCGCCG CGCGCACAGA GCGCTAGTCC TTCGGCGAGC GAGCACCTTC
      ********** ********** ********** ********** ********** **********
 183″ GTGTGCGCTC CGCCCCGCCG CGCGCACAGA GCGCTAGTCC TTCGGCGAGC GAGCACCTTC

1321’ GACGCGGTCC GGGGACCCCC TCGTCGCTGT CCTCCCGACG CGGACCCGCG TGCCCCAGGC
      ********** ********** ********** ********** ********** **********
 243″ GACGCGGTCC GGGGACCCCC TCGTCGCTGT CCTCCCGACG CGGACCCGCG TGCCCCAGGC

1381’ CTCGCGCTGC CCGGCCGGCT CCTCGTGTCC CACTCCCGGC GCACGCCCTC CCGCGAGTCC
      ********** ********** ********** ********** ********** **********
 303″ CTCGCGCTGC CCGGCCGGCT CCTCGTGTCC CACTCCCGGC GCACGCCCTC CCGCGAGTCC

1441’ CGGGCCCCTC CCGCGCCCCT CTTCTCGGCG CGCGCGCAGC ATGGCGCCCC CGCAGGTCCT
      ********** ********** ********** ********** ********** **********
 363″ CGGGCCCCTC CCGCGCCCCT CTTCTCGGCG CGCGCGCAGC ATGGCGCCCC CGCAGGTCCT

1501’ CGCGTTCGGG CTTCTGCTTG CCGCGGCGAC GGCGACTTTT GCCGCAGCTC AGATCAAGAT
      ********** ********** ********** ********** ********** **
 423″ CGCGTTCGGG CTTCTGCTTG CCGCGGCGAC GGCGACTTTT GCCGCAGCTC AG
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