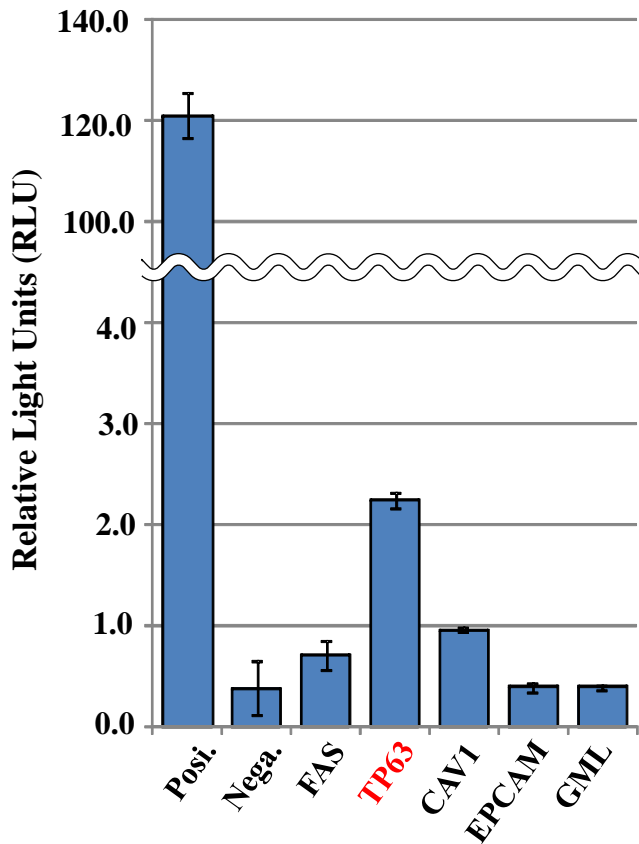
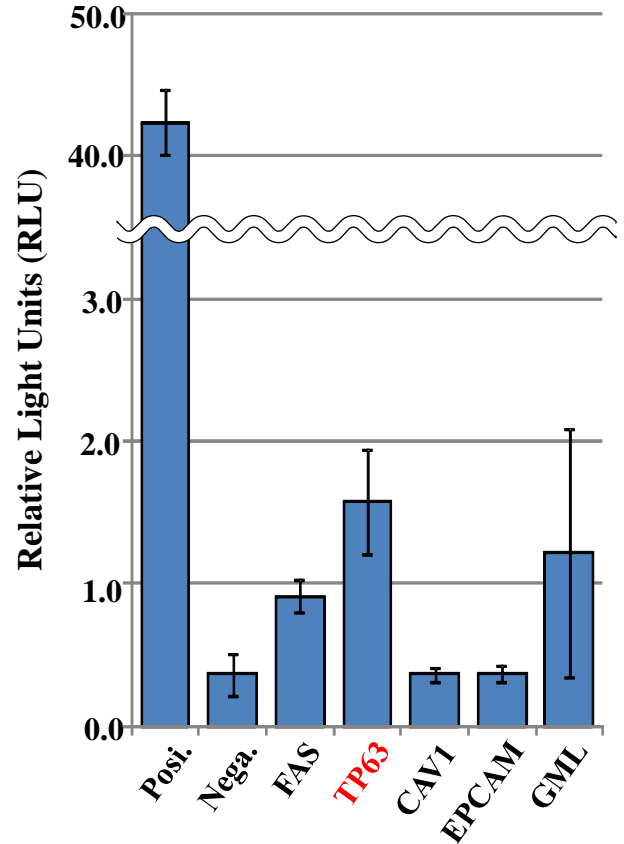


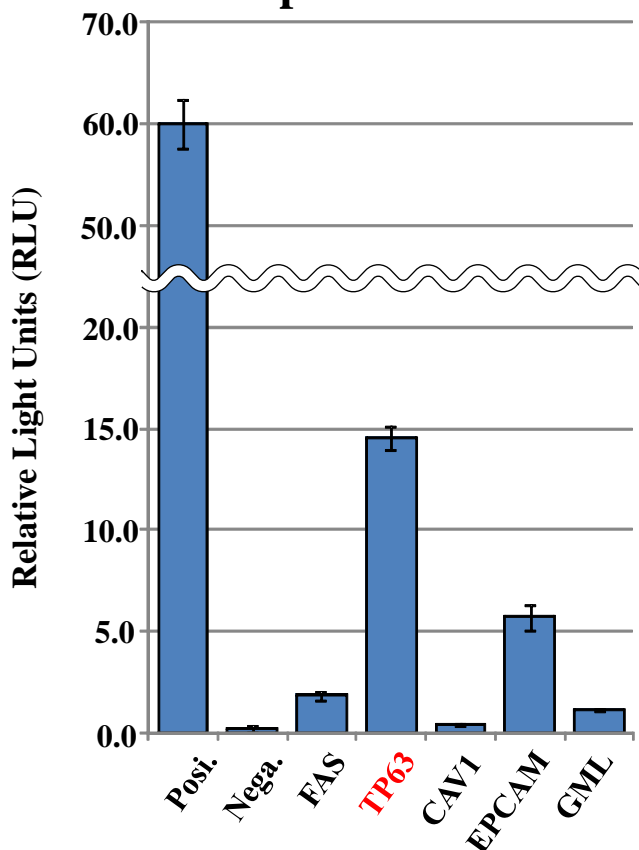
HeLa cells



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)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2010.03.02

1st Nucleotide Sequence

File Name : Reference Seq.gnu
Sequence Size : 5572

2nd Nucleotide Sequence

File Name : RDB7350F.fasta
Sequence Size : 659

Unit Size to Compare = 1
Pick up Location = 1

[98.722% / 626 bp] INT/OPT. Score : < 1956/ 2414 >

```
1'          GG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATG
          ** *****
1'' GTGCCAGAAC ATTTCTCTGG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATG

43' GGCTTTAGAT TGTCTCACAA CTTTGACATC TACTGATGTC ACCTATTTAC AGGTGTGTCC
          *****
61'' GGCTTTAGAT TGTCTCACAA CTTTGACATC TACTGATGTC ACCTATTTAC AGGTGTGTCC

103' TGTGACTAGG GGGTGAAGGG AAGATGTGAA CTCACCATGT TAGTGACCGT TAGATACACA
          *****
121'' TGTGACTAGG GGGTGAAGGG AAGATGTGAA CTCACCATGT TAGTGACCGT TAGATACACA

163' GAGTGGTTTT TTTTCCCCT GTTGGAGTCT ATCCTAACTG AGCTTCTGAA TCATATTTCA
          *****
181'' GAGTGGTTTT TTTTCCCCT GTTGGAGTCT ATCCTAACTG AGCTTCTGAA TCATATTTCA

223' TTCAATTTCC AAATCCACAA AACCAGGATA AGTTTACAGC CCATATTCAG AAAGGAAATA
          *****
241'' TTCAATTTCC AAATCCACAA AACCAGGATA AGTTTACAGC CCATATTCAG AAAGGAAATA
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283' AATTATTTG TGTGTAGACT TTCCTGATAT TACACTGATT TGGGAATATA TGAACAATTT
*****
301" AATTATTTG TGTGTAGACT TTCCTGATAT TACACTGATT TGGGAATATA TGAACAATTT

343' TATGGTTTCC TTTCGAAGTA GGTCAAGTCA AAGCAAACC AAAACAGCA AAAACTGTAA
*****
361" TATGGTTTCC TTTCGAAGTA GGTCAAGTCA AAGCAAACC AAAACAGCA AAAACTGTAA

403' GACATAAAGA ATAGAGTGA GCGACTGAG AGATTAAT AAACAGAA ATTTTATTA
*****
421" GACATAAAGA ATAGAGTGA GCGACTGAG AGATTAAT AAACAGAA ATTTTATTA

463' ACAGGCAATT TGAATAATT TGTGCACTT- CAGAATATTC TACAATAATA TATTATTTCC
*****
481" ACAGGCAATT TGAATAATT TGTGCACTTC CAGAATATTC TACAATAATA TATTATTTCC

522' AATTTAATA TCTTAAGAA AATTACTATA TTATATGTAA GTACATGTGC ATGTGTTTGA
*****
541" AATTTAATA TCTTAAGAA AATTACTATA TTATATGTAA GTACATGTGC ATGTGTTTGA

582' GGTAGGATAT TAA-CTCAA T-AAAGGTT- -ATTTTCTTT TATTCGGGTC AGGCAAAGCT
*****
601" GGTAGGATAT TAACTCAA TAAAGGTTA ATTTTCTTT TATTCGGG GTCAAGGGG

```

1st Nucleotide Sequence

File Name : Reference Seq. gnu
Sequence Size : 5572

2nd Nucleotide Sequence

File Name : RDB7350R.fasta (Complementary)
Sequence Size : 708

Unit Size to Compare = 1
Pick up Location = 1



[99.431% / 703 bp] INT/OPT. Score : < 2636/ 2758 >

721' CCTGTCTTTG CTATTTGAGA TTGTGACCAC AACAGGC-GG TTGGCTGAAA GGG-AAACTG

* ***** ** ***** **

1" CCCACC AACAGGCGGG TTGGCTGAAA GGGAAACTG

779' AAGGGCGGGG AGGGA-GGGA AATAGATGAA AAAACAAAAC AAAACAAAAC TTCCTAAGC

***** **

37" AAGGGCGGGG AGGGAGGGGA AATAGATGAA AAAACAAAAC AAAACAAAAC TTCCTAAGC

838' AGCTCTACAA AACATTTTAG CCCAGAAAT AGTCACAGAA ATCCTCAAAT CAAACCAGTA

***** **

97" AGCTCTACAA AACATTTTAG CCCAGAAAT AGTCACAGAA ATCCTCAAAT CAAACCAGTA

898' TCCAGATACA AGGAAGTGT ATGTAGCTGG AGCAGGGTGG ACACTCATCA GCTCAGTTCA

***** **

157" TCCAGATACA AGGAAGTGT ATGTAGCTGG AGCAGGGTGG ACACTCATCA GCTCAGTTCA

958' GTTACAAAAG TCCAGGCTGC TGAATTTAAA CTCTGATGCC ATTCATGCCA GCATCCAATC

***** **

217" GTTACAAAAG TCCAGGCTGC TGAATTTAAA CTCTGATGCC ATTCATGCCA GCATCCAATC

1018' ACGACAGAGA TCAGAAGTTC AGAGATGCCT CCAGCTCCAA ATTGCCAACA ACAAGTGTGG

***** **

277" ACGACAGAGA TCAGAAGTTC AGAGATGCCT CCAGCTCCAA ATTGCCAACA ACAAGTGTGG

1078' CTA CTACTATACG TCAAGGACTC TGAAGCCGTG AGAGAGGGGG AAGAACAACA GTAGAGAGGA

***** **

337" CTA CTACTATACG TCAAGGACTC TGAAGCCGTG AGAGAGGGGG AAGAACAACA GTAGAGAGGA

1138' TGCCAGCTG GTAAGAATCG AGTGTTTATG AAGTTTTAGT CAATTGATGA ATCTCATTGG

***** **

397" TGCCAGCTG GTAAGAATCG AGTGTTTATG AAGTTTTAGT CAATTGATGA ATCTCATTGG

1198' CTA AAAATCAA GAAACGCTCC GCCTCTTTCG AAATATGTAT GAAGGAGAGA AGTGCCTAAA

***** **

457" CTA AAAATCAA GAAACGCTCC GCCTCTTTCG AAATATGTAT GAAGGAGAGA AGTGCCTAAA



1258' CTTCTATGTC TGATAGCATT TGACCCTATT GCTTTTAGCC TCCCGGCTTT ATATCTATAT

 517" CTTCTATGTC TGATAGCATT TGACCCTATT GCTTTTAGCC TCCCGGCTTT ATATCTATAT

1318' ATACACAGGT ATATGTGTAT ATTTTATATA ATTGTTCTCC GTTCGTTGAT ATCAATCAAG
 ***** ** *****
 577" ATACACAGGT ATTTGTGTAT ATTTTATATA ATTGTTCTCC GTTCGTTGAT ATCAATCAAG

1378' ATCTGGCCTC GCGGCCAAG CTTGGCAATC CGGTACTGTT GGTAAGCCA CCATGGAAGA

 637" ATCTGGCCTC GCGGCCAAG CTTGGCAATC CGGTACTGTT GGTAAGCCA CCATGGAAGA

1438' TGCCAAAAC ATTAAGAAG GCCCAGCGCC ATTCTACCCA CTCGAAGACG GGACCGCCGG
 ***** **
 697" TGCCAAAAC AT