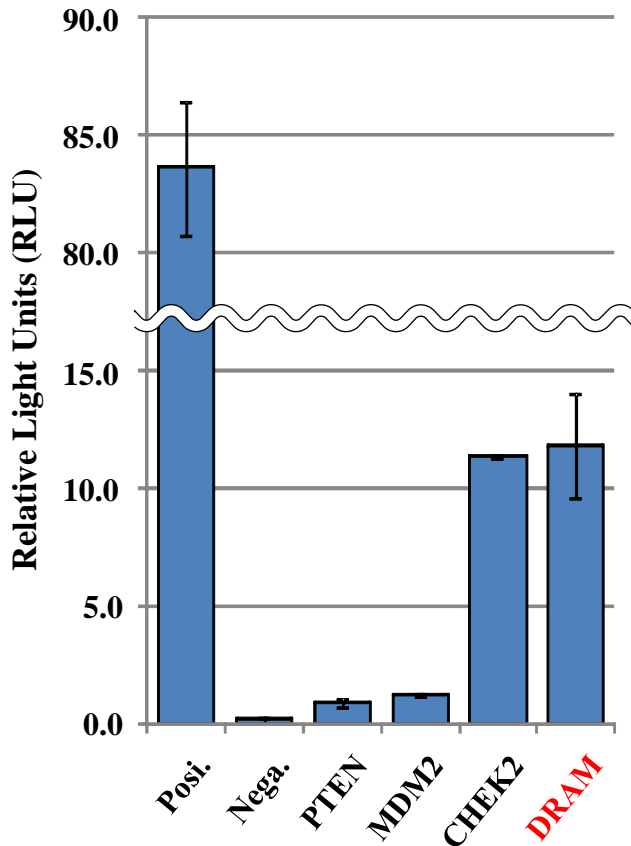
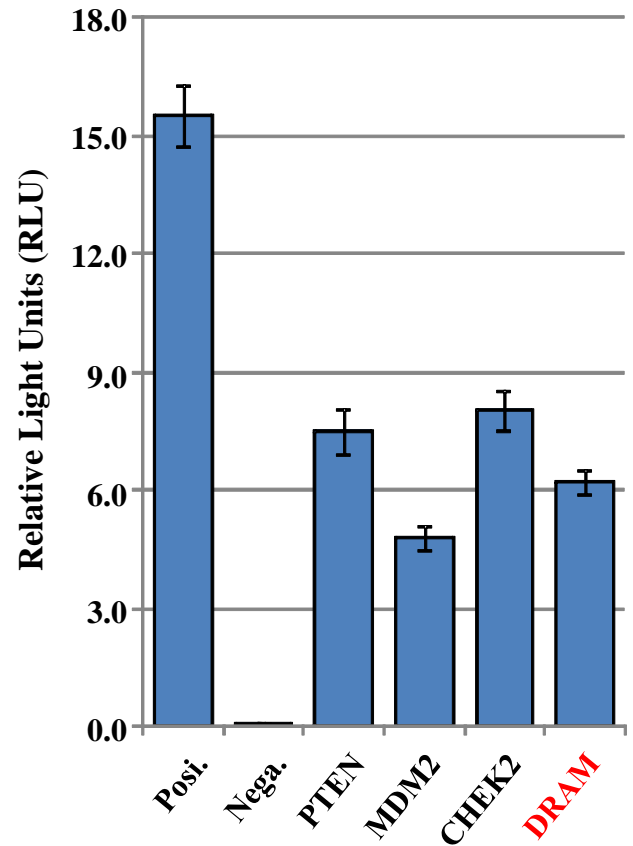


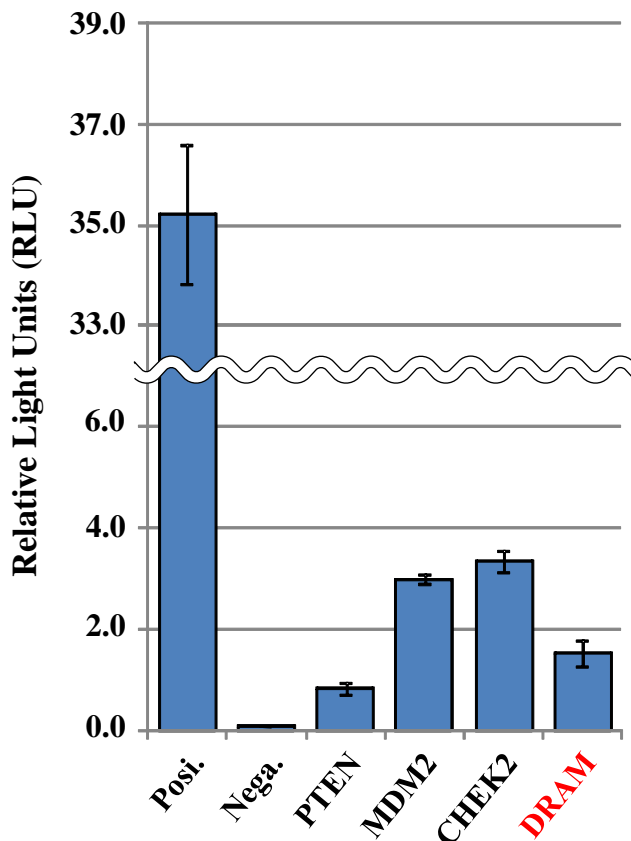
HeLa cells



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 : 2009.06.24

1st Nucleotide Sequence

File Name : Reference Seq.gnu
Sequence Size : 5588

2nd Nucleotide Sequence

File Name : RDB7412F.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 TTGAGCCATG ATGCCTGACT
                                     ***** *****
74"                                     TGAGCCATG ATGCCTGACT

61' AATTTTTTGT ATTTTATAGTA GAGATGGGGT TTCACCATGT TGGCCAGGCT GGTCTCGAAC
    ***** ***** ***** ***** ***** *****
93" AATTTTTTGT ATTTTATAGTA GAGATGGGGT TTCACCATGT TGGCCAGGCT GGTCTCGAAC

121' TCCTGACCTC AGGTGATCCA CCCACCTTGG CCTCCCAAAG TGCTAGGATT ACAGGCATGA
    ***** ***** ***** ***** ***** *****
153" TCCTGACCTC AGGTGATCCA CCCACCTTGG CCTCCCAAAG TGCTAGGATT ACAGGCATGA

181' GCCACCACGC CTGGCCTAAT TTTGTTATTT TGATCTATGA GTGCCTCGT CCTGAGGGTA
    ***** ***** ***** ***** ***** *****
213" GCCACCACGC CTGGCCTAAT TTTGTTATTT TGATCTATGA GTGCCTCGT CCTGAGGGTA

241' CTATTACTAT TTCATCTTTG TAGCCTAGCA TGGCGCCCAT GAAATGTGTT TGTGGCTGAA
    ***** ***** ***** ***** ***** *****
273" CTATTACTAT TTCATCTTTG TAGCCTAGCA TGGCGCCCAT GAAATGTGTT TGTGGCTGAA
```



```

301' AGGAACCTAT CTTTGGTCAC CAATGACCCA ACAATTTTGG CCACATATGT TGGGCTCAGA
*****
333" AGGAACCTAT CTTTGGTCAC CAATGACCCA ACAATTTTGG CCACATATGT TGGGCTCAGA

361' CTCCTAAAC TATCAAATC ATGTGCTTAT ATTATAAGTG CCTCCAGAAC ACAAATCCCT
*****
393" CTCCTAAAC TATCAAATC ATGTGCTTAT ATTATAAGTG CCTCCAGAAC ACAAATCCCT

421' TTCACAGGGC TTGAAATGTA TCAAGTCACT ATTAATCATC TTAGGCCAAG GCTCCGAGTC
*****
453" TTCACAGGGC TTGAAATGTA T

```

1st Nucleotide Sequence

File Name : Reference Seq.gnu
Sequence Size : 5588

2nd Nucleotide Sequence

File Name : RDB7412R.fasta (Complementary)
Sequence Size : 400

Unit Size to Compare = 1
Pick up Location = 1

[99.750% / 400 bp] INT/OPT. Score : < 1594/ 1594 >

```

961' CCCGCGTACT CTCCACCCA CCGTTCCA CCCTGTCTGG GTTTCGGGT GTTACCATT
***
85" CCA CCCTATCTGG GTTTCGGGT GTTACCATT

1021' GAGGTGGGAG CCACATCTGC GCCCGTGAC CTGGCGAACC TCATTGAACA CTTCTGCCG
*****
118" GAGGTGGGAG CCACATCTGC GCCCGTGAC CTGGCGAACC TCATTGAACA CTTCTGCCG

```



1081' ACCCCGCGAG CAGCAGCGCG ACCGGATGGC ATGGGTGTCA CCACGCGGTG GCCACTCTCA

 178" ACCCCGCGAG CAGCAGCGCG ACCGGATGGC ATGGGTGTCA CCACGCGGTG GCCACTCTCA

 1141' CTGCTGCGAA GCGCCGCGG CGGGACCTCG GAGGGGGCGC CCTCGGGGTG CGAGGCCCGG

 238" CTGCTGCGAA GCGCCGCGG CGGGACCTCG GAGGGGGCGC CCTCGGGGTG CGAGGCCCGG

 1201' CACTCCGAA ATCCCCGGG AGGGAGGGT TGGGAGAAAT AAATCCTTTT CTCCAGAGTT

 298" CACTCCGAA ATCCCCGGG AGGGAGGGT TGGGAGAAAT AAATCCTTTT CTCCAGAGTT

 1261' GCGCAAGAGC CAGCGCGGTA GGGCCAGAGT GGAAGGCCA GAGCGGGCGT CCCC GCCAGT

 358" GCGCAAGAGC CAGCGCGGTA GGGCCAGAGT GGAAGGCCA GAGCGGGCGT CCCC GCCAGT

 1321' GACCCACGC CGCCGTCCG CGCCAACCC GGCCTCCGC GAGTGTCAA ACCAAAAGCG

 418" GACCCACGC CGCCGTCCG CGCCAACCC GGCCTCCGC GAGTGTCAA ACCAAAAGCG

 1381' AAAGGAAATC AAGATCTGGC CTCGGCGGCC AAGCTTGCA ATCCGGTACT GTTGGTAAAG

 478" AAAGGAA