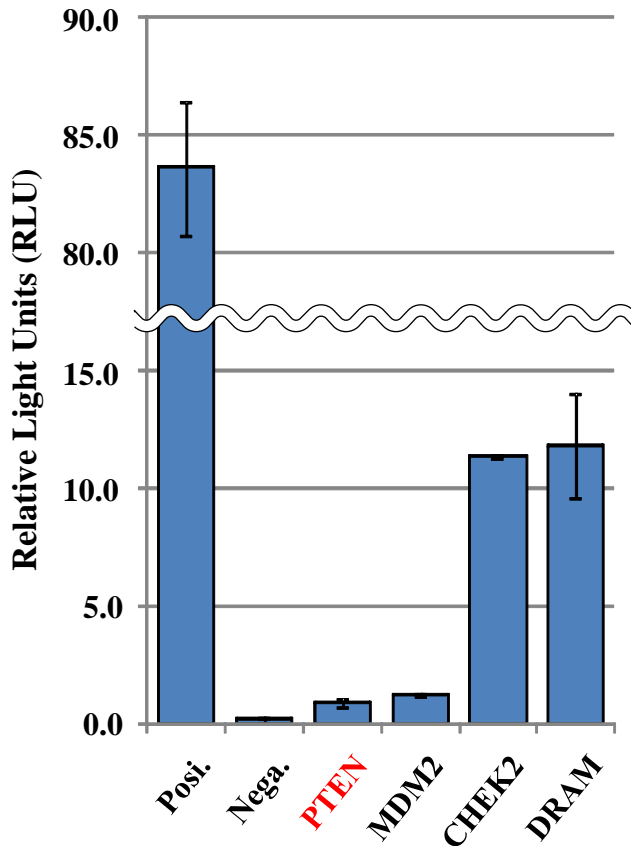
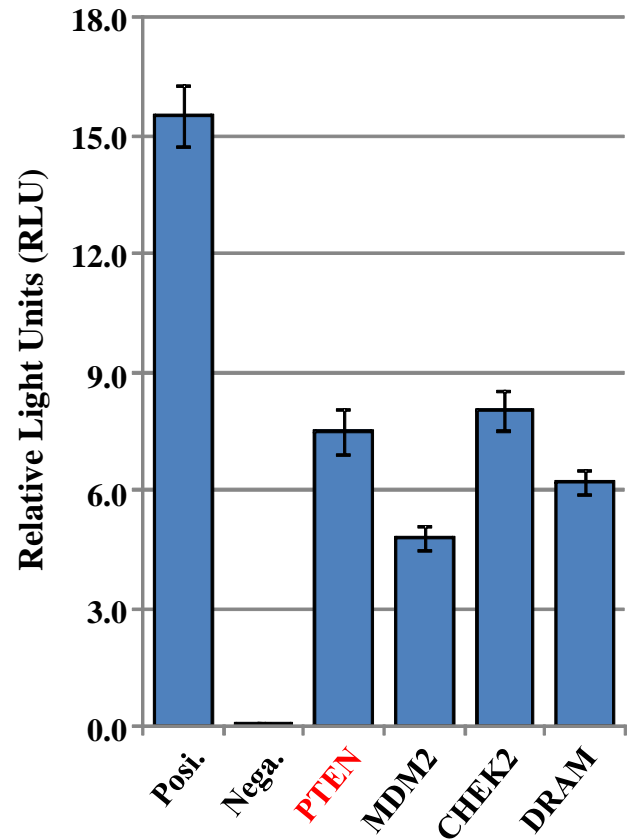


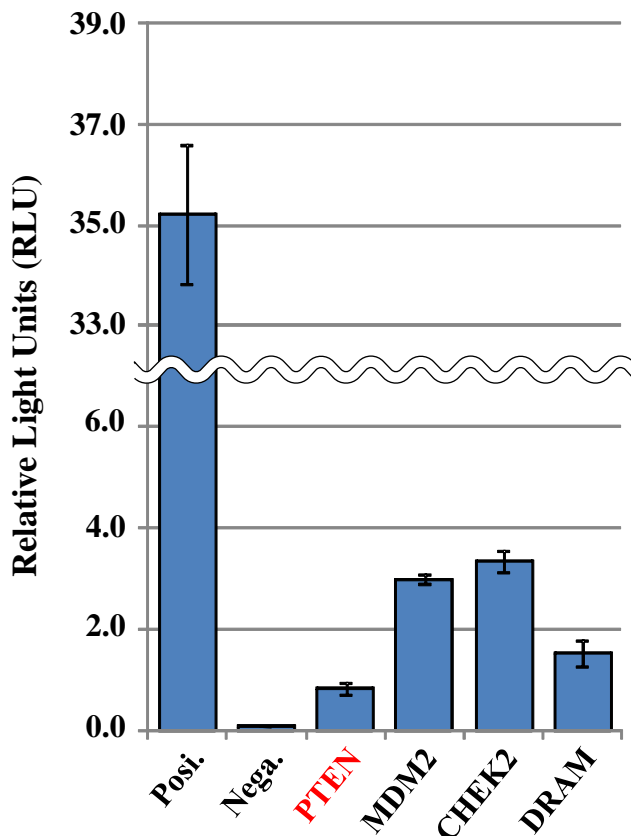
## HeLa cells



## HepG2 cells



## Hep3B cells



Posi.: pGL3 Control Vector  
(SV40 promoter)

Nega.: Empty Vector

**PTEN:** pGL4-phPTEN (RDB# 7400)

MDM2: pGL4-phMDM2 (RDB# 7403)

CHEK2: pGL4-phCHEK2 (RDB# 7407)

DRAM: pGL4-phDRAM (RDB#7412)

[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.06.26

1st Nucleotide Sequence

File Name : Reference Seq. GNU  
Sequence Size : 5684

2nd Nucleotide Sequence

File Name : RDB7400F.fasta  
Sequence Size : 400

Unit Size to Compare = 1  
Pick up Location = 1

[100.000% / 400 bp] INT/OPT. Score : < 1600/ 1600 >

```
1' GGCCTAACTG GCCGGTACCT GAGCTCGCTA GCCTCGAGGA TCGTGTTTGG ATGTGGGTGC
                                     ***** *****
61''                                     CGTGTTTGG ATGTGGGTGC

61' TTGTGTAACC AGTTCCCAA GCGCCAGCCC CGACAGCGCT CCTTCGGGAG GCTGGTCCGA
***** ***** ***** ***** ***** *****
80'' TTGTGTAACC AGTTCCCAA GCGCCAGCCC CGACAGCGCT CCTTCGGGAG GCTGGTCCGA

121' GCCCCTGTTT CCGCCGCGGC GCAGGAAGGG TTGGGGTTCC GCTGCCTGCA CCAGGCAAGA
***** ***** ***** ***** ***** *****
140'' GCCCCTGTTT CCGCCGCGGC GCAGGAAGGG TTGGGGTTCC GCTGCCTGCA CCAGGCAAGA

181' GCACCCCGAG CAAAGGAAGA AGACGACTTG CCTCCGGAGC TATCACTGGG GAGTGGGAAT
***** ***** ***** ***** ***** *****
200'' GCACCCCGAG CAAAGGAAGA AGACGACTTG CCTCCGGAGC TATCACTGGG GAGTGGGAAT

241' TTGAAAGTT CCCCAACTAG GGACACACGT GACCTCCTTC GGAAAGTAGT TCCGACTGTG
***** ***** ***** ***** ***** *****
260'' TTGAAAGTT CCCCAACTAG GGACACACGT GACCTCCTTC GGAAAGTAGT TCCGACTGTG
```



```

301' GCCCGTGTAT CCTCCACCT CCTTTTGAAC CCTCCTAGGT CTCCTCGCCC CGCCCACTCG
*****
320" GCCCGTGTAT CCTCCACCT CCTTTTGAAC CCTCCTAGGT CTCCTCGCCC CGCCCACTCG

361' CTGGGCTGCA GCTTCCTACC GTTCGGTACT TTCCACTCAA CCCGGTAACC CCAAACGTGC
*****
380" CTGGGCTGCA GCTTCCTACC GTTCGGTACT TTCCACTCAA CCCGGTAACC CCAAACGTGC

421' ACGGTCCGGC CGGGGCGCGC GGAGCCTGGC CCCGGGCGAT CCATCCTGCC GGGTTTTCAC
*****
440" ACGGTCCGGC CGGGGCGCGC G

```

1st Nucleotide Sequence

File Name : Reference Seq. GNU  
Sequence Size : 5684

2nd Nucleotide Sequence

File Name : RDB7400R.fasta (Complementary)  
Sequence Size : 250

Unit Size to Compare = 1  
Pick up Location = 1

[82.895% / 228 bp] INT/OPT. Score : < 440/ 576 >

```

1201' TGGGCAGAGG CCGAGGCTTA GCTCGTTATC CTCGCCTCGC GTTGCTGCAA AAGCCGCAGC
                                     * . *
85"          CGCT GGGGGTGGAG AGGCGAGGNA AGTGGATCTG CTGGGGNGGA

1261' AAGTGCAGCT GCAGGCTGGC GGCTGGGAAC CGGCCCGAGC AAGCCCCAGG CAGCTACACT
*** * ** * **, **, ** .** * *** ***** ***** ** **** *
129" AAGCG-AGAA GGAGNGAGGN GGGGNGGGAA CGG-CCGAGC AAGCCCCAGG -AG-TACA-T

```



1321' GGGCATGCTC AGTAGAGCCT GCGGCTTGGG GACTCTGCGC TCGCACCCAG AGCTACCGCT  
 \*\*\*           \*\*\*\*\*           \*\*\*   \*\*\*   \*\*\*   \*\*\*           \*\*\*\*\* \*\* \*\*\*\*\*  
 184" GGG----- AGTAGAG-AG CCGGGCTGGG GACT-TGCG- -TGCACCCAG AG-TACCGCT  
  
 1381' CTGCCCCCTC CTACCGCCCC CTGCCCTGCC CTGCCCTCCC CTCGCCCGGC GCGGTCCCGT  
 \*\*\*\*\*  
 232" CTGCCCCCTC CTACCGCCCC CTGCCCTGCC CTGCCCTCCC CTCGCCCGGC GCGGTCCCGT  
  
 1441' CCGCCTCTCG CTCGCCTCCC GCCTCCCCTC GGTCTTCCGA GGCATCAAGA TCTGGCCTCG  
 \*\*\*\*\*  
 292" CCGCCTCTCG CTCGCCTCCC GCCTCCCCTC GGTCTTCCGA GGC